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BASE COUNT  
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Db	82	ATTATTAAGCTTGGCCGGAGCCGGAGCTGGACCTCCACCTCCGCACTCTGGAGAG	141
QY	62	GAGCCGCGCCGGCCGGCCGGCCCGCCACCGCCATGACCTTCGAGCAGGGAGCTGGT	121
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Db	201	GGGATGTTAGGTGCTGTGACGGTGTCTGGACCTTCCTGCAAGTCCAGCTTTCAAT	260
QY	182	CGCACAGAGATCCAGGCTTGGCCCTCCATCCAGAAACCTATGACTCACCCGGTAC	241
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QY	362	AACCTGGAGTGGCGAGAGCTCAATGACAGGCTGCGGCTGACCCAGAACTATGAGCG	421
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Db 861 TT 862

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DEFINITION	AX205042			
ACCESSION	AX205042.1	GI:15394277		
VERSION				
KEYWORDS				
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			

REFERENCE  
1  
Elson, G. and Gauchat, J.F.  
TITLE  
Scsctf/rnt-1 fusion protein  
JOURNAL  
Patent: WO 0155219-A 1 02-AUG-2001;  
PIERRE FABRE MEDICAMENT (FR)  
Location/Qualifiers

**CDS**

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/db_xref="taxon:9606"  
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BASE COUNT  
ORIGIN

Query Match	82.3%	Score 674;	DB 6;	Length 881;
Best Local Similarity	92.2%;	Pred. NO. 3.8e-145;		
Matches 721; Conservative	0;	Mismatches 60;	Indels 1;	Gaps 1;

Qy	2	ATTATTTAAAGCTTGGCCGGAGCCGGGCTGGCCCTTCCCATCTCCGCAAGCTCTGGAGAG	61
Db	82	ATTATTTAAAGCTTGGCCGGAGCCGGGCTGGCCCTTCCCATCTCCGCAAGCTCTGGAGAG	141
Qy	62	GAGCCGGCCCGGCGCGGCCGCCAGCCCATGAGACTTCCGAGCAGGGAGACTGGTG	121
Db	142	GAGCCGGACCCGGCGGGGCCGG -CCGAGCCCATGAGACTTCCGAGCAGGGAGACTGGTG	200
Qy	122	GGGATGTTTAGCTTGCTTATGCAAGGTGCTGTGGCACTTCCCTGCAGTGCCAGCTTTAAT	181
Db	201	GGGATGTTTAGGTGCTCTGTGCAAGGTGCTGTGGCACTTCCCTGCAAGTCCAGCTTCAAT	260
Qy	182	CGCACAAGAGATCCAGGCGCTTGGGCCCTGCATCCAGAAAACCTTATGACTCAACCGGTAC	241
Db	261	CGCACAAGGGAGCCAGAGGCGCTTGGGCCCTGCATCCAGAAAACCTTATGACTCAACCGGTAC	320
Qy	242	CTGGAGCATCAACTCCGAGCTTAGCTTGGAGCTTACTGAACTACCTTGGGGCCCGCTTTC	301
Db	321	CTGGAGCACCAACTCCGAGCTTAGCTTGGAGCTTACTGAACTACCTTGGGGCCCGCTTTC	380
Qy	302	AACGAGCTCACTTCATTCCTCTCGACTGGGGGCAAAAACCTTGGGCCAAGGCCAGGTC	361
Db	381	AACGAGCACAATTCAACCTTCCCGCTGGGGGCAAGAACTTGGGCCAAGGCCAGGTC	440
Qy	362	AACTTGGAAGTGTGGCAAGCCTCAATGACAGGCTGGGCTGACCCAGAACTATAGAGCG	421
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			Mus musculus neurotrophin-1/B-cell stimulating factor-3 mRNA, complete cds.

FEATURES	Location/Qualifiers
source	1. .819

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QY	661	GGAGCTGCAGACTTGCTATGAGCGTTACGCCAAGGACTTCAACCGCTTTAAGAAAGAAGAT	720
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FEATURES	source
LOCUS	AX205024
DEFINITION	Sequence 1 from Patent WO0155172.
ACCESSION	AX205024
VERSION	AX205024.1
KEYWORDS	GI:15394259
SOURCE	
ORGANISM	Homo sapiens (human)
REFERENCE	Elson, G., Gauchat, J.F., Plun-Favreau, H., Chevalier, S. and Gascan, H. Isolated complex comprising a mt-1 protein and in addition at least a c1f-1 protein and/or a scntfr-g1a) protein Patent: WO 0155172-A-1 02-AUG-2001;
AUTHORS	PIERRE FABRE MEDICAMENT (FR); INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSERM) (FR)
JOURNAL	Location/Qualifiers
	1..881



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

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Run on: February 9, 2004, 06:10:21 ; Search time 3286.64 Seconds

(without alignments)  
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Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

total number of hits satisfying chosen parameters: 5777422

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

## SUMMARIES

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2	819	100.0	819	6	6	AX392089	AX392089 Sequence
3	819	100.0	819	10	10	AF176913	AF176913 Mus muscu
4	674	82.3	881	6	6	AX205042	AX205042 Sequence
5	674	82.3	881	6	6	AX205042	AX205042 Sequence
6	669.4	81.7	797	6	6	AR002595	AR002595 Sequence
7	669.4	81.7	797	6	6	AX392086	AX392086 Sequence
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9	654	79.9	1736	9	9	BC012939	BC012939 Homo sapi
10	627	76.6	1689	9	9	AF172854	AF172854 Homo sapi
11	627	76.6	1710	6	6	BD132824	BD132824 Homo sapi
12	590.4	72.1	680	9	9	AY049579	AY049579 Homo sapi
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16	507.2	61.9	258710	2	2	AC135823	AC135823 Rattus no
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22	428	52.3	169144	2	2	AC005849	AC005849 Homo sapi
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24	137.6	16.8	63347	2	2	AC110526	AC110526 Mus muscu
25	60.6	7.4	230732	2	2	BX510356	BX510356 Dantio rer
26	60.2	7.4	168872	2	2	EX324116	EX324116 Homo sapi
27	52	6.3	396	6	6	BD1429315	BD1429315 Homo sapi
28	50.8	6.2	125020	9	9	AF429315	AF429315 Homo sapi
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30	47.2	5.8	2000	6	6	AX655393	AX655393 Sequence
31	46.2	5.6	47958	2	2	AC091104	AC091104 Homo sapi
32	46	5.6	239300	1	1	AP005026	AP005026 Streptomy
33	45.2	5.5	125020	9	9	AF429315	AF429315 Homo sapi
34	44.4	5.4	167672	2	2	AC132806	AC132806 Homo sapi
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37	44.4	5.4	202414	2	2	AC135051	AC135051 Homo sapi
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## ALIGNMENTS

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ACCESSION	AR002597				linear
VERSION	AR002597.1				PAT 04-DEC-1998
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SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 819)				
TITLE	Chang,M.-S.				
JOURNAL	Neurotrophic factor NNT-1				
FEATURES	Patent: US 5741772-A 4 21-APR-1998;				
	Location/Qualifiers				



## REFERENCE AUTHORS

**TITLE**  
**JOURNAL**  
**COMMENT**

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
1 (bases 1 to 542)  
Klm,N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,  
Oh, K.Y., Cheong, J.E., Sohn, H.Y., Kim, J.W., Park, H.S., Kim, S. and  
Y. S.  
21C Frontier Korean EST Project 2001  
Unpublished  
Contact: Kim YS  
Genome Research Center  
Korea Research Institute of Bioscience & Biotechnology  
52 Boseon-dong Yuseong-gu, Daejeon 305-333, South Korea  
Tel: +82-42-860-4470  
Fax: +82-42-860-4409  
Email: yongsung@mail.kribb.re.kr  
Plate: 9 row: G column: 05  
High quality sequence, atp: 542.

**FEATURES**

**SOURCE**

BASE COUNT ORIGIN	92 a	202 c	155 g	92 t	1 others
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Query March	54.3%;	Score 445;	DB 12;	Length 542;
Best Local Similarity	90.8%;	Pred. No. 6.4e-88;		
Matches 496;	Conservative	0;	Mismatches 46;	Indels 4;
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Qy	493	GGCCCACTTCTGTACAGAGCTTCAGAGGCTCTGGGGAGCAATTGCAGGTGATTGGGAC	552
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Job time : 2214.2 secs

Query Match 54.7%; Score 448; DB 13; Length 448;  
Best Local Similarity 100.0%; Pred. No. 1.3e-88;  
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 CTAGTGGGAGCTTACTGAACTAAGTGGGGCCCCCTTTCAAGAGCTGACTTCAATCC 60
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DB 241 CTGTACAGAGCTTCAGGGGCTGCTGGGAGCATTTGAGGTCATGCGCAGCTTGGCTA 300
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DB 301 CCCACTGCCCCAGCTCTGCGCAGGAGCTGAGCCAGGCTGCGCCCTGCGCTGCCACAG 360
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DB 421 GGGTCAGCGCAAGGACTTCAACCGGCTT 448
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ACCESSION BM841897  
VERSION BM841897.1 GI:19198306  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
1 (bases 1 to 522)  
Kim N.S., Hahn Y., Oh J.H., Lee J.Y., Ahn H.Y., Chu M.Y., Kim M.R.,  
Oh K.J., Cheong D.E., Sohn H.Y., Kim J.M., Park H.S., Kim S. and  
Kim Y.S.  
TITLE 21C Frontiers Korean EST Project 2001  
JOURNAL Unpublished  
COMMENT Contact: Kim YS  
Genome Research Center  
Korea Research Institute of Bioscience & Biotechnology  
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea  
Tel: +82-42-860-4470  
Fax: +82-42-860-4409  
Email: yongsung@mail.kribb.re.kr  
Plate: 34 row: A column: 05  
High quality sequence stop: 522.  
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/note="Vector: PCNS; Site 1: EcoRI; Site 2: NotI. The poly  
(A) + RNA was dephosphorylated with bacterial alkaline  
phosphatase (BAP) and then deacapped with tobacco acid  
pyrophosphatase (TAP). The deacapped intact mRNA was  
ligated with DNA-RNA linker including EcoR I site by  
treatment of T4 RNA ligase and the first strand cDNA was  
synthesized from oligo dt-selected mRNA by priming with  
dt-tailed vector. The dt-tailed vector was adjusted to  
have about 60nt. The cDNA vector was circularized with E.  
coli DNA ligase after digestion of EcoRI which site is  
also included in vector. An RNA strand converted to a DNA  
strand by Okayama-Berg method. The obtained cDNA vectors  
were used for transformation of competent cells E. coli  
Top10F by electroporation method. The cDNA libraries  
constructed by this method are full-length enriched cDNA  
library."

BASE COUNT 90 a 195 c 148 g 89 t  
ORIGIN

Query Match 54.6%; Score 447; DB 12; Length 522;  
Best Local Similarity 92.2%; Pred. No. 2.3e-88;  
Matches 482; Conservative 0; Mismatches 40; Indels 1; Gaps 1;

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QY 35 CTCCCACTCCGACGCTCTGGGAGAGAGAGCGCGCCCGCCGCGCCCGCCAGCCCC 94
DB 1 CTCCCACTCCGACGCTCTGGGAGAGAGAGCGCGCCCGCCGCGCCCGCCAGCCCC 59
QY 95 ATGAGCTTCGAGCAGGGGAGCTGTGGGGAGATGTTAGCTTGTATGACAGGCTGTGG 154
DB 60 ATGAGCTTCGAGCAGGGGAGCTGTGGGGAGATGTTAGCTGTGTGACAGGCTGTGG 119
QY 155 CACCTCCCTGCAAGTGCAGCTTATATGCAAGAGATCCAGGCCCCCTTCCATC 214
DB 120 CACCTCCCTGCAAGTGCAGCTTCAATGCAAGAGGAGCCAGGCGCTGGCCCCCTCCATC 179
QY 215 CAGAAACCTATGACTCAACCCGCTACTGAGAGATCACTCCGAGCTTATGCTGGAGC 274
DB 180 CAGAAACCTATGACTCAACCCGCTACTGAGAGATCACTCCGAGCTTATGCTGGAGC 239
QY 275 TACCTGAATCACTGGGGGCCCCCTTCAACGAGCTGATCAATCTCTCTGACTGGG 334
DB 240 TACCTGAATCACTGGGGGCCCCCTTCAACGAGCTGATCAATCTCTCTGACTGGG 299
QY 335 GCAGAACTCTGCCCCAGGGCCACGCTCACTTGAAGTGTGGCAAGCTCAATGACAG 394
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DB 360 CTGGGAGTGAACCCAGAACTATGAGGCTGATCACTCTCTGTACTTGGTGGAGCTC 419
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DB 420 AACCGTCAAGGCTGCCAGAGCTGAACCTCCAGCTGAGCTGGCCCACTTGTATCAAGCCTC 479
QY 515 CAGGGCTGTGGGAGCAATTCAGAGTGTCAATGGGAGAGCTTGG 557
DB 480 CAGGGCTGTGGGAGCAATTCAGAGTGTCAATGGGAGAGCTTGG 522
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RESULT 15  
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LOCUS K-EST0089713 S19N665307 Homo sapiens cDNA clone S19N665307-9-G05  
DEFINITION 5', mRNA sequence.  
ACCESSION BM821005  
VERSION BM821005.1 GI:19177418  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;



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DE Homo sapiens mRNA; EST DKFZp779H1332_r1 (from clone DKFZp779H1332)
XX EST; expressed sequence tag.
XX Homo sapiens (human)
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Homidae; Homo.
XX [1]
RN 1-634
RP Ottenwälder B., Obermaier B., Deutschenbauer S., Mewes H.W., Weil B.,
RA Amid C., Osengger A., Fobo G., Han M., Wiemann S.;
RT Submitted (07-MAY-2003) to the EMBL/GenBank/DBJ databases.
RL MIPS, Ingolstaedter Landstr.1, D-85764 Neuberg, GERMANY
XX
CC This is the 5' sequence of the clone insert
CC Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
CC Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
CC sequenced by Medigenomix (Martinsried/Germany) within the CDNA
CC No 81 sequencing consortium of the German Genome Project.
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6,
CC 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
XX Key Location/Qualifiers
XX source 1.634
XX /db_xref="taxon:9606"
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XX /organism="Homo sapiens"
XX /clone_1fb="DKFZp779H1332"
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Query Match 57.2%; Score 468.2; DB 2; Length 634;
Best Local Similarity 88.7%; Prid. No. 5.2e-93;
Matches 540; Conservative 0; Mismatches 65; Indels 4; Gaps 3;

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DB 446 GGCANAAATTGGCGGGGATGACAGCTCTGGGCTACCACTGCCAGCGCTGCTGG 505
585 GGCATGAGCAGCGCTGGGCGCCCTGGGCGCCAGTACCTTCCTCCGAAATGATG 644
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645 ACTTGTGCTGTGAAGAGAGCTGACAGCTGCTATGAGCGTTCAGCAAGACTTCAAC 704
566 ACTTGTGCTGTGAAGAGAGCTGACAGCTGCTATGAGCGTTCAGCAAGACTTCAAC 625
DB 705 GGCCTAAGA 713
DB 626 GGCCTAAGA 634

RESULT 12
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LOCUS K-EST0125376 S13KMS581 Homo sapiens CDNA clone S13KMS581-21-A09 5',
DEFINITION mRNA sequence.
ACCESSION BM846370.1 GI:19202769
VERSION BM846370.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 532)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 21 row: A column: 09
High quality sequence scop: 532.
FEATURES
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/lab_host="Top10F"
/clone_1fb="S13KMS581"
/notes="Vector: PCNS; Site 1: EcoRI; Site 2: NotI. The poly
(A) + RNA was dephosphorylated with bacterial alkaline
phosphatase (BAP) and then dephosphorylated with tobacco acid
pyrophosphatase (TAP). The dephosphorylated intact mRNA was
ligated with DNA-RNA linker including BcoRI site by
treatment of T4 RNA ligase and including BcoRI site by
synthesized from oligo dt-selected mRNA by priming with
dt-tailed vector. The dt-tailed vector was adjusted to
have about 60nt. The CDNA vector was circularized with E.
coli DNA ligase after digestion of EcoRI which site is
also included in vector. An RNA strand converted to a DNA
strand by Okayama-Berg method. The obtained CDNA vectors
were used for transformation of competent cells E. coli
Top10F by electroporation method. The CDNA libraries
constructed by this method are full-length enriched CDNA
library. After analyzing and sequencing about 2,000 ~
3,000 colonies in original CDNA library, the abundant
CDNAs were selected and amplified by PCR reaction using
vector region primer including T7 promoter as 5' primer
and N(dt)14 as 3' primer. The PCR products were used as

```

3'); double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p773 vector. RNA provided by Dr. Bertrand Jordan. Library went through three rounds of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

## BASE COUNT

93 a 165 c 126 g 92 t

## ORIGIN

Query Match 58.1%; Score 476; DB 10; Length 476;

Best Local Similarity 100.0%; Pred. No. 9e-95;

Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

203 GGGCCCTCATCAGAAAACCTATGACCTACCGGCTACCTGAGATCAATCCGAGC 262  
1 GGGCCCTCATCAGAAAACCTATGACCTACCGGCTACCTGAGATCAATCCGAGC 60

263 TTAGCTGGAGCTACCTGATGACTGAGGCCCCCTTTCAAGAGCTGACTTCAATCT 322

61 TTAGCTGGAGCTACCTGATGACTGAGGCCCCCTTTCAAGAGCTGACTTCAATCT 120

323 CTGCACTGGGGGAGAAAATCTTGCCAGAGGCCAGCTCACTTGGAGTGGGAGAC 382

121 CCTCAGCTGGGGGAGAAAATCTTGCCAGAGGCCAGCTCACTTGGAGTGGGAGAC 180

383 CTGCACTGGAGCTGAGGCTGAGCCAGAACTATGAGGCGGTACAGTCACTCTGTATAC 442

181 CTGCACTGGAGCTGAGGCTGAGCCAGAACTATGAGGCGGTACAGTCACTCTGTATAC 240

443 TTGCGTGGCTCAACCGCTGAGGCTGAGCCAGAACTATGAGGCGGTACAGTCACTCTGTATAC 502

241 TTGCGTGGCTCAACCGCTGAGGCTGAGCCAGAACTATGAGGCGGTACAGTCACTCTGTATAC 300

503 TGTACAGCTCTCAAGGCTCTGTCAGGAGCAATTGCAAGTGTATGAGCGACGCTTGGCTAC 562

301 TGTACAGCTCTCAAGGCTCTGTCAGGAGCAATTGCAAGTGTATGAGCGACGCTTGGCTAC 360

563 CCAGTGGCCGAGCTCTGTCAGGAGCAATTGCAAGTGTATGAGCGACGCTTGGCTAC 622

361 CCAGTGGCCGAGCTCTGTCAGGAGCAATTGCAAGTGTATGAGCGACGCTTGGCTAC 420

623 GACTTCTCTCAAGAGTGTGATCTTCTGCTGCTGAGAGAGCTGAGAGCTGAGCT 678

421 GACTTCTCTCAAGAGTGTGATCTTCTGCTGCTGAGAGAGCTGAGAGCTGAGCT 476

RESULT 10

AL543945 1028 bp mRNA linear EST 31-MAY-2003

LOCUS AL543945 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA

DEFINITION Clone CS0D1004YM15 5-PRIME, mRNA sequence.

ACCESSION AL543945 GI:31265790

VERSION EST.

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1028)

AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished

COMMENT On Feb 15, 2001 this sequence version replaced gi:12876424.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: segre@genoscope.cns.fr; Web: www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 6127.r For

http://fulllength.invitrogen.com/InvitrogenCorporation1600

Faraday Avenue Genoscope sequence ID: CS0D1004AG80P1.

## FEATURES

## source

1..1028

/organism="Homo sapiens"

/mol\_type="mRNA"

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/clone="CS0D1004YM15"

/issue\_type="PLACENTA COT 25-NORMALIZED"

/clone\_id="Homo sapiens PLACENTA COT 25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo(dT)

primer. Five prime end enriched, double-strand cDNA was

digested with Not I and cloned into the Not I and EcoR V

sites of the pCMVSPORT 6 vector. Library was normalized."

## BASE COUNT

190 a 339 c 283 g 212 t

## ORIGIN

Query Match 57.8%; Score 473.4; DB 9; Length 1028;

Best Local Similarity 88.5%; Pred. No. 4.3e-94;

Matches 525; Conservative 0; Mismatches 66; Indels 2; Gaps 1;

191 GATCCAGGCTCTGGCCCTCCATCCAGAAAACCTATGACTTACCCGCTACCTGAGCAT 250

41 GGTACCGGTCCGGAATTCCCGGATAGAAAACCTATGACTTACCCGCTACCTGAGCAT 100

251 CAATCCGAGCTTATAGCTGAGGAGCACTTACCTGAGGAGGCCCCCTTTCAAGAGCT 310

101 CAATCCGAGCTTATAGCTGAGGAGCACTTACCTGAGGAGGCCCCCTTTCAAGAGCA 160

311 GACTTCAATCTCTCTGCACTGAGGAGGAGAAAATCTGCCCAGAGGCCAGTCACTTGGAA 370

161 GACTTCAATCTCTCTGCACTGAGGAGGAGAAAATCTGCCCAGAGGCCAGTCACTTGGAA 220

371 GTTGGCGAAGCTTCAATGACAGGCTGAGGCTGAGCCAGAACTATGAGGCGGTACAGTAC 430

221 GTTGGCGAAGCTTCAATGACAGGCTGAGGCTGAGCCAGAACTATGAGGCGGTACAGTAC 278

431 CTCCTGTATCTTCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 490

279 CTCCTGTATCTTCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 338

491 CTGGCCCACTTCTGATCAGGCTTCCAGAGGCTGCTGAGGAGCAATTTGCGGGGTATAGCA 550

339 CTGGCCCACTTCTGATCAGGCTTCCAGAGGCTGCTGAGGAGCAATTTGCGGGGTATAGCA 398

551 ACGTGTGCTACCACTGCTCCAGGCTCTGCTGAGGAGCTGAGGAGCTTGGGCCCCCTGAGC 610

399 GCTGTGGGCTACCACTGCTCCAGGCTCTGCTGAGGAGCTGAGGAGCTTGGGCCCCCTGAGC 458

611 CTGGCCCACTGATCTTCTGATCAGGCTTCCAGAGGCTGCTGAGGAGCTTGGGCCCCCTGAGC 670

459 CTGGCCCACTGATCTTCTGATCAGGCTTCCAGAGGCTGCTGAGGAGCTTGGGCCCCCTGAGC 518

671 ACGTGTGCTACCACTGCTCCAGGCTCTGCTGAGGAGCTGAGGAGCTTGGGCCCCCTGAGC 730

519 ACGTGTGCTACCACTGCTCCAGGCTCTGCTGAGGAGCTGAGGAGCTTGGGCCCCCTGAGC 578

731 GCAAGTTAGTACCTGCTGAGGAGCTTGGGAGCTTGGGAGCTTGGGAGCTTGGGAGCTTGGG 783

579 GCAAGTTAGTACCTGCTGAGGAGCTTGGGAGCTTGGGAGCTTGGGAGCTTGGGAGCTTGGG 631

## RESULT 11

HSN090574 standard; RNA; EST; 634 BP.

XX HSN090574

AC BX497225;

SV BX497225.1

XX 09-MAY-2003 (Rel. 75, Created)

DT 09-MAY-2003 (Rel. 75, Last updated, Version 1)

[illegible]

LOCUS	BM840863	573 bp	mRNA	linear	EST 06-MAR-2002
DEFINITION	K-EST0118015 S13KMS5 Homo sapiens cDNA clone S13KMS5-35-D11 5', mRNA sequence.				
ACCESSION	BM840863				
VERSION	BM840863.1	GI:19197272			
KEYWORDS	EST.				
SOURCE	Homo sapiens				
ORGANISM	Homo sapiens (human)				

REFERENCE	1 (bases 1 to 573)
AUTHORS	Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,

TITLE	21C Frontier Korean EST Project 2001
JOURNAL	Unpublished
COMMENT	Contact: Kim YS

Genome Research Center  
Korea Research Institute of Bioscience & Biotechnology  
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea  
Tel: +82-42-860-4470  
Fax: +82-42-860-4409  
Email: yongsung@email.kribb.re.kr  
Plate: 35 row: D column: 11  
High quality sequence stop: 573.

FEATURES	Location/Qualifiers
source	1. .573

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BASE COUNT
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      /tissue_type="myeloma"
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      /lab_host="Top10F."
      /clone_id="S13KMS5"
      /note="vector: pCNS; Site_1: EcoRI; Site_2: NotI; The poly
      (A+) RNA was dephosphorylated with bacterial alkaline
      phosphatase (BAP) and then decapped with tobacco acid
      pyrophosphatase (TAP). The decapped intact mRNA was
      ligated with T4 RNA-ligase including EcoR I site by
      treatment of T4 RNA-ligase and the first strand cDNA was
      synthesized from oligo dT-selected mRNA by priming with
      dT-tailed vector. The dT-tailed vector was adjusted to
      have about 60nt. The cDNA vector was circularized with E.
      coli DNA ligase after digestion of EcoR I which site is
      also included in vector. An RNA strand converted to a DNA
      strand by Okayama-Berg method. The obtained cDNA vectors
      were used for transformation of competent cells E. coli
      Top10F' by electroporation method. The cDNA libraries
      constructed by this method are full-length enriched cDNA
      library."

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Query Match	59.2%	Score 485.2	DB 12	Length 573
Best Local Similarity	91.5%	Pred. No. 9e-97		
Match 525	Conservative	0	Mismatches 48	Indels 1
				Gaps 1

[illegible]

QY	155	TACCTCCCTGAGTGGCAGGCTCTTAATGCGACAGAGATCCAGGCGCTGGGCCCTCCATC	214
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QY	215	CAGAAAACCTATGACCTCACCCGCTACCTGGAGCATCACTCCGACCTTAGCTGGAGCC	274
Db	180	CAGAAAACCTATGACCTCACCCGCTACCTGGAGCATCACTCCGACCTTAGCTGGAGCC	239
QY	275	TACCTGAACTACCTGGGGCCCCCTTTCAAGAGGCTTCAATCTCTCTCCACTTGGGG	334
Db	240	TATCTGAACTACCTGGGGCCCCCTTTCAAGAGGCAACTTCAACCTCCCGCTTGGGG	299
QY	335	GCAGAAACTCTGCGCCAGGGCCACGGCTCAACTTGGAACTGTGGCGAAGCTCAATGACAG	394
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QY	395	CTGCGGCTGACCCAGAACTATGAGGCGTACAGTCACTCCTGTGTGTTCTTGGCTGCGCTC	454
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QY	455	AACGCTAGAGGTGCGACAGCTGAACTCCGAGAGTACCGCTGGGCCCACTTCTGTACAGGCTC	514
Db	420	AACGCTAGAGGTGCGACCTGCTGAGCTGCGCGCGACGCTGGGCCCACTTCTGTACAGGCTC	479
QY	515	CAGGCGCTGTGGGACAGCATTTGACAGTGTATGGCGACGCTTGGCTTACCCACTGCCAG	574
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RESULT 9	476 bp	mRNA	linear	EST 25-AUG-2000
LOCUS	BB632644			
DEFINITION	uv63f01.y1 Soares mouse 3NBWS Mus musculus cDNA clone IMAGE:341865			
ACCESSION	BB632644			
VERSION	BB632644.1			
KEYWORDS	GI:9915332			
SOURCE	EST.			
ORGANISM	Mus musculus (house mouse)			
REFERENCE	Bukatyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.			
AUTHORS	1 (bases 1 to 476)			
TITLE	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .			
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),			
COMMENT	Tumor Gene Index			
	Unpublished			
	Contact: Robert Strausberg, Ph.D.			
	Email: cgapbs-rt@mail.nih.gov			
	This clone is available royalty-free through LIND; contact the			
	IMAGE Consortium ( <a href="mailto:info@image.llnl.gov">info@image.llnl.gov</a> ) for further information.			
	NCI:1087677			
	Seq primer: -40bp from Gbbco			
	High quality sequence stop: 464.			
	Location/Qualifiers			
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/clone_lib="Soares mouse 3nBMS"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
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was primed with a Not I - oligo(dT) primer [5,
TGTTCACCAATCTGAAGTGGAGCGGCCGCTTTTTTTTTTTTTTTTTT
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constructed by this method are full-length enriched cDNA				
		library."		
BASE COUNT	101 a	226 c	164 g	103 t
ORIGIN				

Query Match	61.6%	Score	504.6	DB	12	Length	594
Best Local Similarity	Pred. No. 91.6%		4.8e-101				
Matches	545	Conservative	0	Mismatches	49	Indels	1
						Gaps	1

Fax: +82-42-860-4409  
 Email: yongsung@mail.kribb.re.kr  
 Plate: 48 row: H column: 08  
 High quality sequence stop: 580.  
 Location/Qualifiers  
                   1 580

FEATURES	Location/Qualifiers
source	1. .580

QY	33	CCCTCCCACTCCGACAGGCTCTGGGAGAGAGACCGCCGCCGAGCCGAGCCCGACG	92
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QY	213	TCCAGAAAACCTATATACCTCAACCCGCTACTCTGGAGACTATACCTCCGACGTTAGCTGGGA	272
Db	180	TCCAGAAAACCTATATACCTCAACCCGCTACTCTGGAGACCAACATCCGACGTTGGCTGGGA	239
QY	273	CCTACCTGAACCTACCTGGGGGCCCTTTCAAGAGACCTGACCTTAATCCTCTGCACGTGG	332
Db	240	CCTACCTGAACCTACCTGGGGGCCCTTTCAAGAGACAGACTTCAACCTCTCCCGCTGG	299
QY	333	GGGCGAAGAACTCTGCGCCAGAGGCCACAGCTCAACTTGGAAAGTGGCGAAGCCTCAATGACA	392
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/c/cell_line="KMS-5"
/lab_host="Top10F"
/clone_idb="S13KMS5"
/notes="Vector: PCNS; Site 1: EcoRI, Site 2: NotI; The poly
(A) + RNA was dephosphorylated with bacterial alkaline
phosphatase (BAP) and then decapped with tobacco acid
pyrophosphatase (TAP). The decapped intact mRNA was
ligated with DNA-RNA linker including EcoR I site by
treatment of T4 RNA ligase and the first strand cDNA was
synthesized from oligo dt-selected mRNA by priming with
dt-tailed vector. The dt-tailed vector was adjusted to
have about 60nt. The cDNA vector was circularized with E.
coli DNA ligase after digestion of EcoRI which site is
also included in vector. An RNA strand converted to a DNA
strand by Okayama-Berg method. The obtained cDNA vectors
were used for transformation of competent cells E. coli
Top10F by electroporation method. The cDNA libraries
constructed by this method are full-length enriched cDNA
library."

```

Qy	393	GGCTGGGCTGACCCAGAACTATGAGGGGTAAAGTCACTCTCTGGTATCTTGCGGGC	452
Db	360	AACGTGGGCTGACCCAGAACTAAGAGGCTTAAGCACCCTTGTGGTAACTTGGCGGGC	419
Qy	453	TCAACCGTCAAGGCTGCCACAGTGAATTCCGACGTAGGCTGGGCCCACTTCTGTACCAAGCC	512
Db	420	TCAACCGTCAAGGCTGCCACTGCTGAGCTGCGCCGACAGCTGGGCCCACTTCTGCACAGGCC	479
Qy	513	TCCAGGGGCTGTTGGGACAGCAATTGACAGTGTATATGGCCACAGTTTGGCTATCCCACTGGCCCC	572
Db	480	TCCAGGGGCTGTTGGGACAGCAATTGGGGGGTATGGCAAGCTTGGGCTATCCCACTGGCCCC	539
Qy	573	AGCCTGTGACAGGAGCTGAGCCAGGCTGGGGCCCTGGGCCCTGCCACAGTGACTT	627
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Query Match	60.0%;	Score	491.2;	DB	12;	Length	580;
Best Local Similarity	91.6%;	Pred.	No. 4.33-98;				
Matches	531;	Conservative	0;	Mismatches	48;	Indels	1;
Gaps	1;						

  

QY	35	CTCCCACTCGCCAGCCTTGGGAGAGAGCCGCGCCCGGCGCCGCCAGCCCC	94
DB	2	CTCCCACTCGCCAGCCTTGGGAGAGAGCCGCGCCCGGCGCCGCCAGCCCC	60
QY	95	ATTGAACTCTCGAGAGAGGGAACTCGTGGGGATGTTTAACTTGCCTAATGACGGTCTGTGG	154
DB	61	ATTGAACTCTCGAGAGAGGGAACTCGTGGGGATGTTTAACTTGCCTAATGACGGTCTGTGG	120
QY	155	CACCTCCCTGAGTGCAGCTCTTAATGACAGAGAGATCCAGGSCCTCGGSCCTTCATC	214
DB	121	CACCTCCCTGAGTGCAGCTCTTAATGACAGAGAGATCCAGGSCCTCGGSCCTTCATC	180

RESULT	7
BW848189	
LOCUS	
DEFINITION	BM648189 K-EST0127911 S13KMS Homo sapiens cDNA clone S13KMS-48-H08 5' , 580 bp mRNA linear EST 06-MAR-2001 mRNA sequence.
ACCESSION	BM648189
VERSION	BM648189.1 GI:19204588
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 580) <i>Kim,N.S., Hanh,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.T., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.</i>
AUTHORS	
TITLE	21C Frontler Korean EST Project 2001
JOURNAL	Unpublished
COMMENT	Contact : kim ys

Db	181	CAGAAACCTATGACCTCACCCGGCTACTGGAGCACAACCTCCGAGCTTGCGTGGAGCC	240
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Qy	335	GCAGAACTCTGCCAGGGGCCACGGTCACTTGGAAAGTGGCGCAAGGCTCAATGACAGG	394
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Qy	395	CTGGGGCTGACCCAGAACTATGAGGCGGTACAGTCACTCTGTGTACTTGGCGTGGCTC	454
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Db	421	AAACGTACGGCTGGCACTGCTGAGCTGGGCGGCAAGCTGGGCCCACTTGTGACCAAGCCTC	480

Korea Research Institute of Bioscience & Biotechnology  
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea  
Tel: +82-42-860-4470

Db 481 CAGGCGCTGCTGGGCGAGCATTTGGGGCGCTCATGGCAGCTCTGGGCTACCCACTGCCCCAG 540





218 GGGCCCCCTTTCAACGAGCCAGACTCAACCTCCCGCTGGGGGAGAGACTCTGCC 297  
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OY 469 CACAGCTGACCTCCGACCTGAGCTGAGCTTGTGTTACTTGGCTGAGCTCAACCTGAGGCTGC 528  
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OY 529 CAGCATGAGCTGAGCTGAGCTGAGCTTGTGTTACTTGGCTGAGCTCAACCTGAGGCTGC 588  
DB 478 CAGCATGAGCTGAGCTGAGCTGAGCTTGTGTTACTTGGCTGAGCTCAACCTGAGGCTGC 537  
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RESULT 4  
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DEFINITION BG164929 NIH\_MGC\_89 Homo sapiens cDNA clone IMAGE:445813 5',  
mRNA sequence.  
ACCESSION BG164929  
VERSION BG164929.1 GI:12671563  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
NIH-MGC http://mgi.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: cga@bbs-rcmail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: InCyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLNL0244 row: m column: 14  
High quality sequence start: 3  
High quality sequence stop: 675  
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/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:445813"  
/issue\_type="hyperphicoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_1b="NIH\_MGC\_89"  
/note="Organ: Kidney; Vector: pCMV-Sport6; Site\_1: NotI;

Site 2: SalI; Cloned unidirectionally; oligo-dT primed.  
Average insert size 1.3 kb. Library enriched for  
full-length clones and constructed by Life Technologies.  
Note: This is a NIH\_MGC Library.  
BASE COUNT 210 a 351 c 292 g 200 t  
ORIGIN

Query Match 66.4%; Score 544; DB 10; Length 1053;  
Best Local Similarity 88.2%; Pred. No. 1.2e-109;  
Matches 660; Conservative 0; Mismatches 80; Indels 8; Gaps 6;

OY 24 CGGGCTGCGCCCTCCCACTCCGAGCTCTGGAGAGAGAGCCGCGCCGCGCGG 83  
DB 2 CGGGCTGCGCCCTCCCACTCCGAGCTCTGGAGAGAGAGCCGCGCCGCGCGG 61  
OY 84 CCCCAGCCCATGAGCTCCGAGAGAGAGAGCTGTGGGGATGTAGCTTCAATGCA 143  
DB 62 CCCCAGCTCCCATGAGCTCCGAGAGAGAGAGCTGTGGGGATGTAGCTTCAATGCA 121  
OY 144 CGGTGCTGAGCTCCGAGAGAGAGAGCTTCAATGAGAGATGCAAGGCTGCA 203  
DB 122 CGGTGCTGAGCTCCGAGAGAGAGAGCTTCAATGAGAGATGCAAGGCTGCA 181  
OY 204 GCGCCCTCCATCAGAAAACTATGACCTACCCGCTACCTGAGAGATCACTCCGAGCT 263  
DB 182 GCGCCCTCCATCAGAAAACTATGACCTACCCGCTACCTGAGAGATCACTCCGAGCT 241  
OY 264 TAGCTGAGAGCTTACCTGAGAGAGAGCTTCAATGAGAGATGCAAGGCTGCA 319  
DB 242 TAGCTGAGAGCTTACCTGAGAGAGAGCTTCAATGAGAGATGCAAGGCTGCA 301  
OY 320 CCTCTGAGAGAGAGAGAGAGAGCTTCAATGAGAGAGAGCTTCAATGAGAGAG 378  
DB 302 CCTCTGAGAGAGAGAGAGAGAGCTTCAATGAGAGAGAGCTTCAATGAGAGAG 361  
OY 379 AAGCTCAATGAGAGAGAGAGAGAGCTTCAATGAGAGAGAGCTTCAATGAGAGAG 438  
DB 362 AAGCTCAATGAGAGAGAGAGAGAGCTTCAATGAGAGAGAGCTTCAATGAGAGAG 421  
OY 439 TTAAGCTGAGAGAGAGAGAGAGCTTCAATGAGAGAGAGCTTCAATGAGAGAG 498  
DB 422 TTAAGCTGAGAGAGAGAGAGAGCTTCAATGAGAGAGAGCTTCAATGAGAGAG 481  
OY 499 CTTCTGAGAGAGAGAGAGAGAGCTTCAATGAGAGAGAGCTTCAATGAGAGAG 558  
DB 482 CTTCTGAGAGAGAGAGAGAGAGCTTCAATGAGAGAGAGCTTCAATGAGAGAG 541  
OY 559 CTACCACTGAGAGAGAGAGAGAGCTTCAATGAGAGAGAGCTTCAATGAGAGAG 616  
DB 542 CTACCACTGAGAGAGAGAGAGAGCTTCAATGAGAGAGAGCTTCAATGAGAGAG 601  
OY 617 CACAGTGAATCTTCCAGAGAGAGAGAGCTTCAATGAGAGAGAGCTTCAATGAGAGAG 676  
DB 602 CACAGTGAATCTTCCAGAGAGAGAGAGCTTCAATGAGAGAGAGCTTCAATGAGAGAG 661  
OY 677 CTATGAGCTTCAAGAGAGAGAGAGCTTCAATGAGAGAGAGCTTCAATGAGAGAG 736  
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RESULT 5  
LOCUS BG437538 853 bp mRNA linear EST 14-MAR-2001  
DEFINITION BG437538 NIH\_MGC\_18 Homo sapiens cDNA clone IMAGE:4621530 5',  
mRNA sequence.  
ACCESSION BG437538  
VERSION BG437538.1 GI:13344044  
KEYWORDS EST.  
SOURCE Homo sapiens (human)

# FEATURES

source

Location/Qualifiers

1. .887

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6428214"

/issue\_type="epidermoid carcinoma, cell line"

/lab\_host="DH10B (phage-resistant)"

/clone\_1ib="NIH MGC 101"

/note="Organ: Lung; Vector: pOTB7; Site 1: EcoRI; Site 2: XhoI; cDNA made by oligo-dT priming, directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC library."

BASE COUNT 154 a 325 c 240 g 167 t 1 others

ORIGIN

Query Match 78.7%; Score 644.4; DB 13; Length 887;

Best Local Similarity 92.3%; Pred. No. 8.5e-132;

Matches 700; Conservative 0; Mismatches 56; Indels 2; Gaps 2;

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62 GAGCG 121

65 GAGCG 123

122 GGGATTTAGTTCGCTATGCAAGGCTGTGGAGCTTCCCTGCACTCCGCGAGCTCTTAT 181

124 GGGATTTAGTTCGCTATGCAAGGCTGTGGAGCTTCCCTGCACTCCGCGAGCTCTTAT 183

182 CGCAGAGAGATTCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 241

184 CGCAGAGAGATTCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 243

242 CTGAGAGATTCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 301

244 CTGAGAGATTCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 303

302 AACGAGCGCTTCATCTCTCGAC-TGGGGGAGAACTCTGCGCGCGCGCGCGCG 360

304 AACGAGCGCTTCATCTCTCGAC-TGGGGGAGAACTCTGCGCGCGCGCGCGCG 363

361 CAACTTGAAGTGTGGCGAAGCTCATGACAGGCTGCGCGCTGACCCAGAACTATGAG 420

364 TGACTTGAAGTGTGGCGAAGCTCATGACAGGCTGCGCGCTGACCCAGAACTATGAG 423

421 GTACAGTCACTCTCTGTGTTACTTGGGTGGCTCAACGCTGAGGCTGCAAGTGA 480

424 GTACAGTCACTCTCTGTGTTACTTGGGTGGCTCAACGCTGAGGCTGCAAGTGA 483

481 CGAGGTAGCGTGGCGCACTTCTGTACCAAGCTCCAGGGCGCTGGGAGAGATTGACG 540

484 GCGCGCGAGCGTGGCGCACTTCTGTACCAAGCTCCAGGGCGCTGGGAGAGATTGACG 543

541 TGTTCATGAGAGCTGTGGCTTACCACTGCGCGCGCTGCGCGAGGAGTGAAGCCAG 600

544 GGTTCATGAGAGCTGTGGCTTACCACTGCGCGCGCTGCGCGAGGAGTGAAGCCAG 603

601 GGGCG 660

604 GACTCTGCG 663

661 GGAGGTGAGAGCTGTGGCTTACCACTGCGCGCGCTGCGCGAGGAGTGAAGCCAG 720

664 GGAGGTGAGAGCTGTGGCTTACCACTGCGCGCGCTGCGCGAGGAGTGAAGCCAG 723

721 GCAGCTTCAGAGCTTCAGTCACTGAGCTGAGG 758

Db

724 GCAGCTTCAGAGCTTCAGTCACTGAGCTGAGG 761

## FEATURES

source

Location/Qualifiers

1. .1157

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/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6197786"

/sex="male"

/tissue\_type="sciatic nerve"

/dev\_stage="adult, 70 yr"

/lab\_host="DH10B"

/clone\_1ib="Lupski\_sciatic nerve"

/note="Vector: pCMV-SPORT6 (Life Technologies); Site 1: NotI; Site 2: SalI; cDNA made by oligo-dT priming. Directionally cloned using the following adaptors: 5'-TCGACCAAGCGCTCG-3' and 5'-GACTAGTTCATGATCGCAGGCGCGCGCGCTT(15)-3'. Size selected > 1 kb for average insert length 1.87 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life Technologies."

BASE COUNT 221 a 374 c 346 g 216 t

ORIGIN

Query Match 69.4%; Score 568.6; DB 13; Length 1157;

Best Local Similarity 89.8%; Pred. No. 4.7e-115;

Matches 622; Conservative 0; Mismatches 63; Indels 2; Gaps 1;

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58 AGGGAGCTGTGGGGATGTAGCTTGGCTATGACAGGCTGTGGAGCTTCCCTGACG 117

169 GCCAGCTTATATGCGACAGAGATTCAGGCGCGCGCGCTGCTCATCCGAAAGCTTGA 228

118 GCCAGCTTATATGCGACAGAGATTCAGGCGCGCGCGCTGCTCATCCGAAAGCTTGA 177

229 CCTACCGGCTACCTGAGCATCACTCGAGGCTTACCTGAGGAGCTGAGTACTACT 288

178 CCTACCGGCTACCTGAGCATCACTCGAGGCTTACCTGAGGAGCTGAGTACTACT 237

289 GGGCG 348

Pesole, G., Petrovsky, N., Pillai, R., Pontus, J. U., Qi, D.,  
 Ramachandran, S., Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring,  
 B. Z., Ringwald, M., Sandelin, A., Schneider, C., Sempke, C. A., Setou,  
 M., Shmada, K., Sultana, R., Takemaka, Y., Taylor, M. S., Teasdale,  
 R. D., Tomlita, M., Verardo, R., Wagner, J., Wahlstedt, C., Wang, Y.,  
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 M., Yang, I., Yang, L., Yuan, Z., Zavalon, M., Zhu, Y., Zimmer, A.,  
 Carninci, P., Hayatsu, N., Hirozane-Kitahara, T., Konno, H., Nakamura,  
 M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Atawa, K.,  
 Aokawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii,  
 Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Saeki, D., Shibata,  
 K., Shinagawa, A., Yaunish, A., Yoshino, M., Waterston, R., Lander,  
 E. S., Rogers, J., Birney, E., and Hayashizaki, Y.  
 Analysis of the mouse transcriptome based on functional annotation  
 of 60,770 full-length cDNAs  
 Nature 420, 563-573 (2002)

JOURNAL  
MEDLINE  
PUBMED  
COMMENT

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Fax: 81-45-503-9216

Email: genome-res@sc.riken.go.jp  
URL: <http://genome.gsc.riken.go.jp/>  
Adachi, J., Atsawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda,  
S., Hashizume, M., Hayashida, K., Hirozane, T., Horii, F., Imotani, K.,  
Ishii, Y., Itoh, M., Kageawa, I., Kawai, T., Kojima, Y., Kondo, S., Kon-  
no, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K.,  
Numazaki, R., Ohno, M., Ohashi, N., Saito, R., Sakazume, N., Sano, H.,  
Saeki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Takeda, Y.,  
Waki, K., Watanabe, A., Muramatsu, M. and Hayashizaki, Y. Direct  
Submission

Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences. *Mamm. Genome* 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. *Genome Res.* 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system—384-format sequencing pipeline with 384 multicapillary sequencer. *Genome Res.* 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. *Genome Res.* 11 (2), 281-289 (2001)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

**FEATURES**

**SOURCE**

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ORIGIN

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Best Local Similarity	99.7%	Pred. No. 8.8e-13;		
Matches 672; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0

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 |||||  
 Db 5 ATTATTAAAGCTTCGCCGAGCCGCGGCTGCCCTCCACTCCGCAAGCCTCTGGAGAG 6

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Db	125	GGGATGTTAGCTTGGCTTATGSCACGGTGTCTGTGGCACCCTCCCTGGAGTGC	CACTTTAAT	184
QY	182	CGCACAAGAAATCCAGGCGCTGGCGCCCTCCATCCAGAAAACTATGACCTCAC	CGCGTAC	241
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QY	242	CTGGAGCATGAACCTCCGACCTTAGCTGGGACCTACCTGAACCTACCTGGG	CGCCCTTTC	301
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Db	305	AACGAGCTTGAATTCTCTCTCGACTGGGGGAGAAACTCTGCCAGGGCCA	CGGTC	364
QY	362	AACCTTGAAGTGGGGGAGAGCTCAATGACAGGCTGGGGGTCAGACCAAGAA	CTATGAGCG	421
Db	365	AACCTTGAAGTGGGGGAGAGCTCAATGACAGGCTGGGGGTCAGACCAAGAA	CTATGAGCG	424
QY	422	TACAGTCACCTCTCTGTGTACTTGGCGTGGGCTCAACCGTCAGGCTGGCACA	AGTGAATC	481
Db	425	TATAGTACCTCTCTGTGTACTTGGCGTGGGCTCAACCGTCAGGCTGGCACA	AGTGAATC	484
QY	482	CGAGCTGAGCTGGGCGCCACTTCTGTACAGAGCTCTCAGGGCTGCTGGGCA	bATTGCAAGT	541
Db	485	CGAGTGGAGCTGGGCGCCACTTCTGTACAGAGCTCTCAGGGCTGCTGGGCA	bATTGCAAGT	544
QY	542	GTCATGGACGAGCTTGGACTACCCACTGCGCCAGCTCTGACAGGGAGCTGAG	CCAGCGTGG	601
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DEFINITION	AGNCNCOURT 8813192 NIH_MGC_101 Homo sapiens CDNA clone IMAGE:6428214 5', mRNA sequence.				

ACCESSION	BQ948158	GI:22363636
VERSION	BQ948158.1	
KEYWORDS	EST.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostei  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 887)  
NIH-MGC <http://mgc.ncl.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished  
Contact: Robert Strausberg, Ph.D.

Email: [CGAPds-r@mail.nih.gov](mailto:CGAPds-r@mail.nih.gov)  
Tissue Procurement: ARCC  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
plate: LLCM2614 row: h column: 07  
High quality sequence stop: 674.

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

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9002.070 Million cell updates/sec

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Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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7: em\_estro:\*  
8: em\_hcc:\*  
9: gb\_est1:\*  
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25: em\_gse\_rtd:\*  
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27: em\_gse\_vrl:\*  
28: gb\_gse1:\*  
29: gb\_gse2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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5	543	66.3	853	10	BG437538
6	504.6	61.0	584	12	BM763333
7	491.2	60.6	590	12	BM481819
8	485.2	59.2	573	12	BM840863
9	476	58.1	476	10	BE632644
10	473.4	57.8	1028	9	AL543945
11	468.2	57.2	634	2	HSW090574
12	455.4	55.6	532	12	BM846370
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15	445	54.3	542	12	BM821005
16	441.4	53.9	529	12	BM847924
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18	407.6	49.8	569	12	BM846748
19	390.4	47.7	505	4	BX528877
20	381.4	46.6	388	13	BY022718
21	377.8	46.1	458	12	BM363136
22	363	44.3	668	14	BY734701
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26	329.8	40.3	482	12	BM846622
27	312.4	38.1	407	9	AI752561
28	295.8	36.1	392	13	BY012378
29	278.4	34.0	663	14	BY722568
30	263	32.1	281	10	BB864730
31	261.2	31.9	488	9	AA015243
32	257	31.4	359	13	BY009925
33	255.8	31.2	377	13	BY017916
34	252.2	30.8	473	14	CB729926
35	251.2	30.7	357	13	BY185798
36	246.8	30.1	552	10	BG095271
37	228.4	27.9	440	10	BG148676
38	228	27.8	385	13	BY018063
39	228	27.8	913	12	BI912197
40	186	22.7	681	9	AL857796
41	172.8	21.1	915	10	BF035982
42	155.8	19.0	560	9	AL800340
43	151.8	18.5	617	9	AL959824
44	151.8	18.5	659	9	AL865000
45	128.8	15.7	381	13	BY093116

## ALIGNMENTS

RESULT 1  
BY735168  
LOCUS  
DEFINITION  
BY735168 RIKEN full-length enriched, mammary gland RCB-0527  
Jyg-MC(B) CDNA Mus musculus cDNA clone G330015622 5', mRNA  
Sequence.  
ACCESSION  
BY735168  
VERSION  
BY735168.1 GI:27148295  
KEYWORDS  
EST.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
1 (bases 1 to 678)  
Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,  
Nikaido, I., Otsato, N., Saito, R., Suzuki, H., Yamana, I., Kiyosawa, H.,  
Yagi, K., Tomaru, Y., Hasegawa, Y., Nogi, A., Schonbach, C.,  
Gojobori, T., Baldarelli, R., Hill, D.P., Bull, C., Hume, D.A.,  
Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S.,  
Beisel, K.W., Blake, J.A., Brade, D., Brusic, V., Chochia, C., Corbani,  
L.E., Cousine, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest,  
A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A.,  
Gough, J., Grimmond, S., Guenichon, S., Hirokawa, N., Jackson, I.J.,  
Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedziarski, R.M.,  
King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons,  
P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Mikl,  
H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G.,

PR 15-SEP-2000; 2000US-0663561.  
PR 20-OCT-2000; 2000US-0693325.  
PR 30-NOV-2000; 2000US-0728422.

XX  
XX  
XX (HSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;  
PI Zhao Q, Wang D, Zhang J, Ren F, Chen R, Wang ZW;  
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;

XX WPI: 2001-476283/51.  
DR P-PSDB; AAM78415.

PT Nucleic acids encoding polypeptides with cytokine-like activities,  
PI useful in diagnosis and gene therapy -

PS Claim 1, Page 711-712; 6221pp; English.

XX  
XX  
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the  
CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to  
CC cytokine, cell proliferation or cell differentiation or which may induce  
CC production of other cytokines in other cell populations. The  
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or  
CC peptide therapy. The polypeptides have various cytokine-like activities,  
CC e.g. stem cell growth factor activity, haematopoiesis regulating  
CC activity, tissue growth factor activity, immunomodulatory activity and  
CC activin/inhibin activity and may be useful in the diagnosis and/or  
CC treatment of cancer, leukemia, nervous system disorders, arthritis and  
CC inflammation.  
CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666  
CC (AAM80020) are omitted as the relevant pages from the sequence listing  
CC were missing at the time of publication.

XX Sequence 1008 BP; 183 A; 374 C; 247 G; 204 T; 0 other;

Query Match 71.2%; Score 583.2; DB 22; Length 1008;  
Best Local Similarity 90.8%; Pred. No. 96-137;  
Matches 621; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY	100	CCTCCGAGAGGGGACTCGTGGGGATGTTAGCTTGCATGACGGTCTGTGGACCT	159
DB	236	CCTGCCACAGGGGACTCGTGGGGATGTTAGCTTGCATGACGGTCTGTGGACCT	355
QY	160	CCCTGAGTCCAGCTCTTAATGCGACAGAGATCCAGGCGCTGGGCCCTCCATCCAGAA	219
DB	356	CCCTGAGTCCAGCTCTTAATGCGACAGAGATCCAGGCGCTGGGCCCTCCATCCAGAA	415
QY	220	AACCTATGACTTACCCGCTACCTGGAGCATCACTCCGACCTTAGTGGAGCTTACT	279
DB	416	AACCTATGACTTACCCGCTACCTGGAGCATCACTCCGACCTTAGTGGAGCTTACT	475
QY	280	GAACCTACTGGGGGCCCCCTTTCAAGAGGCTGACTTCAATCTCTTCGACTGGGGCAGA	339
DB	476	GAACCTACTGGGGGCCCCCTTTCAAGAGGCTGACTTCAATCTCTTCGACTGGGGCAGA	535
QY	340	AACCTGAGCCAGAGGCGAGGTCACCTTGGAGATGTTGGGAGCTCAATGACAGGCTGG	399
DB	536	GAACCTGAGCCAGAGGCGAGGTCACCTTGGAGATGTTGGGAGCTCAATGACAGGCTGG	595
QY	400	GCTGACCCAGAACTATGAGGCGTACAGTCACTCTCTGTGTACTTGCCTGAGCTCAACG	459
DB	596	GCTGACCCAGAACTATGAGGCGTACAGTCACTCTCTGTGTACTTGCCTGAGCTCAACG	655
QY	460	TAGAGCTGCGACAGTGAATCCGAGCTAGCTGGGCCCACTTGTATACAGGCTCCAGGG	519
DB	656	TAGAGCTGCGACAGTGAATCCGAGCTAGCTGGGCCCACTTGTATACAGGCTCCAGGG	715
QY	520	CCTGCTGGGACAGATTGAGGTGTATAGGCGAGCGCTTGGCTACCACTGCCCCAGCTCT	579
DB	716	CCTGCTGGGACAGATTGAGGTGTATAGGCGAGCGCTTGGCTACCACTGCCCCAGCTCT	775
QY	580	GCACAGGACTGAGCAGCTGGGCCCCCTGGCCCAAGTGAATTCTCCAGAAAT	639

DB	776	GCTGGAGCTGAACCCACTTGGACTCTGGCCCTGGCCACAGTGAATCTCTCCAGAAAT	835
QY	640	GGATGACTTCTGGCTGCTGGAAGAGCTGCAACCTGGCTATAGGCTTACGCCAAGACTT	699
DB	836	GGAGCACTTCTGGCTGCTGGAAGAGCTGCAACCTGGCTATAGGCTTACGCCAAGACTT	895
QY	700	CAACCGGCTTAAGAAGATGACAGCTCCAGAGCTTCACTCAACCTGCACTTGGAGGC	759
DB	896	CAACCGGCTTAAGAAGATGACAGCTCCAGAGCTTCACTCAACCTGCACTTGGAGGC	955
QY	760	ACATGTTTCTGACCTTGACCTT	783
DB	956	TCATGGCTTCTGACCTTGAACCTT	979

Search completed: February 9, 2004, 08:10:58  
Job time : 285.291 secs

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RESULT 14
AAD04201
ID AAD04201 standard; cDNA; 729 BP.
XX
XX AAD04201;
XX
XX 02-JUL-2001 (first entry)
XX
XX Human cardiotrophin-like cytokine (CLC) cDNA.
DE
XX Human; biologically active complex; haemopoietin receptor; NR6;
XX cardiotrophin-like cytokine; CLC; therapy; prophylaxis; proliferation;
XX differentiation; cell survival; neurotrophic activity; ss.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 11..679
XX /tag= a
XX /product= "Human cardiotrophin-like cytokine (CLC)
XX protein"
XX /note= "CDS does not include stop codon"
XX /partial
XX sig_peptide 11..91
XX /tag= b
XX mat_peptide 92..679
XX /tag= c
XX /product= "Human mature cardiotrophin-like cytokine
XX (CLC) protein"
XX
XX WO200127157-A1.
XX
XX 19-APR-2001.
XX
XX 06-OCT-2000; 2000WO-AU01216.
XX
XX 08-OCT-1999; 99AU-0003327.
XX
XX 12-MAY-2000; 2000AU-0007489.
XX
XX (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
XX Nash A, Jachno KM, Fabri LJ, Reid K, Bartlett PF, Hilton DJ;
XX Nakata Y, Hasegawa M;
XX
XX MPI; 2001-281978/29.
XX
XX P-PSDB; AAE00828.
XX
XX New biologically active complex comprising NR6 and
XX cardiotrophin-like cytokine, for facilitating proliferation,
XX differentiation and/or survival of a cell -
XX
XX Claim 31; Page 112-114; 123pp; English.
XX
XX The present invention relates to a biologically active complex comprising
XX a haemopoietin receptor, NR6 and cardiotrophin-like cytokine (CLC).
XX The complex is useful in the manufacture of a medicament for the
XX treatment and/or prophylaxis of a subject, as it is involved in
XX facilitating proliferation, differentiation and/or survival of a cell.
XX The complex or its components have neurotrophic activity. The present
XX sequence is human cardiotrophin-like cytokine (CLC) cDNA.
XX
XX Sequence 729 BP; 132 A; 261 C; 196 G; 140 T; 0 other;
XX
XX Query Match 73.3%; Score 600.2; DB 22; Length 729;
XX Best Local Similarity 91.6%; Pred. No. 4.5e-141;
XX Matches 635; Conservative 0; Mismatches 58; Indels 0; Gaps 0;
XX
XX 91 CCCCATGACCTCCGACGAGGGGAGCTGGGGGATGTTAGCTTGCCTATGACGGTCT 150
XX |||||
XX 7 CCCCATGACCTCCGACGAGGGGAGCTGGGGGATGTTAGCTTGCCTATGACGGTCT 66
```

```
QY 151 GTGGACCTTCCTGAGTGCAGCTCTTAATCCGACAGAGATCAGAGCCCTGAGCCCTC 210
DB 67 CTGGCACTCCCTCGAGGTGCGAGCTCTCAATGCCAGAGGGGACCCAGGGCTG6CCCTC 126
QY 211 CATCCAGAAAACTATGACTCTACCCGCTACTGAGAGCATCAATCCGAGCTTTAGCTGG 270
DB 127 CATCCAGAAAACTATGACTCTACCCGCTACTGAGAGCATCAATCCGAGCTTTAGCTGG 186
QY 271 GACCTACCTGAACTACTGAGGGGGCCCTTTCAACGAGCCGTAATCAATCCTGCACT 330
DB 187 GACCTATCTGAATCTAGCTGGGGCCCTTTCAACGAGCCGTAATCAATCCTGCACT 246
QY 331 GGGGGGAGAACTCTGCGCAGAGGCGCAGGCTCACTTGAAGTGTGGCGAAGCCTCAATGA 390
DB 247 GGGGGGAGAGACTCTGCGCAGAGGCGCAGGCTCACTTGAAGTGTGGCGAAGCCTCAATGA 306
QY 391 CAGGCTGCGGCTGACCCGAGAACTATGAGGCGTACAGTCACTCTGTGTTACTTGGCGTGG 450
DB 307 CAAACTGCGGCTGACCCGAGAACTATGAGGCGTACAGTCACTCTGTGTTACTTGGCGTGG 386
QY 451 CCTCAACCGTCAGAGGCGTCCAGAGCTGAACTCCGAGCTGCGGCGCACTTCTGTACAG 510
DB 367 CTTCAACCGTCAGAGGCGTCCAGAGCTGAACTCCGAGCTGCGGCGCACTTCTGTACAG 426
QY 511 CCTCAGAGGCTGCTGGGCGAGCATTTGAGGTGTCATGAGCGAGCGCTTGGCTAACCACTGCC 570
DB 427 CTTCAACCGTCAGAGGCGTCCAGAGCTGAACTCCGAGCTGCGGCGCACTTCTGTACAG 486
QY 571 CCAAGCTCTGCGAGGAGCTGAGCCAGCCCTGGGCGCCCTGAGCTTGGCTTCTTCT 630
DB 487 CCAAGCTCTGCGAGGAGCTGAGCCAGCCCTGGGCGCCCTGAGCTTGGCTTCTTCTTCT 546
QY 631 CCAAGAGATGAGATGATCTTCTGCTGCTGAAGAGAGCTGAGAGCTGAGCTTCTTCTTCT 650
DB 547 CCAAGAGATGAGAGATGATCTTCTGCTGCTGAAGAGAGCTGAGAGCTGAGCTTCTTCTTCT 606
QY 691 CAAGACTTCAACCGGCTTAAGAGAGATGAGAGCTTCCAGAGAGCTTCACTGACCTGGA 750
DB 607 CAAGACTTCAACCGGCTTAAGAGAGATGAGAGCTTCCAGAGAGCTTCACTGACCTGGA 666
QY 751 CTTGAGAGGACATGCTTCTGACCTTGAACCTT 783
DB 667 CTTGAGAGGACATGCTTCTGACCTTGAACCTT 699
RESULT 15
AAK51548
ID AAK51548 standard; cDNA; 1008 BP.
XX
XX AAK51548;
XX
XX 06-NOV-2001 (first entry)
XX
XX Human polynucleotide SEQ ID NO 93.
XX
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
XX vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
XX tissue growth factor; immunomodulatory; cancer; leukaemia;
XX nervous system disorder; arthritis; inflammation; ss.
XX
XX Homo sapiens.
XX
XX WO200157190-A2.
XX
XX 09-AUG-2001.
XX
XX 05-FEB-2001; 2001WO-US04098.
XX
XX 03-FEB-2000; 2000US-0496914.
XX
XX 27-APR-2000; 2000US-0560875.
XX
XX 20-JUN-2000; 2000US-0598075.
XX
XX 19-JUL-2000; 2000US-0620325.
XX
XX 01-SEP-2000; 2000US-0654936.
```



CC rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,  
 CC Alzheimer's disease, Parkinson's disease, neurodegenerative and  
 CC neurological disorders.

XX Sequence 768 BP; 137 A; 278 C; 217 G; 136 T; 0 other;

Query Match 80.6%; Score 660; DB 22; Length 768;  
 Best Local Similarity 92.1%; Pred. No. 4.3e-156;  
 Matches 707; Conservative 0; Mismatches 60; Indels 1; Gaps 1;

QY 2 ATTATTAAGCTTGGCGGAGCGCGGCTCCGCTCCGACCTCCGACGCTCTGGAGAG 61  
 DB 2 ATTATTAAGCTTGGCGGAGCGCGGCTCCGCTCCGACCTCCGACGCTCTGGAGAG 61  
 QY 62 GAGCCG 121  
 DB 62 GAGCCG 120  
 QY 122 GGGATGTAGCTTGGCTTATGACAGGCTGTGTGACCTCTGCTGACGCTCTTAAAT 181  
 DB 121 GGGATGTAGCTTGGCTTATGACAGGCTGTGTGACCTCTGCTGACGCTCTTAAAT 180  
 QY 182 CGCAGCAGAGATCCAGAGCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 241  
 DB 181 CGCAGCAGAGATCCAGAGCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240  
 QY 242 CTGAGCATCAACTCCGAGCTTATGAGTGGGAGCTTACCTGAGCTGAGGCGCGCTTTC 301  
 DB 241 CTGAGCATCAACTCCGAGCTTATGAGTGGGAGCTTACCTGAGCTGAGGCGCGCTTTC 300  
 QY 302 AACGAGCTGACTTCAATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 361  
 DB 301 AACGAGCTGACTTCAATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360  
 QY 362 AACTTGAAGTGTGGGAGAGCTTCAATGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 421  
 DB 361 AACTTGAAGTGTGGGAGAGCTTCAATGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420  
 QY 422 TACAGTCACTCTGTGCTTACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 481  
 DB 421 TACAGTCACTCTGTGCTTACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480  
 QY 482 CGAGTGAAGCTTGGGAGAGCTTCAATGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 541  
 DB 481 CGAGTGAAGCTTGGGAGAGCTTCAATGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540  
 QY 542 GTCATGTGGCAGCTTGGGAGAGCTTCAATGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 601  
 DB 541 GTCATGTGGCAGCTTGGGAGAGCTTCAATGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600  
 QY 602 GCGCGTGGCGCTGCGCGAGTCACTTCCGAGAGATGAGTGAATTTGGCTGCTGAGG 661  
 DB 601 ACTCTGGCGCTGCGCGAGTCACTTCCGAGAGATGAGTGAATTTGGCTGCTGAGG 660  
 QY 662 GAGTGCAGAGCTTGGCTTATGAGCTTGGCTTATGAGCTTGGCTTATGAGCTTGGCTTATGAG 721  
 DB 661 GAGTGCAGAGCTTGGCTTATGAGCTTGGCTTATGAGCTTGGCTTATGAGCTTGGCTTATGAG 720  
 QY 722 CAGCTTCCAGAGCTTCAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 769  
 DB 721 CAGCTTCCAGAGCTTCAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 768

RESULT 12

AAAB8547 standard; DNA; 648 BP.

AAAB8547;

22-JAN-2001 (first entry)

Mouse Interleukin-B60 (IL-B60) gene.

XX

KW Interleukin-B60; IL-B60; mouse; cytokine; cytokine-like factor-1;  
 KW haematopoietic; inflammation; antiinflammatory; autoimmune disease;  
 KW therapy; ds.

OS Mus musculus.

FX Key Location/Qualifiers  
 FT CDS 1..648  
 FT sig\_peptide /+tag= a  
 FT mat\_peptide /+tag= b  
 FT /+tag= c

PN MO200053631-A1.

PD 14-SEP-2000.

PF 09-MAR-2000; 2000MO-US06182.

PR 11-MAR-1999; 99US-0267901.

PA (SCHE) SCHERING CORP.

PI Opmann B, Timans JC, Kastelein RA, Bazan JF;

DR WPI: 2000-587426/55.

PT P-PSDB; AAB19587.

PS Cytokine-like factor 1 (CLF-1) and interleukin (IL)-B60 complexes,  
 PT polypeptides, and nucleic acids, useful in research, diagnosis and for  
 treating inflammatory and autoimmune disorders -

PS Claim 17; Page 17; 97pp; English.

CC The present sequence is that of DNA encoding mouse interleukin-B60  
 CC (IL-B60, see AAB19587), a novel, small soluble cytokine-like protein  
 CC of 215 amino acids that exhibits structural motifs characteristic  
 CC of a member of the long-chain cytokines, and which shows homology  
 CC to granulocyte colony stimulating factor and interleukin-6. IL-60B  
 CC may have either stimulatory or inhibitory effects on haematopoietic  
 CC cells, including e.g. lymphoid cells, such as T-cells, B-cells,  
 CC natural killer cells, macrophages, dendritic cells, haematopoietic  
 CC progenitors, etc. Methods are provided for modulating the  
 CC physiology or development of a cell or tissue culture cells by  
 CC contacting the cell with an agonist or antagonist of IL-B60 or an  
 CC agonist of antagonist of a complex of mature IL-B60 and its  
 CC partner, cytokine-like factor-1 (CLF-1, see AAB19588). The  
 CC IL-B60/CLF-1 cytokine serves as a key physiological factor in motor  
 CC neuron development and regeneration. IL-60B, its agonists and  
 CC antagonists may be used to treat inflammatory or autoimmune  
 CC disorders and also for drug screening.

SQ Sequence 648 BP; 130 A; 217 C; 170 G; 131 T; 0 other;

Query Match 78.9%; Score 646.4; DB 21; Length 648;  
 Best Local Similarity 99.8%; Pred. No. 1.1e-152;  
 Matches 647; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 125 ATGTAGCTTGGCTTATGACAGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 184  
 DB 1 ATGTAGCTTGGCTTATGACAGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60

QY 185 ACAGAGATCCAGGCGCTGCGCTCCATCCAGAAACCTATGACCTGACCGGCTACCTG 244  
 DB 61 ACAGAGATCCAGGCGCTGCGCTCCATCCAGAAACCTATGACCTGACCGGCTACCTG 120

QY 245 GAGCATCAATCCGAGCTTATGCTGAGACCTGACCTGACCTGACCTGACCTGACCTGACCT 304  
 DB 121 GAGCATCAATCCGAGCTTATGCTGAGACCTGACCTGACCTGACCTGACCTGACCTGACCT 180

QY 305 GAGCTGACTTCAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 364



CC encoded by a NNT1 nucleotide sequence, its fragment or naturally  
 CC occurring variant, and diagnosing an IGE-related disease or  
 CC susceptibility of an IGE-related disease based on the presence or amount  
 CC of expression of the polypeptide and a pharmaceutical composition for use  
 CC in treating IGE-related disease, comprising the NNT1 inhibitor.  
 CC The NNT1 inhibitor is useful for preventing and treating IGE-related  
 CC disease, modulating IGE levels, and creating allergic diseases e.g.  
 CC Type I allergic disease, allergic rhinitis, eczema, dermatitis,  
 CC pollinosis, asthma, immune diseases and disorders, diseases involving  
 CC abnormal cell proliferation including cancer, arteriosclerosis and  
 CC vascular stenosis, diseases and conditions relating to dysfunction of  
 CC immune system including rheumatoid arthritis, psoriatic arthritis,  
 CC inflammatory arthritis, osteoarthritis, inflammatory joint disease,  
 CC autoimmune disease, multiple sclerosis, lupus, diabetes, inflammatory  
 CC bowel disease, transplant rejection, and graft versus host disease, and  
 CC reproductive diseases and disorders including infertility, miscarriage,  
 CC preterm labour and delivery, and endometriosis. The present sequence  
 CC encodes human NNT1.

XX Sequence 797 BP; 139 A; 297 C; 218 G; 143 T; 0 other;

Query Match 81.7%; Score 669.4; DB 24; Length 797;

Best Local Similarity 92.0%; Pred. No. 1.9e-158;

Matches 717; Conservative 0; Mismatches 61; Indels 1; Gaps 1;

5 ATTAAGCTTGGCCGAGGCGGCGGCTCCGACCTCCGACGCTCTGGAGAGAG 64  
 1 ATTAAGCTTGGCCGAGGCGGCGGCTCCGACCTCCGACGCTCTGGAGAGAG 60  
 65 CCGCGCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 124  
 61 CCGGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 119  
 125 ATGTTAGCTTGGCTATGACGCGTGTGCGGCGGCGGCGGCGGCGGCGGCGG 184  
 120 ATGTTAGCTTGGCTATGACGCGTGTGCGGCGGCGGCGGCGGCGGCGGCGG 179  
 185 AAGAGAGATTCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 244  
 180 AAGAGAGATTCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 239  
 245 GAGCATCACTCCGAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCT 304  
 240 GAGCATCACTCCGAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCT 299  
 305 GAGCTGACTTCAATCTCTCTGAGCTTGGGCGGCGGCGGCGGCGGCGGCGG 364  
 300 GAGCTGACTTCAATCTCTCTGAGCTTGGGCGGCGGCGGCGGCGGCGGCGG 359  
 365 TTGGAAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 424  
 360 TTGGAAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 419  
 425 AGTCACCTCTGTTACTTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 484  
 420 AGTCACCTCTGTTACTTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 479  
 485 CGTACCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 544  
 480 CGTACCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 539  
 545 ATGGGAGGCTTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 604  
 540 ATGGGAGGCTTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 599  
 605 CTTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 664  
 600 CTTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 659  
 665 CTGACAGCTTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 724  
 660 CTGACAGCTTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 719

Oy 725 CCTCAGAGCTTGCATGACACCTGACATTTGAGAGGACATGAGTTCTGACCTTGAACCT 783  
 Db CCTCAGAGCTTGCATGACACCTGACATTTGAGAGGACATGAGTTCTGACCTTGAACCT 778

RESULT 11  
 AAH99772

ID AAH99772 standard; cDNA; 768 BP.

AAH99772;

16-OCT-2001 (first entry)

Human protein encoding cDNA sequence SEQ ID NO:607.

Human; cancer; ulcer; HIV infection; human immunodeficiency virus;  
 antiinflammatory; antirheumatic; antirheumatic; immunosuppressive;  
 antibacterial; endocrine; cardiac; central nervous system; virucide;  
 anti-HIV; fungicide; antimutagen; cardiovascular; antianemic; anaemia;  
 dermatological; antiallergic; antiaesthetic; antidiabetic; cytostatic;  
 neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;  
 immunomodulant; gene therapy; antisense therapy; vaccine; inflammation;  
 antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;  
 cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;  
 genetic disease; haematopoietic disorder; platelet disorder; asthma;  
 thrombocytopenia; osteoporosis; severe combined immunodeficiency;  
 allergic rhinitis; diabetes; multiple sclerosis; depression;  
 Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;  
 neurological disorder; ss.

Hom sapiens.

WO200153455-A2.

26-JUL-2001.

22-DEC-2000; 2000WO-US35017.

23-DEC-1999; 99US-0471275.

21-JAN-2000; 2000US-0488725.

25-APR-2000; 2000US-0552317.

(HYSE-) HYSBQ INC.

Tang YT, Liu C, Dermanac RT;

WPI; 2001-457603/49.

P-PSDB; AAM25831.

Isolated human polynucleotides encoding polypeptides, useful for the

treatment and diagnosis of e.g. cancer, ulcers and HIV infection -

Claim 1; Page 638; 1217BP; English.

AAH99166 to AAH99904 encode the human proteins given in AAM25225 to  
 AAM25963. The proteins can have activities based on the tissues and  
 cells they are expressed in, such as: antiinflammatory; antirheumatic;  
 antiallergic; immunosuppressive; antibacterial; endocrine; cardiac;  
 central nervous system; virucide; anti-HIV; fungicide; antimutagen;  
 cardiovascular; antianemic; antiallergic; haematopoietic; vulnery;  
 antidiabetic; osteopathic; dermatological; antiallergic; antiaesthetic;  
 antiparkinsonian; and immunostimulant. The proteins and polynucleotides  
 encoding them can be used in gene therapy, antisense therapy and vaccine  
 production. The proteins and polynucleotides are useful for screening for  
 agonists or antagonists of a protein and for the treatment and diagnosis  
 of disorders associated with the activity of a protein e.g. inflammation,  
 rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,  
 neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal  
 infections, autoimmunity, genetic diseases, haematopoietic disorders,  
 anaemia, platelet disorders, thrombocytopenia, wounds, burns, ulcers,  
 osteoporosis, severe combined immunodeficiency, eczema, allergic

PI Chang M;  
 XX MPI: 2000-338492/29.  
 DR P-PSDB; AAY87813.  
 XX  
 PT New nucleic acids encoding neurotrophic factors useful for stimulating  
 PT growth of motor or sympathetic neurons for treating neuron cell damage  
 PT  
 XX  
 PS Claim 1a; Fig 1; 42pp; English.  
 XX  
 CC This invention describes a novel nucleic acid molecule (I) encoding a  
 CC novel neurotrophic factor (NNT-1) (II) which has neurotrophic,  
 CC neuroprotective, anticonvulsant, antiparkinsonian, antidiabetic and  
 CC ophthalmological activity. (I) is useful for producing NNT-1  
 CC polypeptides which are useful for treating patients in whom various  
 CC cells of the central, autonomic, or peripheral nervous system have  
 CC degenerated and/or have been damaged by congenital disease, trauma,  
 CC mechanical damage, surgery, stroke, ischemia, infection, metabolic  
 CC disease, nutritional deficiency, malignancy and/or toxic agents. NNT-1  
 CC proteins are used to treat diseases like Alzheimer's, Parkinson's,  
 CC amyotrophic lateral sclerosis, Charcot-Marie-Tooth syndrome, Huntington's  
 CC disease, peripheral neuropathy induced by diabetes or other metabolic  
 CC disorders, and/or dystrophies or degeneration of the neural retina such  
 CC as retinitis pigmentosa, drug-induced retinopathies, stationary forms of  
 CC night blindness, progressive cone-rod degeneration, immune disorders and  
 CC hematoepietic disorders. (I) is effective in treating neurological  
 CC conditions and promotes neuron regeneration. Neural functions are  
 CC effectively restored in patients suffering from various neurological  
 CC disorders. This sequence encodes the human NNT-1 protein described in the  
 CC method of the invention.  
 XX  
 SQ Sequence 797 BP; 139 A; 297 C; 218 G; 143 T; 0 other;  
 Query Match 81.7%; Score 669.4; DB 21; Length 797;  
 Best Local Similarity 92.0%; Pred. No. 1.9e-158;  
 Matches 717; Conservative 0; Mismatches 61; Indels 1; Gaps 1;

QY 545 ATGGCAGCGCTTGGCTACCCAGTGGCCAGCCTTGGCCAGGAGCTGAGCCAGCTGGCC 604  
 DB 540 ATGGCAGCTCTGGGCTACCCAGTGGCCAGCCTTGGCCAGGAGCTGAGCCAGCTGG 599  
 QY 605 CCTGGCCCTGCCCAAGTACTTCTCCAGAAAGATGATGACTTCTGGCTGGAAGAG 664  
 DB 600 CTGGGCCCTGCCCAAGTACTTCTCCAGAAAGATGATGACTTCTGGCTGGAAGAG 659  
 QY 665 CTGGCAGCCTGGCTATGGGCTTACGCGAAGACTTCAACCGGCTTAAGAAAGATGAG 724  
 DB 660 CTGGCAGCCTGGCTATGGGCTTACGCGAAGACTTCAACCGGCTTAAGAAAGATGAG 719  
 QY 725 CCTCCAGCAGCTTCACTGACCTCCAGCCTTGAAGGACATGGTTTCTGACCTGACCT 783  
 DB 720 CCTCCAGCAGCTGACCTCACTGACCTCCAGCCTTGAAGGACATGGTTTCTGACCT 778

RESULT 10  
 ABK11647  
 ID ABK11647 standard; cDNA; 797 BP.  
 XX  
 AC ABK11647;  
 XX  
 DT 05-JUN-2002 (first entry)  
 XX  
 DE Human cDNA encoding novel neurotrophic factor NNT1.  
 XX  
 KW Human; ss; gene; NNT1; neurotrophic factor; IGF-related disease;  
 KW Type I allergic disease; allergic rhinitis; eczema; dermatitis;  
 KW pollinosis; asthma; immune disease; cancer; arteriosclerosis;  
 KW vascular stenosis; rheumatoid arthritis; psoriatic arthritis;  
 KW inflammatory arthritis; osteoarthritis; inflammatory joint disease;  
 KW autoimmune disease; multiple sclerosis; lupus; diabetes; endometriosis;  
 KW inflammatory bowel disease; transplant rejection; reproductive disorder;  
 KW graft versus host disease; infertility; miscarriage; preterm labour.  
 XX  
 OS Homo sapiens.  
 XX  
 PD 28-FEB-2002.  
 XX  
 PF 17-AUG-2001; 2001WO-US25906.  
 XX  
 PR 18-AUG-2000; 2000US-226436P.  
 PR 16-AUG-2001; 2001US-0931704.  
 XX  
 PA (AMGE-) AMGEN INC.  
 XX  
 PI Senaldi G;  
 XX  
 DR MPI: 2002-280867/32.  
 DR P-PSDB; AAU78176.  
 XX  
 PT Treating immunoglobulin E-related disease, modulating IGE levels in a  
 PT patient, preventing IGF-related disease and treating allergic diseases,  
 PT involve administering NNT-1 inhibitor to a patient  
 XX  
 PS Claim 2; Fig 1; 63pp; English.  
 XX  
 CC The invention relates to treating immunoglobulin E (IGE)-related disease,  
 CC modulating IGE levels in a patient, preventing an IGF-related disease,  
 CC and treating allergic diseases, comprising administering a  
 CC therapeutically effective amount of novel neurotrophic factor (NNT)-1  
 CC inhibitor to a patient. Also included are a method of diagnosing an  
 CC IGE-related disease or susceptibility to an IGF-related disease, by  
 CC determining the presence or amount of expression of an NNT1 polypeptide

RESULT 8  
AAV22652  
ID AAV22652 standard; cDNA; 797 BP.  
XX  
AC AAV22652;  
XX  
DT 13-JUL-1998 (first entry)  
XX  
DE cDNA encoding human neurotrophic factor NNT-1.  
XX  
KW Human; neurotrophic factor; NNT-1; growth; motor; sympathetic; neuron;  
KW treatment; neurological disease; degeneration; Parkinson's disease;  
KW amyotrophic lateral sclerosis; ALS; Alzheimers's disease; stroke; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 90..767  
FT /tag= a  
FT sig\_peptide 90..170  
FT /tag= b  
FT mat\_peptide 171..764  
FT /tag= c  
XX  
PN US5741772-A.  
XX  
PD 21-APR-1998.  
XX  
PF 03-FEB-1997; 97US-0792019.  
XX  
PR 03-FEB-1997; 97US-0792019.  
XX  
PA (AMGE-) AMGEN INC.  
XX  
PI Chang M;  
XX  
DR WPI; 1998-260526/23.  
XX  
P-PSDB; AAM56141.  
XX  
PT Neurotrophic factor NNT-1 polypeptide and related nucleic acids -  
PT useful for stimulating growth of motor and sympathetic neurons  
XX  
PS Disclosure; Fig 1; 41pp; English.  
XX  
CC The present sequence encodes a human neurotrophic factor, designated  
CC NNT-1, which is capable of stimulating growth of motor or sympathetic  
CC neurons. The NNT-1 protein is useful in the treatment of neurological  
CC diseases characterized by the degeneration and death of particular  
CC classes of neurons. These diseases specifically include Parkinson's  
CC disease, amyotrophic lateral sclerosis (ALS), Alzheimers's disease,  
CC stroke and various degenerative disorders affecting vision.  
SQ Sequence 797 BP; 139 A; 297 C; 218 G; 143 T; 0 other;  
Query Match 81.7%; Score 669.4; DB 19; Length 797;  
Best Local Similarity 92.0%; Pred. No. 1.9e-158;  
Matches 717; Conservative 0; Mismatches 61; Indels 1; Gaps 1;  
QY 5 ATTAAGCTTCGCGGAGCGCGGCTCGCCCTCCCACTCCGCGCAGCTTGGAGAGAG 64  
DB 1 ATTAAGCTTCGCGGAGCGCGGCTCGCCCTCCCACTCCGCGCAGCTTGGAGAGAG 60  
QY 65 CCG 124  
DB 61 CCG 119  
QY 125 ATGTAGCTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 184  
DB 120 ATGTAGCTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 179  
QY 185 ACAGAGATCCAGGCG 244

DB 180 ACAGGAGACCCAGGCG 239  
QY 245 GAGCATCACTCCGAGCTTGTGCTGGGACCTACCTGAGCTGCGGCGCGCGCGCGCG 304  
DB 240 GAGCATCACTCCGAGCTTGTGCTGGGACCTACCTGAGCTGCGGCGCGCGCGCGCG 299  
QY 305 GAGCGTGAATCAATCCCTCTGCACTGGGCGGAGAACTGCGCGCGCGCGCGCGCGCG 364  
DB 300 GAGCGTGAATCAATCCCTCTGCACTGGGCGGAGAACTGCGCGCGCGCGCGCGCGCG 359  
QY 365 TTGGAAGTGGCGGAGCGCTCAATGACAGCTGCGCGCGCGCGCGCGCGCGCGCGCG 424  
DB 360 TTGGAAGTGGCGGAGCGCTCAATGACAGCTGCGCGCGCGCGCGCGCGCGCGCGCG 419  
QY 425 AGTCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 484  
DB 420 AGTCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 479  
QY 485 CGTAGCGTGGCG 544  
DB 480 CGTAGCGTGGCG 539  
QY 545 ATGGCAGCTTGGCTGACCACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 604  
DB 540 ATGGCAGCTTGGCTGACCACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 599  
QY 605 CCGGCG 664  
DB 600 CCGGCG 659  
QY 665 CTGCGAGCTTGGCTGACCACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 724  
DB 660 CTGCGAGCTTGGCTGACCACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 719  
QY 725 CCTCAGCAGCTTGAATGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 783  
DB 720 CCTCAGCAGCTTGAATGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 778  
RESULT 9  
AAA39481  
ID AAA39481 standard; cDNA; 797 BP.  
XX  
AC AAA39481;  
XX  
DT 24-AUG-2000 (first entry)  
XX  
DE Human NNT-1 cDNA.  
XX  
KW NNT-1; human; neurotrophic factor; nootropic; neuroprotective; treatment;  
KW anticonvulsant; antiparkinsonian; antidiabetic; ophthalmological;  
KW nervous system degeneration; Alzheimer's disease; Parkinson's disease;  
KW amyotrophic lateral sclerosis; Charcot-Marie-Tooth syndrome;  
KW Huntington's disease; peripheral neuropathy; neural retina degeneration;  
KW retinopathy; immune disorder; hematopoietic disorder; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 90..767  
FT /tag= a  
FT /product= "NNT-1"  
XX  
PN US6054294-A.  
XX  
PD 25-APR-2000.  
XX  
PF 12-DEC-1997; 97US-0988819.  
XX  
PR 03-FEB-1997; 97US-0792019.  
XX  
PA (AMGE-) AMGEN INC.  
XX

```
QY 662 GAGCTGCAGACCTGGCTATGCGCTTCAGCCAGACTTCAACCGGCTTAAAGAAAGATG 721
DB 699 GAGCTGCAGACCTGGCTATGCGCTTCAGCCAGACTTCAACCGGCTTAAAGAAAGATG 758
QY 722 CAGCTTCAGACCTTCACTGACCTTCAGCTTGGAGGACATGGTTTCTGACCTTGACC 781
DB 759 CAGCTTCAGACCTTCACTGACCTTCAGCTTGGAGGACATGGTTTCTGACCTTGACC 818
QY 782 CT 783
DB 819 TT 820

RESULT 7
AAV47510
ID AAV47510 standard; cDNA; 797 BP.
AC AAV47510;
XX
XX
XX 09-NOV-1998 (first entry)
XX
XX
XX Human neurotrophic factor NNT-1 cDNA.
DE
XX NNT-1; neurotrophic factor; human; antiinflammatory; adjuvant;
XX Alzheimer's disease; Parkinson's disease; Huntington's disease;
XX amyotrophic lateral sclerosis; Charcot-Marie-Tooth syndrome;
XX peripheral neuropathy; dystrophy; neural retina degeneration;
XX common variable immunodeficiency; CVID; selective IgA deficiency;
XX hypogammaglobulinaemia; X-linked agammaglobulinaemia; antiseptic;
XX therapy; ss.
XX
XX Homo sapiens.
OS
XX
XX
XX Key Location/Qualifiers
XX FH 90..767
XX FT CDS /*tag= a
XX FT sig_peptide 90..170
XX FT /*tag= b
XX FT mat_peptide 171..764
XX FT /*tag= c
XX
XX WO9833922-A1.
XX
XX 06-AUG-1998.
XX
XX 02-FEB-1998; 98WO-US02363.
XX
XX 30-JAN-1998; 98US-0016534.
XX PR 03-FEB-1997; 97US-0792019.
XX
XX (AMGE-) AMGEN INC.
XX
XX PA
XX PI Chang M, Elliot GS, Sarmiento U, Senaldi G;
XX DR WPI; 1998-437475/37.
XX DR P-PSDB; AAW29715.
XX
XX Newly isolated nucleic acid encoding human or murine neurotrophic
XX factor NNT-1 - useful for treatment of neurological and
XX immunological diseases or inflammation, also as vaccine adjuvant
XX
XX Claim 3; Fig 1; 120p; English.
XX
XX This newly isolated human cDNA sequence (deposited at ATCC 98295)
XX codes for a novel neurotrophic factor, designated NNT-1 (see
XX AAW29715), that is a growth factor for neurons and for B or T cells.
XX It was obtained from a T-cell lymphoma cDNA library by expressed
XX sequence tag analysis on the basis of homology to CNTF. The
XX isolated NNT-1 cDNA was used as probe to isolated NNT-1 genomic
XX DNA (see AAV47511). Vectors containing the cDNA or genomic DNA and
XX host cells are provided for use in the production of NNT-1
XX polypeptides. These are used to treat: (i) neurological or
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CC immunological diseases, specifically Alzheimer's, Parkinson's or
CC Huntington's diseases, amyotrophic lateral sclerosis,
CC Charcot-Marie-Tooth syndrome, peripheral neuropathy, dystrophy and
CC degeneration of the neural retina, or conditions characterised by T
CC or B cell defects, e.g. common variable immunodeficiency (CVID),
CC selective IgA deficiency, hypogammaglobulinaemia and X-linked
CC agammaglobulinaemia (claimed), but many others disclosed; and (ii)
CC inflammation. NNT-1 is also able to boost immunoreactivity and
CC antibody production following vaccination, and, since it inhibits
CC tumour necrosis factor production, it may also be useful for
CC treating sepsis. NNT-1 nucleic acid fragments are also used as
CC hybridisation probes in diagnostic assays. In addition, cells that
CC have been engineered to express NNT-1 can be implanted, or nucleic
CC acids are delivered in gene therapy vectors.
XX
XX Sequence 797 BP; 139 A; 297 C; 218 G; 143 T; 0 other;
SQ
Query Match 81.7%; Score 669.4; DB 19; Length 797;
Best Local Similarity 92.0%; Pred. No. 1.9e-158;
Matches 717; Conservative 0; Mismatches 61; Indels 1; Gaps 1;
QY 5 ATTTAAAGCTTCCGCGAGCGCGGCTCCGCTCCCACTCCGCGAGCTTGGAGAGAG 64
DB 1 ATTTAAAGCTTCCGCGAGCGCGGCTCCGCTCCCACTCCGCGAGCTTGGAGAGAG 60
QY 65 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 124
DB 61 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 119
QY 125 ATGTTAGCTTGGCTTATGACAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 184
DB 120 ATGTTAGCTTGGCTTATGACAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 179
QY 185 ACAGAGATCCAGGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 244
DB 180 ACAGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 239
QY 245 GAGCATCACTCCGAGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 304
DB 240 GAGCATCACTCCGAGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 299
QY 305 GAGCTGACTTCAATCTCTCTGACCTGTGGGCGAGAACTGTGCGCGCGCGCGCGCG 364
DB 300 GAGCTGACTTCAATCTCTCTGACCTGTGGGCGAGAGACTGTGCGCGCGCGCGCGCG 359
QY 365 TTGGAAGTGTGGCGAGGCTTCAATGACAGGCTGTGCGCGCGCGCGCGCGCGCGCG 424
DB 360 TTGGAAGTGTGGCGAGGCTTCAATGACAGGCTGTGCGCGCGCGCGCGCGCGCGCG 419
QY 425 AGTCACTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 484
DB 420 AGTCACTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 479
QY 485 CGTAGCTGTGCGCACTTCTGTATCAAGGCTTCAAGGCGCTGTGCGCGCGCGCGCGCG 544
DB 480 CGTAGCTGTGCGCACTTCTGTATCAAGGCTTCAAGGCGCTGTGCGCGCGCGCGCGCG 539
QY 545 ATGCGCAGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 604
DB 540 ATGCGCAGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 599
QY 605 CCGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 664
DB 600 CCGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 659
QY 665 CTGCGAGACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 724
DB 660 CTGCGAGACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 719
QY 725 CTTCCAGAGCTTCAATGACCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 783
DB 720 CTTCCAGAGCTTCAATGACCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 778
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Qy	362	AACTTGAAGTGTGGGAAGCCTCAATGACAGGCTGCGGCTGACCCGAAATATGAAGCG	4421
Dd	441	GACTTGAAGTGTGGGAAGCCTCAATGACAACTGCGCTGACCCGAAATATGAAGCG	5000
Qy	422	TACAGTCACCTCTGTGTACTTGGCGTCAACGTCAGGCTGCCACAGCTGAATC	4811
Dd	501	TACAGCACCTCTGTGTACTTGGCGTCAACCGTCAGGCTGCCACAGCTGAATC	5600
Qy	482	CGACGTAAAGCTGGGCCCACTTGTATCAAGAGCTCCAGGGGCTGTGGGAGATGCAAGT	5411
Dd	561	CGCGGAGCCTGGGCCCACTTGTATCAAGAGCTCCAGGGGCTGTGGGAGATGCAAGT	6200
Qy	542	GTCATGGCGACGCTTGGTCAACCACTGCCCCAGCCTCTGCAGAGGATGAGCCAGCTGG	6011
Dd	621	GTCATGGCGACGCTTGGTCAACCACTGCCCCAGCCTCTGCAGAGGATGAGCCAGCTGG	6800
Qy	602	GCCCCCTGGGCTGCCCAAGTAGACTTCTCCAGAAAGATGATGACTTGTGCTGCTGAG	6611
Dd	681	ACTCTGGGCCCTGCCCAAGTAGACTTCTCCAGAAAGATGATGACTTGTGCTGCTGAG	7400
Qy	662	GAGCTGCAGACTGTGCTATATGGGCTTCAGGCAAGACTTCAACCGGCTTAAGAAAGATG	7211
Dd	741	GAGCTGCAGACTGTGCTATATGGGCTTCAGGCAAGACTTCAACCGGCTTAAGAAAGATG	8000
Qy	722	CAGCCTTCAGAGCTTCAAGTCACCTGCACTTGAAGGCAATGCTTCTGAACCTTGACC	7811
Dd	801	CAGCCTTCAGAGCTTCAAGTCACCTGCACTGAGGGGCTCATAGGCTTCTGAACCTTGACC	8600
Qy	782	CT 783	
Dd	861	TT 862	

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RESULT 6
AAAB8546
ID AAAB8546 standard; DNA, 1790 BP.
XX
XX
AC AAAB8546;
XX
DT 22-JAN-2001 (first entry)
XX
DE Human Interleukin-B60 (IL-B60) gene.
XX
KW Interleukin-B60; IL-B60; human; cytokine; chromosome 11;
KW cytokine-like factor-1; haematopoietic; inflammation;
KW antiinflammatory; autoimmune disease; therapy; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 162..809
FT /*tag= a
FT sig_peptide 162..212
FT /*tag= b
FT mat_peptide 213..806
FT /*tag= c
XX
PV WC200053631-A1.
XX
PD 14-SEP-2000.
XX
PF 09-MAR-2000; 2000MO-US06182.
XX
PR 11-MAR-1999; 99US-0267901.
XX
PA (SCHE ) SCHERING CORP.
XX
PI Oppmann B, Timans JC, Kastelein RA, Bazan JF;
XX
XX WPI; 2000-587426/55.
XX
XX P-PSDB; AAB19686.
XX
XX
XX Cytokine-like factor 1 (CLF-1) and interleukin (IL)-B60 complexes,

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polypeptides, and nucleic acids, useful in research, diagnosis and for treating inflammatory and autoimmune disorders - and for

Claim 17, Page 15-16; 97pp; English.

The present sequence is that of DNA encoding human interleukin-860 (IL-860, see AAB19586), a novel, small soluble cytokine-like protein of 198 amino acids that exhibits structural motifs characteristic of a member of the long-chain cytokines, and which shows homology to granulocyte colony stimulating factor and interleukin-6. IL-608 may have either stimulatory or inhibitory effects on haematopoietic cells, including e.g. Lymphoid cells, such as T-cells, B-cells, natural killer cells, macrophages, dendritic cells, haematopoietic progenitors, etc. Methods are provided for modulating the physiology or development of a cell or tissue culture cells by contacting the cell with an agonist or antagonist of IL-860 or an agonist of antagonist of a complex of mature IL-860 and its partner, cytokine-like factor-1 (CLF-1, see AAB19588). The IL-860/CLF-1 cytokine serves as a key physiological factor in motor neuron development and regeneration. IL-608, its agonists and antagonists may be used to treat inflammatory or autoimmune disorders and also for drug screening. The IL608 gene maps to human chromosome 11.

Sequence 1790 BP; 381 A; 560 C; 474 G; 375 T; 0 other;

Query Match	82.3%	Score 674;	DB 21;	Length 1790;
Best Local Similarity	92.2%;	Pred. No. 1.6e-159;		
Matches 721;	Conservative 0;	Mismatches 60;	Indels 1;	Gaps 1
QY	2	ATTATTAAGCTTGGCCGAGACCCGCGCTCGCCCTCCCACTCCGCGACCTCTGGAGAG	61	
DB	40	ATTATTAAGCTTGGCCGAGACCCGCGCTCGCCCTCCCACTCCGCGACCTCTGGAGAG	99	
QY	62	GAGCGCGCCCGCGCGCGCCGCGCCCGCCCGCCCATGAGACTTCCGAGAGGGAGACTGTGG	121	
DB	100	GAGCGCGACCCGCGCGCGCCCGCGCGCCCGCCCGCCCATGAGACTTCCGAGAGGGAGACTGTGG	158	
QY	122	GGAGTGTAGCTTGGCTTATGACGAGGTGTGTGGCACTTCCCTGACAGTGGCACTTTAAT	181	
DB	159	GGAGTGTAGCTTGGCTTGTGACGAGGTGTGTGGCACTTCCCTGACAGTGGCACTTTAAT	218	
QY	182	CGCACAAGAGATCCAGAGCCCTGGGCCCTTCATCCAGAAACCTAAGACTCACCCGCTAC	241	
DB	219	CGCACAAGGAGACCCAGAGGCCCTGGGCCCTTCATCCAGAAACCTAAGACTCACCCGCTAC	278	
QY	242	CTGGAGACTCAACTCCGAGGCTTGTAGCTGAGGACTCACTGAACTACTCTGGGGGCCCTTTC	301	
DB	279	CTGGAGACCAACTCCGAGGCTTGTAGCTGAGGACTCACTGAACTACTCTGGGGGCCCTTTC	338	
QY	302	AACGAGCTGACTTCAATCTCTTGACTGGGGGAGAGAACTCTGCCAGGGCCACGCTC	361	
DB	339	AACGAGCCAGACTTCAATCTCTTGACTGGGGGAGAGAACTCTGCCAGGGCCACGCTC	398	
QY	362	AACCTTGAAGTGTGGCGAAGCTCTCAATGACAGGCTGGCTGTACCCAGAGCTATGAGCGG	421	
DB	399	GACTTGGAGGTGTGGCGAAGCTCTCAATGACAACTGCGGCTGTAGCCAGAACTTACAGAGGCC	458	
QY	422	TACAGTCACTCTCTGTATTACTCTGGCTGTGGCCCTCAACCGTCAGGCGTGGCACTGTAATC	481	
DB	459	TACAGTCACTCTCTGTATTACTCTGGCTGTGGCCCTCAACCGTCAGGCGTGGCACTGTAATC	518	
QY	482	CGACGTACCTCTGGCCCACTTCTGTATGACAGCTTCAAGGGCTTGTGGGAGACTTTCAGGT	541	
DB	519	CGCGCAAGCTTGTGGCCCACTTCTGTATGACAGCTTCAAGGGCTTGTGGGAGACTTTCAGGT	578	
QY	542	GTCAATGCGACGCTTGTGGTCACTCCACTGCCCCAGGCTTGTGCCAGGGAGCTGAGCAGCTGG	601	
DB	579	GTCAATGCGACGCTTGTGGTCACTCCACTGCCCCAGGCTTGTGCCAGGGAGCTGAGCAGCTGG	638	
QY	602	GCCCCCTGGCCCTGGCCCACTGACTTCTCCAGAGAGATGAGATGACTTTCGTGGCTGGAG	661	
DB	639	ACTCTGGCCCTGGCCCACTGACTTCTCCAGAGAGATGAGATGACTTTCGTGGCTGGAG	698	

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QY 181 TCGCAGAGGATTCAGAGCCCTGCCCCCTCCATCCAGAAAACTTAGACTCAACCGCTA 240
    |||
DB 181 TCGCAGAGGATTCAGAGCCCTGCCCCCTCCATCCAGAAAACTTAGACTCAACCGCTA 240
QY 241 CCGAGAGCATCACTCCGAGCTTAAAGTGGAGCTTAACTTAACCTTGGGGCCCTTTT 300
    |||
DB 241 CCGAGAGCATCACTCCGAGCTTAAAGTGGAGCTTAACTTAACCTTGGGGCCCTTTT 300
QY 301 CAAAGAGCTGACTTCAATCTCTCCAGCTGGGGGAGAAACTCTGGCCAGAGGACAGT 360
    |||
DB 301 CAAAGAGCTGACTTCAATCTCTCCAGCTGGGGGAGAAACTCTGGCCAGAGGACAGT 360
QY 361 CAACTTGAAGTGTGGGAGAGCTCAATGAAGGCTGGCTGAACCCAGAACTATAGAGC 420
    |||
DB 361 CAACTTGAAGTGTGGGAGAGCTCAATGAAGGCTGGCTGAACCCAGAACTATAGAGC 420
QY 421 GTACAGTCACTCTGTGTGTTACTTGGCTGGCTCAACCGTCAAGGCTGCCACAGCTGAACT 480
    |||
DB 421 GTACAGTCACTCTGTGTGTTACTTGGCTGGCTCAACCGTCAAGGCTGCCACAGCTGAACT 480
QY 481 CCGACGTAGGCTGGCCCACTTCTGTACAGGCTCCAGAGGCTGCTGGGAGAGATTGGAGG 540
    |||
DB 481 CCGACGTAGGCTGGCCCACTTCTGTACAGGCTCCAGAGGCTGCTGGGAGAGATTGGAGG 540
QY 541 TGTGATGGCGAGCGCTTGGCTAACCCACTGCCAGGCTCTGGCCAGGACTGAGCCAGCTG 600
    |||
DB 541 TGTGATGGCGAGCGCTTGGCTAACCCACTGCCAGGCTCTGGCCAGGACTGAGCCAGCTG 600
QY 601 GGGCCCTGGCCCTGGCCCAAGTGAATCTTCCAGAAAGATGAGTCTTGGCTGTGAA 660
    |||
DB 601 GGGCCCTGGCCCTGGCCCAAGTGAATCTTCCAGAAAGATGAGTCTTGGCTGTGAA 660
QY 661 GGAGCTGAGAGCTGCTATGAGGCTTCAAGGAGAGACTTCAACCGGCTTAAAGAAAGAT 720
    |||
DB 661 GGAGCTGAGAGCTGCTATGAGGCTTCAAGGAGAGACTTCAACCGGCTTAAAGAAAGAT 720
QY 721 GGAGCTTCCAGAGCTTCACTCACTGCACTTGAAGGAGCATGATTTCTGACCTTGAC 780
    |||
DB 721 GGAGCTTCCAGAGCTTCACTCACTGCACTTGAAGGAGCATGATTTCTGACCTTGAC 780
QY 781 CCTTAACCCCCACACTTCCAGGCGCCAGTCAAGCTGTGCTT 819
    |||
DB 781 CCTTAACCCCCACACTTCCAGGCGCCAGTCAAGCTGTGCTT 819

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XX 26-JAN-2001; 2001WO-FR00253.
PF
XX
PR 27-JAN-2000; 2000PR-0001035.
PR 12-OCT-2000; 2000PR-0013089.
PA (FABR ) FABRE MEDICAMENT SA PIERRE.
PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
PI Elson G, Gauchat J, Plun-Favreau H, Chevalier S, Gascan H;
DR WPI; 2001-488773/53.
DR P-PSDB; AAG63543.
PT A complex comprising a NNT-1 protein and a CLF-1 and/or SCNTFRalpha
PT protein useful to treat neurodegenerative disease including Parkinson's
PT and Huntington's, obesity and cancer
XX
PS Disclosure; Page 57-58; 67pp; French.
XX
CC The present sequence encodes a human NNT-1 protein. The specification
CC describes a complex comprising a NNT-1 protein and a CLF-1 and/or
CC SCNTFRalpha protein. The NNT-1/CLF-1 complex is used to modulate
CC activity of the SCNTFRalpha/gp130/LiFbeta receptor complex, or to
CC induce phosphorylation of the tyrosine of gp130 and LiFbeta,
CC particularly where cells expressing the receptor complex are in the
CC central or peripheral nervous system, in neurons implicated in
CC neuro-muscular function or in skeletal muscle. The complex or
CC antibodies are also used to decrease the survival, growth or
CC proliferation of tumor cells or to facilitate the proliferation and/or
CC inhibit differentiation of cells stocks. The complex is also used to
CC modulate activity of the gp130/LiFbeta receptor or cells expressing
CC that receptor, particularly those cells implicated in the immune,
CC haematopoietic, nervous or reproductive system, the liver or skeletal
CC muscle. Molecules of the invention may be used to prevent or treat
CC neurodegenerative diseases including amyotrophic lateral sclerosis,
CC Parkinson's and Huntington's disease, to repair or regenerate nervous
CC or muscular tissue or to maintain muscular mass in paralysis patients.
CC They may also be used to treat cancer, obesity and associated diseases,
CC and to improve fertility, particularly to avoid endometriosis and/or
CC assist blastocyst implantation, thrombosis, or retinal disease,
CC particular retinal pigmentosis.
XX
SQ Sequence 881 BP; 158 A; 318 C; 246 G; 159 T; 0 other;

```

```

Query Match 82.3%; Score 674; DB 22; Length 881;
Best Local Similarity 92.2%; Pred. No. 1.4e-159;
Matches 721; Conservative 0; Mismatches 60; Indels 1; Gaps 1;

```

```

QY 2 ATTATTAAGCTTGGCGGAGCGGCGCTGCGCTCCCACTCGGACGCTTGGGAGAG 61
    |||
DB 82 ATTATTAAGCTTGGCGGAGCGGCGCTGCGCTCCCACTCGGACGCTTGGGAGAG 141
QY 62 GAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 121
    |||
DB 142 GAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 200
QY 122 GGAATGTTAGCTTGGCTATGACAGGCTGTGTGGCACTTCCCTGCAAGTGCAGCTTTAAT 181
    |||
DB 201 GGAATGTTAGCTTGGCTATGACAGGCTGTGTGGCACTTCCCTGCAAGTGCAGCTTTAAT 260
QY 182 GCGACAGAGATGACAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 241
    |||
DB 261 GCGACAGAGATGACAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 320
QY 242 CTGAGCATCAACTCCGAGCTTAGCTGAGACTGAATGAATGAATGAATGAATGAATGAAT 301
    |||
DB 321 CTGAGCATCAACTCCGAGCTTAGCTGAGACTGAATGAATGAATGAATGAATGAATGAAT 380
QY 302 AAGAGCTGACTTCAATCTCTGAGCTGGGGGAGAAACTCTGAGGAGGAGGAGGCTC 361
    |||
DB 381 AAGAGCTGACTTCAATCTCTGAGCTGGGGGAGAGAGACTCTGCCAGGAGGAGGAGGCTT 440

```

RESULT 5  
 AAH74484  
 ID AAH74484 standard; DNA; 881 BP.  
 XX  
 AC AAH74484;  
 XX  
 DT 15-OCT-2001 (first entry)  
 XX  
 DE Nucleotide sequence of a human NNT-1 protein.  
 XX  
 KW NNT-1; CLF-1; SCNTFRalpha; nervous system; neuron; nervous system;  
 KW neuro-muscular function; tumour; immune system; haematopoietic system;  
 KW reproductive system; liver; skeletal muscle; neurodegenerative disease;  
 KW amyotrophic lateral sclerosis; Parkinson's disease; Huntington's disease;  
 KW muscular mass; paralysis; cancer; obesity; fertility; endometriosis;  
 KW blastocyst implantation; thrombosis; retinal disease;  
 KW retinal pigmentosis; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 174..851  
 FT /tag= a  
 FT /product= "NNT-1"  
 XX  
 PN WO200155172-A2.  
 XX  
 PD 02-AUG-2001.





CC The present sequence encodes a murine neurotrophic factor, designated  
CC NNT-1, which is capable of stimulating growth of motor or sympathetic  
CC neurons. The NNT-1 protein is useful in the treatment of neurological  
CC diseases characterized by the degeneration and death of particular  
CC classes of neurons. These diseases specifically include Parkinson's  
CC disease, amyotrophic lateral sclerosis (ALS), Alzheimer's disease,  
CC stroke and various degenerative disorders affecting vision.

XX Sequence 819 BP; 156 A; 288 C; 218 G; 157 T; 0 other;

Query Match 100.0%; Score 819; DB 19; Length 819;

Best Local Similarity 100.0%; Pred. No. 5,1e-196;

Matches 819; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 TATTTATTAAGCTTCCCGAGCGCGGCTGCGCTCCCACTCCGCGAGCCTTGGAGAG 60
DB 1 TATTTATTAAGCTTCCCGAGCGCGGCTGCGCTCCCACTCCGCGAGCCTTGGAGAG 60
OY 61 GGAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
DB 61 GGAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
OY 121 GGGGATGTTAGCTTGCCTTATGACAGGCTGCTGTGGCACTTCCCTGCACTGCTTAA 180
DB 121 GGGGATGTTAGCTTGCCTTATGACAGGCTGCTGTGGCACTTCCCTGCACTGCTTAA 180
OY 181 TGGCAGAGAGATCCAGGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
DB 181 TGGCAGAGAGATCCAGGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
OY 241 CCTGGAGCATCACTCCGAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAG 300
DB 241 CCTGGAGCATCACTCCGAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAG 300
OY 301 CAACGAGCTGACTTCAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
DB 301 CAACGAGCTGACTTCAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
OY 361 CAACCTGGAAGTGTGGCGAAGCTCAATGACAGGCTGCGCGCGCGCGCGCGCGCG 420
DB 361 CAACCTGGAAGTGTGGCGAAGCTCAATGACAGGCTGCGCGCGCGCGCGCGCGCG 420
OY 421 GTACAGTCACTCTGTGTACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
DB 421 GTACAGTCACTCTGTGTACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
OY 481 CCGAGCTGAGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540
DB 481 CCGAGCTGAGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540
OY 541 TGTGATGAGGAGCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
DB 541 TGTGATGAGGAGCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
OY 601 GGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660
DB 601 GGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660
OY 661 GGAAGCTGCAAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
DB 661 GGAAGCTGCAAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
OY 721 GGAAGCTGCAAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
DB 721 GGAAGCTGCAAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
OY 781 CCTTAACCCCACTCCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 819
DB 781 CCTTAACCCCACTCCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 819
```

RESULT 3  
AAA39483

```

ID AAA39483 standard; cDNA; 819 BP.
XX
AC AAA39483;
XX
DT 24-AUG-2000 (first entry)
XX
DE Murine NNT-1 cDNA.
XX
XX NNT-1; neurotrophic factor; neuroprotective; treatment;
XX anticonvulsant; antiparkinsonian; antidiabetic; ophthalmological;
XX nervous system degeneration; Alzheimer's disease; Parkinson's disease;
XX amyotrophic lateral sclerosis; Charcot-Marie-Tooth syndrome; murine;
XX Huntington's disease; peripheral neuropathy; neural retina degeneration;
XX retinopathy; immune disorder; hematopoietic disorder; ss.
XX
XX Mus sp.
XX
XX Key Location/Qualifiers
XX CDS 95..772
XX FT /tag= a
XX FT /product= "NNT-1"
XX
XX US6054294-A.
XX
XX 25-APR-2000.
XX
XX 12-DEC-1997; 97US-0988019.
XX
XX 03-FEB-1997; 97US-0792019.
XX
XX (AMGE-) AMGEN INC.
XX
XX Chang M;
XX
XX WPI; 2000-338492/29.
XX
XX P-PSDB; AAY87814.
XX
XX New nucleic acids encoding neurotrophic factors useful for stimulating
XX growth of motor or sympathetic neurons for treating neuron cell damage
XX
XX Claim 2a; Fig 4; 42bp; English.
XX
XX This invention describes a novel nucleic acid molecule (i) encoding a
XX novel neurotrophic factor (NNT-1) (ii) which has neurotrophic,
XX neuroprotective, anticonvulsant, antiparkinsonian, antidiabetic and
XX ophthalmological activity. (I) is useful for producing NNT-1
XX polypeptides which are useful for treating patients in whom various
XX cells of the central, autonomic, or peripheral nervous system have
XX degenerated and/or have been damaged by congenital disease, trauma,
XX mechanical damage, surgery, stroke, ischemia, infection, metabolic
XX disease, nutritional deficiency, malignancy and/or toxic agents. NNT-1
XX proteins are used to treat diseases like Alzheimer's, Parkinson's,
XX amyotrophic lateral sclerosis, Charcot-Marie-Tooth syndrome, Huntington's
XX disease, peripheral neuropathy induced by diabetes or other metabolic
XX disorders, and/or dystrophies or degeneration of the neural retina such
XX as retinitis pigmentosa, drug-induced retinopathies, stationary forms of
XX night blindness, progressive cone-rod degeneration, immune disorders and
XX hematopoietic disorders. (I) is effective in treating neurological
XX conditions and promotes neuron regeneration. Neural functions are
XX effectively restored in patients suffering from various neurological
XX disorders. This sequence encodes the murine NNT-1 protein described in
XX the method of the invention.
XX
XX Sequence 819 BP; 156 A; 288 C; 218 G; 157 T; 0 other;
XX
XX
XX Query Match 100.0%; Score 819; DB 21; Length 819;
XX Best Local Similarity 100.0%; Pred. No. 5,1e-196;
XX Matches 819; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 1 TATTTATTAAGCTTCCCGAGCGCGGCTGCGCTCCCACTCCGCGAGCCTTGGAGAG 60
DB 1 TATTTATTAAGCTTCCCGAGCGCGGCTGCGCTCCCACTCCGCGAGCCTTGGAGAG 60
```



XX 02-FEB-1998; 98WO-US02363.  
 XX  
 XX 30-JAN-1998; 98US-0016534.  
 PR 03-FEB-1997; 97US-0792019.  
 XX  
 XX (AMGE-) AMGEN INC.  
 XX  
 XX Chang M, Elliot GS, Sarmiento U, Senaldi G;  
 XX  
 XX WPI: 1998-437475/37.  
 DR P-PSDB; AAW56142.  
 XX  
 XX Newly isolated nucleic acid encoding human or murine neurotrophic  
 PT factor NNT-1 - useful for treatment of neurological and  
 PT immunological diseases or inflammation, also as vaccine adjuvant  
 XX  
 XX Disclosure; Fig 4; 120p; English.

XX This newly isolated mouse cDNA sequence codes for a novel  
 CC neurotrophic factor, designated NNT-1 (see AAW56142), that is a  
 CC growth factor for neurons and for B or T cells. Vectors and  
 CC host cells are provided for use in the production of murine and  
 CC human NNT-1 polypeptides. These are used to treat: (1) neurological  
 CC or immunological diseases, specifically Alzheimer's, Parkinson's or  
 CC Huntington's diseases, amyotrophic lateral sclerosis, or  
 CC Charcot-Marie-Tooth syndrome, peripheral neuropathy, dystrophy and  
 CC degeneration of the neural retina, or conditions characterized by T  
 CC or B cell defects, e.g. common variable immunodeficiency (CVID),  
 CC selective IgA deficiency, hypogammaglobulinemia and X-linked  
 CC agammaglobulinemia (claimed), but many others disclosed; and (11)  
 CC inflammation. NNT-1 is also able to boost immunoreactivity and  
 CC antibody production following vaccination, and, since it inhibits  
 CC tumour necrosis factor production, it may also be useful for  
 CC treating sepsis. NNT-1 nucleic acid fragments are also used as  
 CC hybridisation probes in diagnostic assays. In addition, cells that  
 CC have been engineered to express NNT-1 can be implanted, or nucleic  
 CC acids are delivered in gene therapy vectors.

XX Sequence 819 BP; 156 A; 288 C; 218 G; 157 T; 0 other;

XX Query Match 100.0%; Score 819; DB 19; Length 819;  
 XX Best Local Similarity 100.0%; Pred. No. 5.1e-156;  
 XX Matches 819; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATTATTAAAGCTTGGCCGAGCCCGGCTGCTCCCACTCCCGCAAGCTCTGGAGA 60  
 DB 1 TATTATTAAAGCTTGGCCGAGCCCGGCTGCTCCCACTCCCGCAAGCTCTGGAGA 60  
 QY 61 GGAGCCGCGCCCGGCGCCGCGCCCGCCAGCCCAAGGAGCGAGAGAGGAGGAGGAG 120  
 DB 61 GGAGCCGCGCCCGGCGCCGCGCCCGCCAGCCCAAGGAGCGAGAGAGGAGGAGGAG 120  
 QY 121 GGGGATGTTAGCTTATGACGCGTGTGAGCACTCCCTGAGAGTGCAGCTCTTAA 180  
 DB 121 GGGGATGTTAGCTTATGACGCGTGTGAGCACTCCCTGAGAGTGCAGCTCTTAA 180  
 QY 121 GGGGATGTTAGCTTATGACGCGTGTGAGCACTCCCTGAGAGTGCAGCTCTTAA 180  
 DB 121 GGGGATGTTAGCTTATGACGCGTGTGAGCACTCCCTGAGAGTGCAGCTCTTAA 180  
 QY 181 TCGCACAGAGATCCAGGCGCTGCGCTCCATCCAGAAAACCTTAGACCTGACCCGCTA 240  
 DB 181 TCGCACAGAGATCCAGGCGCTGCGCTCCATCCAGAAAACCTTAGACCTGACCCGCTA 240  
 QY 191 TCGCACAGAGATCCAGGCGCTGCGCTCCATCCAGAAAACCTTAGACCTGACCCGCTA 240  
 DB 191 TCGCACAGAGATCCAGGCGCTGCGCTCCATCCAGAAAACCTTAGACCTGACCCGCTA 240  
 QY 241 CCTGAGAGATCAATCCGCAAGCTTAGCTGGAGCACTGAACTGAGGAGGAGGAGGAG 300  
 DB 241 CCTGAGAGATCAATCCGCAAGCTTAGCTGGAGCACTGAACTGAGGAGGAGGAGGAG 300  
 QY 301 CAACGAGCTGAGCTTCAATCTCTGAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAG 360  
 DB 301 CAACGAGCTGAGCTTCAATCTCTGAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAG 360  
 QY 361 CAACCTTGAAGTGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420  
 DB 361 CAACCTTGAAGTGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420

QY 421 GTACAGTACCTCTGTTGTTACTTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480  
 DB 421 GTACAGTACCTCTGTTGTTACTTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480  
 QY 481 CCGAGTACCTGAGCCCACTTCTGTACAGGCTTCAGGAGGCTGTGGGAGCACTTGCAGG 540  
 DB 481 CCGAGTACCTGAGCCCACTTCTGTACAGGCTTCAGGAGGCTGTGGGAGCACTTGCAGG 540  
 QY 541 TGTGATGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600  
 DB 541 TGTGATGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600  
 QY 601 GGGCCCTGAGCCCTGAGCCCACTTCTGTACAGGCTTCAGGAGGAGGAGGAGGAGGAG 660  
 DB 601 GGGCCCTGAGCCCTGAGCCCACTTCTGTACAGGCTTCAGGAGGAGGAGGAGGAGGAG 660  
 QY 661 GAGAGCTGAGAGCTTGTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720  
 DB 661 GAGAGCTGAGAGCTTGTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720  
 QY 721 GCAAGCTTCCAGAGCTTCACTGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780  
 DB 721 GCAAGCTTCCAGAGCTTCACTGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780  
 QY 781 CCTTACCCCACTTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840  
 DB 781 CCTTACCCCACTTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840

# RESULT 2

ID AAV22654 standard; cDNA; 819 BP.

AAV22654;

13-JUN-1998 (first entry)

cDNA encoding murine neurotrophic factor NNT-1.

Mouse; neurotrophic factor; NNT-1; growth; motor; sympathetic; neuron;

treatment; neurological disease; degeneration; Parkinson's disease;

amyotrophic lateral sclerosis; ALS; Alzheimer's disease; stroke; 88.

Mus sp.

Key

CDS

sig\_peptide

mat\_peptide

US5741772-A.

21-APR-1998.

03-FEB-1997; 97US-0792019.

03-FEB-1997; 97US-0792019.

(AMGE-) AMGEN INC.

Chang M;

WPI: 1998-260526/23.

P-PSDB; AAW56142.

Neurotrophic factor NNT-1 polypeptide and related nucleic acids -

useful for stimulating growth of motor and sympathetic neurons

Disclosure; Fig 4; 41p; English.



Search completed: February 9, 2004, 09:36:34  
Job time : 381.326 secs

/ TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer  
/ FILE REFERENCE: 44921-5028-WO  
/ CURRENT APPLICATION NUMBER: US/09/880,107.  
/ CURRENT FILING DATE: 2001-06-14  
/ PRIOR APPLICATION NUMBER: US 60/211,379  
/ PRIOR FILING DATE: 2000-06-14  
/ PRIOR APPLICATION NUMBER: US 60/237,054  
/ PRIOR FILING DATE: 2000-10-02  
/ NUMBER OF SEQ ID NOS: 3950  
/ SOFTWARE: Patencin Ver. 2.1  
/ SEQ ID NO 3440  
/ LENGTH: 1578  
/ TYPE: DNA  
/ ORGANISM: Homo sapiens  
/ FEATURE:  
/ OTHER INFORMATION: Genbank Accession No. US20020142981A1 UB2108  
US-09-880-107-3440

Query Match 5.2%; Score 42.4; DB 10; Length 1578;  
Best Local Similarity 52.9%; Pred. No. 0.047;  
Matches 91; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

QY 512 CTCGAGGGCTCTGGGAGCATTTGAGGTGTCATGCGAGCGCTTGCTACCCACTGCC 571  
DB 377 CTCGCGCGGCGGAGCTGACGTGACCGAGAGATGGCCGAGGGCTCCACCGCC 436  
QY 572 CAGCTCTGCCAGGACTGAGCAGCTTGGGCCCCCTGGCCCTCCACAGTACCTTCC 631  
DB 437 CACGACCCCTGGAGAGCCGAGAGCTGAGGAGACACACCGGAGCCACAGCTCCGAA 496  
QY 632 CAGAGATGATGATCTTGTGCTGCTGAAGAGCTGACAGCTGGCTATGGC 683  
DB 497 GCGAAGAGGATGTCAGTGGGCCCCCTGAGGAGAGCTGCGCCCTCGGCTTGGC 548

RESULT 15  
US-10-108-260A-1682  
/ Sequence 1682, Application US/10108260A  
/ Publication No. US20040005560A1  
/ GENERAL INFORMATION:  
/ APPLICANT: HELIX RESEARCH INSTITUTE  
/ TITLE OF INVENTION: No. US20040005560A1 full length cDNA  
/ FILE REFERENCE: H1-A0106  
/ CURRENT APPLICATION NUMBER: US/10/108,260A  
/ CURRENT FILING DATE: 2002-03-27  
/ NUMBER OF SEQ ID NOS: 5458  
/ SOFTWARE: Patencin Ver. 2.1  
/ SEQ ID NO 1682  
/ LENGTH: 2750  
/ TYPE: DNA  
/ ORGANISM: Homo sapiens  
US-10-108-260A-1682

Query Match 5.0%; Score 40.8; DB 12; Length 2750;  
Best Local Similarity 51.8%; Pred. No. 0.14;  
Matches 116; Conservative 0; Mismatches 107; Indels 1; Gaps 1;

QY 19 GAGAGCGGCGCTCGCCCTCCACTCGCCAGCCTTGGAGAGAGAGCCGCCGCCGCG 78  
DB 1285 GAAAGCAGTGAAGCTCCAGGCCCCCACCACACGACCCCTGTCTCCCCACCCCA 1344  
QY 79 CCGGCGCCGAGCCCATGAGCACTCCGAGCGGGGACTGTGGGGATGTAGCTTGCT 138  
DB 1345 ACTGCCCCCACTCTCTGGGATCCCTCATGAGCGCGCTTCTATGGGGTGAAGCA 1404  
QY 139 ATGCAAGGTGCTGTGAGCACTCTCCAGTGC-CAGCTTTATGCAACAGAGATCCAG 197  
DB 1405 GGGCCAGGGGTGGGGGCCCGCGCGAGTGACACACTTCAACGCTCAACCCCGGG 1464  
QY 198 GCGCTGGCCCTTCATCCAGAAACCTTATGACTCACCCGCTAC 241  
DB 1465 TCTGTGCCCCCTGCGACCCAGCCCACTCTCCAGCCAC 1508

NAME/KEY: Site  
LOCATION: (306)  
OTHER INFORMATION: n equals any nucleotide  
FEATURE:  
NAME/KEY: Site  
LOCATION: (360)  
OTHER INFORMATION: n equals any nucleotide  
FEATURE:  
NAME/KEY: Site  
LOCATION: (371)  
OTHER INFORMATION: n equals any nucleotide  
FEATURE:  
NAME/KEY: Site  
LOCATION: (377)  
OTHER INFORMATION: n equals any nucleotide  
FEATURE:  
NAME/KEY: Site  
LOCATION: (383)  
OTHER INFORMATION: n equals any nucleotide  
US-10-212-793-7

Query Match  
Best Local Similarity 6.3%; Score 52; DB 15; Length 396;  
Matches 58; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 716 AGAGTACAGCTTCAGAGCTTCAGTACCTGAGGACAGTGTCTGACCT 775  
DB 4 ACAGGACAGCTTCAGAGCTTCAGTACCTGAGGACAGTGTCTGACCT 63  
QY 776 CTGACCT 783  
DB 64 CTGACCT 71

RESULT 12

US-10-156-761-1403/c  
Sequence 1403, Application US/10156761  
Publication No. US20030119018A1

GENERAL INFORMATION:

APPLICANT: OMURA, SATOSHI  
APPLICANT: IKEDA, HARUO  
APPLICANT: ISHIKAWA, JUN  
APPLICANT: HORIKAWA, HIROSHI  
APPLICANT: SHIBA, TADAYOSHI  
APPLICANT: SAKAKI, YOSHIYUKI  
APPLICANT: HATTORI, MASAHIRA

TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

FILE REFERENCE: 249-262

CURRENT APPLICATION NUMBER: US/10/156,761

CURRENT FILING DATE: 2002-05-29

PRIOR APPLICATION NUMBER: JP 2001-204089

PRIOR FILING DATE: 2001-05-30

PRIOR APPLICATION NUMBER: JP 2001-272697

PRIOR FILING DATE: 2001-08-02

NUMBER OF SEQ ID NOS: 15109

SEQ ID NO 1403

LENGTH: 951

TYPE: DNA

ORGANISM: Streptomyces avermitilis

FEATURE:

NAME/KEY: CDS

LOCATION: (1)..(951)

US-10-156-761-1403

Query Match  
Best Local Similarity 5.6%; Score 46; DB 15; Length 951;  
Matches 103; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

QY 430 CCTCTGTGTTACTTGGCGGCTTCAACCTGACAGCTGCAAGCTGGAAGCTGAGCTG 489  
DB 562 CCTTCAGGCTGAAGCCAGGCGGAGCGTCCGCCGCCAGGCTGTGCTGAGGCTCA 503  
QY 490 CCTGCCACCTTCTGTACAGAGCTTCAGGCGCTGTGCTGAGCAGATTGAGTGTATGSC 549

DB 502 TCTGCCACAGCTTCGCCAGTCCGACGAGGTGCGGTCCGTACTGTCTCGCGTCCA 443  
QY 550 GAGCTTGGCTACCCATGCTCCCGAGCTTCTGACAGGAGTACGAGCTGAGGCTG 609  
DB 442 GAGCATTGTACGCTTCTGCGCCCATCAGGAGCGGTGAGCGAGCTTCCGCTCC 383  
QY 610 CCTGCCACAGTGAATT 627  
DB 382 ACCTACCTGCGCGTCTT 365

RESULT 13

US-10-156-761-1

Sequence 1, Application US/10156761

Publication No. US20030119018A1

GENERAL INFORMATION:

APPLICANT: OMURA, SATOSHI

APPLICANT: IKEDA, HARUO

APPLICANT: ISHIKAWA, JUN

APPLICANT: HORIKAWA, HIROSHI

APPLICANT: SHIBA, TADAYOSHI

APPLICANT: SAKAKI, YOSHIYUKI

APPLICANT: HATTORI, MASAHIRA

TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

FILE REFERENCE: 249-262

CURRENT APPLICATION NUMBER: US/10/156,761

CURRENT FILING DATE: 2002-05-29

PRIOR APPLICATION NUMBER: JP 2001-204089

PRIOR FILING DATE: 2001-05-30

PRIOR APPLICATION NUMBER: JP 2001-272697

PRIOR FILING DATE: 2001-08-02

NUMBER OF SEQ ID NOS: 15109

SEQ ID NO 1

LENGTH: 9025608

TYPE: DNA

ORGANISM: Streptomyces avermitilis

FEATURE:

NAME/KEY: misc feature

LOCATION: (4187715)

OTHER INFORMATION: a, t, c, g, other or unknown

US-10-156-761-1

Query Match  
Best Local Similarity 5.6%; Score 46; DB 15; Length 9025608;  
Matches 103; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

QY 430 CCTCTGTGTTACTTGGCGGCTTCAACCTGACAGCTGCAAGCTGGAAGCTGAGCTG 489  
DB 1746625 CCTTCAGGCTGAAGCCAGGCGGAGCGTCCGCCGCCAGGCTGTGCTGAGGCTCA 1746684  
QY 490 CCTGCCACCTTCTGTACAGAGCTTCAGGCGCTGTGCTGAGCAGATTGAGTGTATGSC 549  
DB 1746685 TCTGCCACAGCTTCGCCAGTCCGAGTGGAGGTGCGTCCGTCTGTGCGGTCA 1746744  
QY 550 GAGCATTGTACGCTTCTGCGCCCATCAGGAGCGGTGAGCGAGCTTCCGCTCC 609  
DB 1746745 GAGCATTGTACGCTTCTGCGCCCATCAGGAGCGGTGAGCGAGCTTCCGCTCC 1746804  
QY 610 CCTGCCACAGTGAATT 627  
DB 1746805 ACCTACCTGCGCGTCTT 365

RESULT 14

US-09-880-107-3440

Sequence 3440, Application US/09880107

Patent No. US20020142981A1

GENERAL INFORMATION:

APPLICANT: Horne, Darci T.

APPLICANT: Vockley, Joseph G.

APPLICANT: Scherf, Uwe

APPLICANT: Gene Logic, Inc.

US-10-027-632-134702

Query Match 19.3% Score 158; DB 13; Length 809;  
Best Local Similarity 88.5%; Pred. No. 7.9e-35;  
Matches 170; Conservative 1; Mismatches 21; Indels 0; Gaps 0;

Qy 100 CCTCCGAGGAGGAGCTCGTGGGGAGTGTAGCTTCCCTTATCCACGCTGTGGACCT 159  
| | | | |  
Db 46 CCTGCCACAGGGAGCTCGTGGGGAGTGTAGCTTCCCTTATCCACGCTGTGGACCT 105  
| | | | |  
Qy 160 CCTTCGAGTGGCAGCTCTTAAATGCGACAGAGATCCAGGCTTGGCCCTTCATCCAGAA 219  
| | | | |  
Db 106 CCTTCGAGTGGCAGCTCTTAAATGCGACAGAGATCCAGGCTTGGCCCTTCATCCAGAA 165  
| | | | |  
Qy 220 AACCTATGACTCACCCTGCTTACCTGGAGCATCACTCGCAGCTTAGTGGAGCTTACT 279  
| | | | |  
Db 166 AACCTATGACTCACCCTGCTTACCTGGAGCATCACTCGCAGCTTAGTGGAGCTTACT 225  
| | | | |  
Qy 280 GAACCTAGCTGGG 291  
| | | | |  
Db 226 GAGTATCCAGCG 237  
| | | | |

RESULT 9  
US-10-027-632-134702  
; Sequence 134702, Application US/10027632  
; GENERAL INFORMATION:

; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; TITLE OF INVENTION: Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; PRIOR FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 134702  
; LENGTH: 809  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-134702

Query Match 19.3% Score 158; DB 14; Length 809;  
Best Local Similarity 88.5%; Pred. No. 7.9e-35;  
Matches 170; Conservative 1; Mismatches 21; Indels 0; Gaps 0;

Qy 100 CCTCCGAGGAGGAGCTCGTGGGGAGTGTAGCTTCCCTTATCCACGCTGTGGACCT 159  
| | | | |  
Db 46 CCTGCCACAGGGAGCTCGTGGGGAGTGTAGCTTCCCTTATCCACGCTGTGGACCT 105  
| | | | |  
Qy 160 CCTTCGAGTGGCAGCTCTTAAATGCGACAGAGATCCAGGCTTGGCCCTTCATCCAGAA 219  
| | | | |  
Db 106 CCTTCGAGTGGCAGCTCTTAAATGCGACAGAGATCCAGGCTTGGCCCTTCATCCAGAA 165  
| | | | |  
Qy 220 AACCTATGACTCACCCTGCTTACCTGGAGCATCACTCGCAGCTTAGTGGAGCTTACT 279  
| | | | |  
Db 166 AACCTATGACTCACCCTGCTTACCTGGAGCATCACTCGCAGCTTAGTGGAGCTTACT 225  
| | | | |  
Qy 280 GAACCTAGCTGGG 291  
| | | | |

Db 226 GAGTATCCAGCG 237

RESULT 10  
US-09-908-975-29446  
; Sequence 29446, Application US/09908975  
; Publication No. US20030165843A1  
; GENERAL INFORMATION:

; APPLICANT: SHOSHAN, Avi  
; APPLICANT: MASSEMAN, Alon  
; APPLICANT: MINTZ, Eli  
; APPLICANT: MINTZ, Liat  
; APPLICANT: FAIGLER, Simchon  
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLIC  
; TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME  
; FILE REFERENCE: 36688-0005  
; CURRENT APPLICATION NUMBER: US/09/908,975  
; PRIOR FILING DATE: 2001-07-20  
; PRIOR APPLICATION NUMBER: US 60/287,724  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: US 60/221,607  
; PRIOR FILING DATE: 2000-07-28  
; NUMBER OF SEQ ID NOS: 32337  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 29446  
; LENGTH: 65  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-09-908-975-29446

Query Match 7.9% Score 65; DB 13; Length 65;  
Best Local Similarity 100.0%; Pred. No. 1.2e-09;  
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 656 CTGAAGAGCTGCGAGACTGCGCTATGCGCTTACGCAAGACTTCAACCGGCTTAAGAAG 715  
| | | | |  
Db 1 CTGAAGAGCTGCGAGACTGCGCTATGCGCTTACGCAAGACTTCAACCGGCTTAAGAAG 60  
| | | | |  
Qy 716 AAGAT 720  
| | | | |  
Db 61 AAGAT 65  
| | | | |

RESULT 11  
US-10-212-793-7  
; Sequence 7, Application US/10212793  
; Publication No. US20030087395A1  
; GENERAL INFORMATION:

; APPLICANT: Shi et al.  
; TITLE OF INVENTION: Cardiotrophin-Like Cytokine  
; FILE REFERENCE: P0385D1C1  
; CURRENT APPLICATION NUMBER: US/10/212,793  
; PRIOR FILING DATE: 2002-08-07  
; PRIOR APPLICATION NUMBER: US 09/438,299  
; PRIOR FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: US 09/106,182  
; PRIOR FILING DATE: 1998-06-29  
; PRIOR APPLICATION NUMBER: US 60/051,311  
; PRIOR FILING DATE: 1997-06-30  
; NUMBER OF SEQ ID NOS: 24  
; SEQ ID NO 7  
; LENGTH: 396  
; TYPE: DNA

; ORGANISM: homo sapiens  
; FEATURE:  
; NAME/KEY: Site  
; LOCATION: (199)  
; OTHER INFORMATION: n equals any nucleotide  
; FEATURE:  
; NAME/KEY: Site  
; LOCATION: (293)  
; OTHER INFORMATION: n equals any nucleotide  
; FEATURE:









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QY 1 TATTATTAAGCTTGGCCGAGCCGCGCTGCTCCCTCCCACTCCGCGAGCTCTGGAGAG 60
DB 1 TATTATTAAGCTTGGCCGAGCCGCGCTGCTCCCTCCCACTCCGCGAGCTCTGGAGAG 60
QY 61 GGAGCCGCGCCGCGCCGCGCCGCGCCGCGCCGCGCCGCGCCGCGCCGCGCCGCGCCGCG 120
DB 61 GGAGCCGCGCCGCGCCGCGCCGCGCCGCGCCGCGCCGCGCCGCGCCGCGCCGCGCCGCG 120
QY 121 GGGGATGTTAGCTTGGCTTGAAGGCTGTGGCACTTCCCTGCGAGTGGCACTTGA 180
DB 121 GGGGATGTTAGCTTGGCTTGAAGGCTGTGGCACTTCCCTGCGAGTGGCACTTGA 180
QY 181 TGGCAGAGAGATCCAGAGCCCTGCGCCCTCCATCCGAGAAACCTTATGACCTACCGGCTA 240
DB 181 TGGCAGAGAGATCCAGAGCCCTGCGCCCTCCATCCGAGAAACCTTATGACCTACCGGCTA 240
QY 241 CTTGAGAGCTCAACTCCGAGCTTAGCTGGAGCTTACCTGAACTACCTGGGGCCCTTTT 300
DB 241 CTTGAGAGCTCAACTCCGAGCTTAGCTGGAGCTTACCTGAACTACCTGGGGCCCTTTT 300
QY 301 CAACGAGCTGACTTCAATCTCTCTGAGTGGGGGCGAGAACTTGGCCGAGGCGCAAGGT 360
DB 301 CAACGAGCTGACTTCAATCTCTCTGAGTGGGGGCGAGAACTTGGCCGAGGCGCAAGGT 360
QY 361 CAACCTTGGAGTGTGGCGAGAGCTCAATGACAGGCTGCGGCTGAGCCGAGAACTTGAAGGC 420
DB 361 CAACCTTGGAGTGTGGCGAGAGCTCAATGACAGGCTGCGGCTGAGCCGAGAACTTGAAGGC 420
QY 421 GTACAGTCACTCTGTGTATTACTTGGGTGGCTCAACCGTCAAGGCTGCGACAGCTGAAGT 480
DB 421 GTACAGTCACTCTGTGTATTACTTGGGTGGCTCAACCGTCAAGGCTGCGACAGCTGAAGT 480
QY 481 CCGAGCTGAGCTTGGCCCACTTCTGTAACAGCTCCAGGGCTGCTGGGGAGATTTGACAG 540
DB 481 CCGAGCTGAGCTTGGCCCACTTCTGTAACAGCTCCAGGGCTGCTGGGGAGATTTGACAG 540
QY 541 TGTCAATGGGAGCTTGGCTTACCACTGCGCCGAGCTCTGCGAGGAGATTTGACAGCTG 600
DB 541 TGTCAATGGGAGCTTGGCTTACCACTGCGCCGAGCTCTGCGAGGAGATTTGACAGCTG 600
QY 601 GGGCCCTGGCCCTGCGCCAGAGTACTTCTCCAGAAATGATGACTTGTGCTGCTGA 660
DB 601 GGGCCCTGGCCCTGCGCCAGAGTACTTCTCCAGAAATGATGACTTGTGCTGCTGA 660
QY 661 GAGAGCTGAGAGCTTGGCTTACCACTGCGCCGAGCTTCAACCGGCTTGAAGAAAT 720
DB 661 GAGAGCTGAGAGCTTGGCTTACCACTGCGCCGAGCTTCAACCGGCTTGAAGAAAT 720
QY 721 GAGAGCTGAGAGCTTGGCTTACCACTGCGCCGAGCTTCAACCGGCTTGAAGAAAT 780
DB 721 GAGAGCTGAGAGCTTGGCTTACCACTGCGCCGAGCTTCAACCGGCTTGAAGAAAT 780
QY 781 CTTAATCCCGCCACACTTCCAGGCGCGAGTCAAGCTTGTGCTT 819
DB 781 CTTAATCCCGCCACACTTCCAGGCGCGAGTCAAGCTTGTGCTT 819
RESULT 2
US-09-931-704-1
; Sequence 1, Application US/09311704
; Patent No. US20020041873A1
; GENERAL INFORMATION:
; APPLICANT: Senaldi, Giorgio
; TITLE OF INVENTION: Method and Compositions for Treating IGF-Related Disease Using N
; FILE REFERENCE: A-695
; CURRENT APPLICATION NUMBER: US/09/931,704
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: US 60/226,436
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
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LENGTH: 797
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (90)..(764)
OTHER INFORMATION:
NAME/KEY: mat peptide
LOCATION: (171)..()
OTHER INFORMATION: Met at -27
US-09-931-704-1

Query Match 81.7% Score 669.4; DB 9; Length 797;
Best Local Similarity 92.0%; Pred. No. 1.2e-179;
Matches 717; Conservative 0; Mismatches 61; Indels 1; Gaps 1;

QY 5 ATTAAAGCTTGGCCGAGCCGCGCTGCTCCCTCCCACTCCGCGAGCTCTGGAGAGAG 64
DB 1 ATTAAAGCTTGGCCGAGCCGCGCTGCTCCCTCCCACTCCGCGAGCTCTGGAGAGAGAG 60
QY 65 CCGGCGCCGCGCCGCGCCGCGCCGCGCCGCGCCGCGCCGCGCCGCGCCGCGCCGCG 124
DB 61 CCGGCGCCGCGCCGCGCCGCGCCGCGCCGCGCCGCGCCGCGCCGCGCCGCGCCGCG 119
QY 125 ATGTTAGCTTGGCTTGAAGGCTGTGGCACTTCCCTGCGAGTGGCACTTGAATGGC 184
DB 120 ATGTTAGCTTGGCTTGAAGGCTGTGGCACTTCCCTGCGAGTGGCACTTGAATGGC 179
QY 185 ACAGAGAGATCCAGAGCCCTGCGCCCTCCATCCAGAAACCTTATGACCTACCGGCTA 244
DB 180 ACAGAGAGATCCAGAGCCCTGCGCCCTCCATCCAGAAACCTTATGACCTACCGGCTA 239
QY 245 GAGCATCACTCCGAGCTTAGCTGGAGCTTAACTTGAAGCTTGGGGCCCTTTTCAAC 304
DB 240 GAGCATCACTCCGAGCTTAGCTGGAGCTTAACTTGAAGCTTGGGGCCCTTTTCAAC 299
QY 305 GAGCTGACTTCAATCCCTCCCTGCGAGCTGGGGGCGAGAACTTGGCCGAGGCGCAAGTCAAC 364
DB 300 GAGCTGACTTCAATCCCTCCCTGCGAGCTGGGGGCGAGAACTTGGCCGAGGCGCAAGTCAAC 359
QY 365 TTGGAAGTGTGGCGAGAGCTTCAATGACAGGCTGCGGCTGAGCCAGAACTATGAGGCGTAC 424
DB 360 TTGGAAGTGTGGCGAGAGCTTCAATGACAGGCTGCGGCTGAGCCAGAACTATGAGGCGTAC 419
QY 425 AGTCACTCTCTGTGTACTTGGCTTCAACCGTCAAGGCTGCGCACTTGAATCCGA 484
DB 420 AGTCACTCTCTGTGTACTTGGCTTCAACCGTCAAGGCTGCGCACTTGAATCCGA 479
QY 485 GGTAGCTTGGCCCACTTCTGTAACAGGCTTCCAGGGGCTGCGGAGAGATTTGACAGTGTG 544
DB 480 GGTAGCTTGGCCCACTTCTGTAACAGGCTTCCAGGGGCTGCGGAGAGATTTGACAGTGTG 539
QY 545 ATGCGAGAGCTTGGCTTACCACTGCGCCGAGCTTGGCGAGGAGCTGAGCCGAGCTGAGCC 604
DB 540 ATGCGAGAGCTTGGCTTACCACTGCGCCGAGCTTGGCGAGGAGCTGAGCCGAGCTGAGCC 599
QY 605 CTTGCGCTTCCCAAGTACTTCTTCCAGAAATGATGACTTGTGCTGCTTGAAGAGAG 664
DB 600 CTTGCGCTTCCCAAGTACTTCTTCCAGAAATGATGACTTGTGCTGCTTGAAGAGAG 659
QY 665 CTTGAGAGCTTGGCTTGAAGGCTTGAAGGAGCTTGAAGGAGCTTGAAGGAGCTTGAAGGAG 724
DB 660 CTTGAGAGCTTGGCTTGAAGGCTTGAAGGAGCTTGAAGGAGCTTGAAGGAGCTTGAAGGAG 719
QY 725 CTTGAGAGCTTGAAGGAGCTTGAAGGAGCTTGAAGGAGCTTGAAGGAGCTTGAAGGAGCT 783
DB 720 CTTGAGAGCTTGAAGGAGCTTGAAGGAGCTTGAAGGAGCTTGAAGGAGCTTGAAGGAGCT 778
RESULT 3
US-10-212-793-1
; Sequence 1, Application US/10212793
; Publication No. US20030087395A1
```



APPLICANT: Seedorf, Klaus  
APPLICANT: Ullrich, Axel  
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT  
TITLE OF INVENTION: OF TKA-1 RELATED  
TITLE OF INVENTION: DISORDERS  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/665,037  
FILING DATE: June 13, 1996  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/005,167  
FILING DATE: October 13, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 220/156  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1642 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Coding Sequence  
LOCATION: 97...1446  
US-08-665-037-1

Query Match 5.2%; Score 42.4; DB 2; Length 1642;  
Best Local Similarity 52.9%; Pred. No. 0.057;  
Matches 91; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

QY 512 CTCGAGGCGCTCTGGGAGCATGTGAGGTGTCATGGCGACCGCTTGAGTACCCACTGCGCC 571  
DB 379 CTCGCGCGGCGGAGCTGATCGGAGAGATGGCCAGCGGCGCTCCACCGCGCC 438  
QY 572 CAGCCTCTGCCAGGAGCTGAGCGAGCGCTGGCCCTGGCCGACAGTGAATTCTTC 631  
DB 439 CACGACCCCTGGAGGCCGAGGACCACTGGGACACACACCGGACGACGCTCCGAGCT 498  
QY 632 CAGAGAGATGATGATCTTGTGCTGCTGAGAGAGCTGACAGCTTGAGTATGCG 683  
DB 499 GGCAAGAGATGTGATGTGGGCGCCCTGAGGAGAGCTCGGCTGCGCTGCGC 550

RESULT 15  
US-08-666-067-1  
Sequence 1, Application US/08666067  
GENERAL INFORMATION:  
APPLICANT: Seedorf, Klaus  
APPLICANT: Ullrich, Axel  
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT  
TITLE OF INVENTION: OF TKA-1 RELATED  
TITLE OF INVENTION: DISORDERS

NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/666,067  
FILING DATE: June 13, 1996  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/005,421  
FILING DATE: October 13, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 220/157  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1642 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Coding Sequence  
LOCATION: 97...1446  
US-08-666-067-1

Query Match 5.2%; Score 42.4; DB 2; Length 1642;  
Best Local Similarity 52.9%; Pred. No. 0.057;  
Matches 91; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

QY 512 CTCGAGGCGCTCTGGGAGCATGTGAGGTGTCATGGCGAGCGCTTGACTACCCACTGCGCC 571  
DB 379 CTCGCGCGGCGGAGCTGATCGGAGAGATGGCCAGCGGCGCTCCACCGCGCC 438  
QY 572 CAGCCTCTGCCAGGAGCTGAGCGAGCGCTGGCCCTGGCCGACAGTGAATTCTTC 631  
DB 439 CACGACCCCTGGAGGCCGAGGACCACTGGGACACACACCGGACGACGCTCCGAGCT 498  
QY 632 CAGAGAGATGATGATCTTGTGCTGCTGAGAGAGCTGACAGCTTGAGTATGCG 683  
DB 499 GGCAAGAGATGTGATGTGGGCGCCCTGAGGAGAGCTCGGCTGCGCTGCGC 550

Search completed: February 9, 2004, 06:13:16  
Job time : 79.8985 secs



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RESULT 10
US-09-016-534-3
; Sequence 3, Application US/09016534
; Patent No. 6143874
; GENERAL INFORMATION:
; APPLICANT: CHANG, MING-SHI
; APPLICANT: ELLIOTT, GARY S.
; APPLICANT: SARMIENTO, ULLA
; APPLICANT: SEMALDI, GIORGIO
; TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC.
; STREET: ONE AMGEN CENTER
; CITY: THOUSAND OAKS
; STATE: CA
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,534
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/792,019
; FILING DATE: 03-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: COOK, ROBERT R.
; REGISTRATION NUMBER: 31,602
; REFERENCE/DOCKET NUMBER: A-442B
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5087 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 137_138 /Producte "INTERVENING UNSEQUENCED
; OTHER INFORMATION: REGION OF >1KB"
; US-09-016-534-3
Query Match 52.5%; Score 429.6; DB 3; Length 5087;
Best Local Similarity 90.4%; Pred. No. 2,8e-103;
Matches 459; Conservative 0; Mismatches 49; Indels 0; Gaps 0;
QY 276 ACTGTAACCTCTGAGGAGCCCTTTCAAGAGCCGTAATCTCTCGACTGGGGG 335
DB 3363 AGGTGAACCTCTGAGGAGCCCTTTCAAGAGCCGTAATCTCTCGACTGGGGG 3422
QY 336 CAGAACTCTGAGGAGCCCTTTCAAGAGCCGTAATCTCTCGACTGGGGG 395
DB 3423 CAGAACTCTGAGGAGCCCTTTCAAGAGCCGTAATCTCTCGACTGGGGG 3482
QY 396 TGGGCTGACCCAGAACTATGAGGAGCTACGCTCTGTTACTTGGGCTGCA 455
DB 3463 TGGGCTGACCCAGAACTATGAGGAGCTACGCTCTGTTACTTGGGCTGCA 3542
QY 456 ACCGTGAGCTGCAAGCTGCAAGCTGCAAGCTGCAAGCTGCAAGCTGCA 515
DB 3543 ACCGTGAGCTGCAAGCTGCAAGCTGCAAGCTGCAAGCTGCAAGCTGCA 3602
QY 516 AGGGCTGCTGGGCGAGCTTGCAGGTGCTATGAGGAGCTTGGCTACCACTGCCCAGC 575
DB 3603 AGGGCTGCTGGGCGAGCTTGCAGGTGCTATGAGGAGCTTGGCTACCACTGCCCAGC 3662
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QY 576 CTGTCCAGGAGCTAGAGCAGAGCTGAGGAGCCCTGAGCCCTGACAGAGTACTTCTCCAGA 635
DB 3663 CGTGGCTGGAGACTGAAACCACTTGAGACTCTTGAGCCCTGACAGAGTACTTCTCCAGA 3722
QY 636 AGATGATGACTTCTGAGCTGAGAGAGCTGAGAGCTGAGAGCTTATGAGGCTTACAGCAAG 695
DB 3723 AGATGAGAGACTTCTGAGCTGAGAGAGCTGAGAGCTGAGAGCTGAGGCTGAGGCTGAGCAAG 3782
QY 696 ACTTCAACCGGCTTAAGAAAGAGTGAAGAGCTTCAAGAGCTTCAAGTCAAGCTGACCTTGG 755
DB 3783 ACTTCAACCGGCTTAAGAAAGAGTGAAGAGCTTCAAGAGCTTCAAGTCAAGCTGACCTTGG 3842
QY 756 AGGACATGAGTTTCTGAGCTTGAACCTT 783
DB 3843 GGGCTCATGGCTTCTGAGCTTGAACCTT 3870
RESULT 11
US-09-106-182-7
; Sequence 7, Application US/09106182
; Patent No. 6046035
; GENERAL INFORMATION:
; APPLICANT: Shi, Yangu
; APPLICANT: Ruben, Steve
; TITLE OF INVENTION: Cardiotrophin-Like Cytokine
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc
; STREET: 9410 Key West Ave
; CITY: Rockville
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/106,182
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/051,053
; FILING DATE: 30-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF385
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 396 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-09-106-182-7
Query Match 6.3%; Score 52; DB 3; Length 396;
Best Local Similarity 85.3%; Pred. No. 0.00011;
Matches 58; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 716 AAGATGAGCTTCCAGAGCTTCAAGTCAAGCTTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 775
DB 4 AAGATGAGCTTCCAGAGCTTCAAGTCAAGCTTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 63
QY 776 CTGACCTT 783
DB 64 CTGACCTT 71
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QY 605 CTTGGCCCTGCCCCACAGTACTTCTCCAGAAATGATGACTTGTGGCTGTGAAGAG 664  
DB 600 CTTGGCCCTGCCCCACAGTACTTCTCCAGAAATGATGACTTGTGGCTGTGAAGAG 659  
QY 665 CTGCAAGACTTGGCTTATGCGCTTACGCAAGACTTCAACCGCTTAAAGAAATGACAG 724  
DB 660 CTGCAAGACTTGGCTTATGCGCTTACGCAAGACTTCAACCGCTTAAAGAAATGACAG 719  
QY 725 CTTCAAGCACTTCACTGACCTTGTGAGGCAATGTTTCTGACTTGTGACCTT 783  
DB 720 CTTCAAGCACTTCACTGACCTTGTGAGGCAATGTTTCTGACTTGTGACCTT 778

RESULT 7  
US-09-106-182-1  
Sequence 1, Application US/09106182  
Patent No. 6046035  
GENERAL INFORMATION:  
APPLICANT: Shi, Yangu  
APPLICANT: Ruben, Steve  
TITLE OF INVENTION: Cardiotrophin-Like Cytokine  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc  
STREET: 9410 Key West Ave  
CITY: Rockville  
STATE: MD  
COUNTRY: US  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/106,182  
FILING DATE: Herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/051,053  
FILING DATE: 30-JUN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Brookes, A. Anders  
REGISTRATION NUMBER: 36,373  
TELEPHONE: 301-309-8504  
TELEFAX: 301-309-8504  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1710 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 46..720  
FEATURE:  
NAME/KEY: sig\_peptide  
LOCATION: 46..126  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 127..720  
US-09-106-182-1

Query Match 76.6%; Score 627; DB 3; Length 1710;  
Best Local Similarity 91.7%; Pred. No. 3.8e-155;  
Matches 674; Conservative 0; Mismatches 60; Indels 1; Gaps 1;  
QY 49 GCCTCTGGAGAGAGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCAGCCCTCGAC 108  
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DB 1 GCCTCCGGAGAGAGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCAGCCCTCGAC 59  
QY 109 AGGGGACTGATGGGGGATGTTAGCTTGTGACAGGCTGTGACAGCTCCCTGACGT 168  
DB 60 AGGGGACTGATGGGGGATGTTAGCTTGTGACAGGCTGTGACAGCTCCCTGACGT 119  
QY 169 GCCAGCTTATATGACAGAGATTCAGAGCCCTGAGCCCTTCATCCAGAAACCTATGA 228  
DB 120 GCCAGCTTATATGACAGAGATTCAGAGCCCTGAGCCCTTCATCCAGAAACCTATGA 179  
QY 229 CTTACCCGCTACTGAGACATCACTCCGACCTTGTGAGTGTGACCTGACCT 288  
DB 180 CTTACCCGCTACTGAGACATCACTCCGACCTTGTGAGTGTGACCTGACCT 239  
QY 289 GGGGCCCCCTTCAACGAGCTGACTTCAATCTCTGCTGATGAGGGGGAGAACTCTGCC 348  
DB 240 GGGGCCCCCTTCAACGAGCTGACTTCAATCTCTGCTGATGAGGGGGAGAACTCTGCC 299  
QY 349 CAGGCGCAAGCTCACTTGAAGTGTGCGAAGCTCAATGACAGGCTGCGGCTGACCA 408  
DB 300 CAGGCGCAAGCTTGTGACTTGAAGTGTGCGAAGCTCAATGACAGGCTGCGGCTGACCA 359  
QY 409 GAATATAGAGCGTACAGTCACTCTGTGTACTTGTGCTGCTGCTCAACCTGAGCTGC 468  
DB 360 GAATATAGAGCGTACAGTCACTCTGTGTACTTGTGCTGCTGCTCAACCTGAGCTGC 419  
QY 469 CACAGCTGAACTCCGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 528  
DB 420 CACTGTGAGTGTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 479  
QY 529 CAGATTCAGAGTGTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 588  
DB 480 CAGATTCAGAGTGTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 539  
QY 589 TGAGCAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 648  
DB 540 TGAGCAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 599  
QY 649 CTGCTGTGAAAGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 708  
DB 600 CTGCTGTGAAAGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 659  
QY 709 TAAAGAAAGATGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 768  
DB 660 TAAAGAAAGATGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 719  
QY 769 CTGACTTGTGACCTT 783  
DB 720 CTGACTTGTGACCTT 734

RESULT 8  
US-08-792-019B-3  
Sequence 3, Application US/08792019B  
Patent No. 5741772  
GENERAL INFORMATION:  
APPLICANT: CHANG, MING-SHI  
TITLE OF INVENTION: THE NEUROTROPIC FACTOR NNT-1  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: AMGEN INC.  
STREET: 1840 DEHAVILLAND DRIVE  
CITY: THOUSAND OAKS  
STATE: CA  
COUNTRY: USA  
ZIP: 91320  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/792,019B





STATE: CA  
COUNTRY: USA  
ZIP: 91320  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/792,019B  
FILING DATE: 03-FEB-1997  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: COOK, ROBERT R.  
REGISTRATION NUMBER: 31,602  
REFERENCE/DOCKET NUMBER: A-442  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 797 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 90..764  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 171..764  
FEATURE:  
NAME/KEY: sig\_peptide  
LOCATION: 90..170  
US-08-792-019B-1

Query Match 81.7%; Score 669.4; DB 1; Length 797;  
Best Local Similarity 92.0%; Pred. No. 2.4e-166;  
Matches 717; Conservative 0; Mismatches 61; Indels 1; Gaps 1;

QY 5 ATTAAGCTTCCCGGAGCGCGCTCGCTCCCACTCCGACCTCTTGGAAGAG 64  
DB 1 ATTAAGCTTCCCGGAGCGCGCTCGCTCCCACTCCGACCTCTTGGAAGAG 60  
QY 65 CCGGCG 124  
DB 61 CCGGCG 119  
QY 125 ATGTTAGCTTGGCTATGACGGTGTGTGTGCACTTCCCTGCACTGCACTTATGCG 184  
DB 120 ATGTTAGCTTGGCTATGACGGTGTGTGTGCACTTCCCTGCACTGCACTTATGCG 179  
QY 185 ACAAGAGATCCAGGCGCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 244  
DB 180 ACAAGAGATCCAGGCGCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 239  
QY 245 GAGCATCAACTCCGAGCTTGTAGCTGAGACTGAGACTGAGACTGAGACTGAGACT 304  
DB 240 GAGCATCAACTCCGAGCTTGTAGCTGAGACTGAGACTGAGACTGAGACTGAGACT 299  
QY 305 GAGCGTGAATTCCTCTCTGACTGAGGAGGAGAACTGTGCGGAGGAGGAGGAGG 364  
DB 300 GAGCGTGAATTCCTCTCTGACTGAGGAGGAGAACTGTGCGGAGGAGGAGGAGG 359  
QY 365 TTGGAAGTGTGGGAGGAGCTCAATGACAGGCTGCGGCTGACCCAGAACTATGAGGCT 424  
DB 360 TTGGAAGTGTGGGAGGAGCTCAATGACAGGCTGCGGCTGACCCAGAACTATGAGGCT 419  
QY 425 AGTCACTCTCTGTTACTTGTGCTGCTCAACCGTCAAGGCTGAGCACTGCACTGCA 484  
DB 420 AGTCACTCTCTGTTACTTGTGCTGCTCAACCGTCAAGGCTGAGCACTGCACTGCA 479  
QY 485 CGTAGCTGCGCACTTCTGTATCAAGCTTCAAGGCGCTGTGCGGAGCACTGCACTG 544  
DB 480 CGTAGCTGCGCACTTCTGTATCAAGCTTCAAGGCGCTGTGCGGAGCACTGCACTG 539

QY 545 ATGGGACGCTTGGGCTACCCAGCTGCGCCAGCGCTGCGCGGAGGAGGAGGAGGAGG 604  
DB 540 ATGGGACGCTTGGGCTACCCAGCTGCGCCAGCGCTGCGCGGAGGAGGAGGAGGAGG 599  
QY 605 CTTGCGCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 664  
DB 600 CTTGCGCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 659  
QY 665 CTGCAAGCTTGGCTATGAGGCTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 724  
DB 660 CTGCAAGCTTGGCTATGAGGCTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 719  
QY 725 CTTGCAAGCTTGGCTATGAGGCTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 783  
DB 720 CTTGCAAGCTTGGCTATGAGGCTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 778

RESULT 5  
US-08-988-819-1  
Sequence 1, Application US/08988819  
Patent No. 6054294

GENERAL INFORMATION:  
APPLICANT: CHANG, MING-SHI  
TITLE OF INVENTION: NEUTROTROPHIC FACTOR NNT-1  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: AMGEN INC.  
STREET: ONE AMGEN CENTER DRIVE  
CITY: THOUSAND OAKS  
STATE: CA  
COUNTRY: USA  
ZIP: 91320

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/988,819  
FILING DATE: 12-DEC-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/792,019  
FILING DATE: 03-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: COOK, ROBERT R.  
REGISTRATION NUMBER: 31,602  
REFERENCE/DOCKET NUMBER: A-442A  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 797 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA

FEATURE:  
NAME/KEY: CDS  
LOCATION: 90..764  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 171..764  
FEATURE:  
NAME/KEY: sig\_peptide  
LOCATION: 90..170  
US-08-988-819-1

Query Match 81.7%; Score 669.4; DB 3; Length 797;  
Best Local Similarity 92.0%; Pred. No. 2.4e-166;  
Matches 717; Conservative 0; Mismatches 61; Indels 1; Gaps 1;  
QY 5 ATTAAGCTTCCCGGAGCGCGCTCGCTCCCACTCCGACCTCTTGGAAGAG 64

QY 541 TGTGATGGGAGCGCTTGGTACCTGACCTGCCCCAGCCTTGCCAGGAGCATGAGCCAGCTTG 600  
Db 541 TGTGATGGGAGCGCTTGGTACCTGACCTGCCCCAGCCTTGCCAGGAGCATGAGCCAGCTTG 600  
QY 601 GGGCCCTGGCCCTGCCCCAGGATGATCTTCTCCGAAAGATGATGATCTTGGCTGCTGAA 660  
Db 601 GGGCCCTGGCCCTGCCCCAGGATGATCTTCTCCGAAAGATGATGATCTTGGCTGCTGAA 660  
QY 661 GGAGCTGAGAGCTGCTATGAGCTTCAAGCCAGGAGCTTCAACCGGCTTAAGAAAGAT 720  
Db 661 GGAGCTGAGAGCTGCTATGAGCTTCAAGCCAGGAGCTTCAACCGGCTTAAGAAAGAT 720  
QY 721 GGAGCTTCAAGAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAG 780  
Db 721 GGAGCTTCAAGAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAG 780  
QY 781 CCTTAACCCCAACCTTCAAGCCAGGAGCTTCAAGCTTCAAGCTTCAAGCTTCAAG 819  
Db 781 CCTTAACCCCAACCTTCAAGCCAGGAGCTTCAAGCTTCAAGCTTCAAGCTTCAAG 819

RESULT 3  
US-09-016-534-4

; Sequence 4, Application US/09016534

; Patent No. 613874

; GENERAL INFORMATION:

; APPLICANT: CHANG, MING-SHI

; APPLICANT: ELLIOTT, GARY S.

; APPLICANT: SARMIENTO, ULLA

; APPLICANT: SENALDI, GIORGIO

; TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1

; NUMBER OF SEQUENCES: 16

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: AMGEN INC.

; STREET: ONE AMGEN CENTER

; CITY: THOUSAND OAKS

; STATE: CA

; COUNTRY: USA

; ZIP: 91320

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/016,534

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/792,019

; FILING DATE: 03-FEB-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: COOK, ROBERT R.

; REGISTRATION NUMBER: 31,602

; REFERENCE/DOCKET NUMBER: A-442B

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 819 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 95..769

; FEATURE:

; NAME/KEY: mat\_peptide

; LOCATION: 176..769

; FEATURE:

; NAME/KEY: sig\_peptide

; LOCATION: 95..175

; US-09-016-534-4

Query Match 100.0%; Score 819; DB 3; Length 819;  
Best Local Similarity 100.0%; Pred. No. 1.5e-205;  
Matches 819; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATTTATTAAGCTTGGCCGAGCCGCGGCTGCGCTTCCCACTCCGACCTCTGGGAGA 60  
Db 1 TATTTATTAAGCTTGGCCGAGCCGCGGCTGCGCTTCCCACTCCGACCTCTGGGAGA 60  
QY 61 GGAAGCGGCG 120  
Db 61 GGAAGCGGCG 120  
QY 121 GGGAGATGTTAGCTTGGCTTATGACAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 180  
Db 121 GGGAGATGTTAGCTTGGCTTATGACAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 180  
QY 181 TGGCAGAGAGATTCAGAGCCCTGCGCCCTTCATTCAGAAACCTTATGACCTTACCCGCTA 240  
Db 181 TGGCAGAGAGATTCAGAGCCCTGCGCCCTTCATTCAGAAACCTTATGACCTTACCCGCTA 240  
QY 241 CCTGAGAGATTCAGAGCCCTGCGCCCTTCATTCAGAGAGCTTATGACCTTATGACCTTATG 300  
Db 241 CCTGAGAGATTCAGAGCCCTGCGCCCTTCATTCAGAGAGCTTATGACCTTATGACCTTATG 300  
QY 301 CAACGAGCTGACTTCAATCTCTCTGACTGAGGAGGAGAACTTGTGCCAGGAGGAGAGCT 360  
Db 301 CAACGAGCTGACTTCAATCTCTCTGACTGAGGAGGAGAACTTGTGCCAGGAGGAGAGCT 360  
QY 361 CAACCTTGAAGT 420  
Db 361 CAACCTTGAAGT 420  
QY 421 GTTACGATCACTCTCTGT 480  
Db 421 GTTACGATCACTCTCTGT 480  
QY 481 CCGAGCTAGCTTGGCCCACTTCTGTACCAAGCTTCCAGGAGGCTGTGTGTGTGTGTGTGT 540  
Db 481 CCGAGCTAGCTTGGCCCACTTCTGTACCAAGCTTCCAGGAGGCTGTGTGTGTGTGTGTGT 540  
QY 541 TGTGATGGGAGCGCTTGGTACCTGACCTGCCCCAGCCTTGCCAGGAGCATGAGCCAGCTTG 600  
Db 541 TGTGATGGGAGCGCTTGGTACCTGACCTGCCCCAGCCTTGCCAGGAGCATGAGCCAGCTTG 600  
QY 601 GGGCCCTGGCCCTGCCCCAGGATGATCTTCTCCGAAAGATGATGATCTTGGCTGCTGAA 660  
Db 601 GGGCCCTGGCCCTGCCCCAGGATGATCTTCTCCGAAAGATGATGATCTTGGCTGCTGAA 660  
QY 661 GGAGCTGAGAGCTGCTATGAGCTTCAAGCCAGGAGCTTCAACCGGCTTAAGAAAGAT 720  
Db 661 GGAGCTGAGAGCTGCTATGAGCTTCAAGCCAGGAGCTTCAACCGGCTTAAGAAAGAT 720  
QY 721 GGAGCTTCAAGAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAG 780  
Db 721 GGAGCTTCAAGAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAG 780  
QY 781 CCTTAACCCCAACCTTCAAGCCAGGAGCTTCAAGCTTCAAGCTTCAAGCTTCAAG 819  
Db 781 CCTTAACCCCAACCTTCAAGCCAGGAGCTTCAAGCTTCAAGCTTCAAGCTTCAAG 819

## RESULT 4

US-08-792-019B-1

; Sequence 1, Application US/08792019B

; Patent No. 5741772

; GENERAL INFORMATION:

; APPLICANT: CHANG, MING-SHI

; TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1

; NUMBER OF SEQUENCES: 16

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: AMGEN INC.

; STREET: 1840 DEHAVILLAND DRIVE

; CITY: THOUSAND OAKS

1 TATTATTAAAGCTTGGCCGAGAGCCGAGGCTGCTCCCACTCCGCGCAGAGCTCTGGAGAGA 60  
1 TATTATTAAAGCTTGGCCGAGAGCCGAGGCTGCTCCCACTCCGCGCAGAGCTCTGGAGAGA 60  
61 GAGAGCCGCGCCGCGCGCCGCGCCGCGCCGCGCCGCGCCGCGCCGCGCCGCGCCGCGCCGCG 120  
61 GAGAGCCGCGCCGCGCGCCGCGCCGCGCCGCGCCGCGCCGCGCCGCGCCGCGCCGCGCCGCG 120  
121 GGGGATGTTAGCTTGGCTATGCAAGGCTGCTGAGCACTCTCCCTGAGAGGCTCTTAA 180  
121 GGGGATGTTAGCTTGGCTATGCAAGGCTGCTGAGCACTCTCCCTGAGAGGCTCTTAA 180  
181 TCGCAGAGAGATCCAGAGCCCTGCGCCCTCCATCCAGAAAACCTATGACCTTACCCGCTA 240  
181 TCGCAGAGAGATCCAGAGCCCTGCGCCCTCCATCCAGAAAACCTATGACCTTACCCGCTA 240  
241 CTGAGAGATCAATCCGAGAGCTTGAAGCTGAGCACTTACCTGAACTAAGGAGGAGGAGGAGG 300  
241 CTGAGAGATCAATCCGAGAGCTTGAAGCTGAGCACTTACCTGAACTAAGGAGGAGGAGGAGG 300  
301 CAACGAGCTGACCTTCAATCTCTGCTGAGCTGGGGGAGAAAATCTGCGCCAGGAGGAGGAGG 360  
301 CAACGAGCTGACCTTCAATCTCTGCTGAGCTGGGGGAGAAAATCTGCGCCAGGAGGAGGAGG 360  
361 CAACGAGCTGACCTTCAATCTCTGCTGAGCTGGGGGAGAAAATCTGCGCCAGGAGGAGGAGG 420  
361 CAACGAGCTGACCTTCAATCTCTGCTGAGCTGGGGGAGAAAATCTGCGCCAGGAGGAGGAGG 420  
421 GTACAGTCACTCTGCTGTTACTTCTGCTGAGCTGGGGGAGAAAATCTGCGCCAGGAGGAGGAG 480  
421 GTACAGTCACTCTGCTGTTACTTCTGCTGAGCTGGGGGAGAAAATCTGCGCCAGGAGGAGGAG 480  
481 CGAGCTGAGCTGCGCCGAGCTTGTATCCAGAGCTCCAGGGGCTGCTGGGGGAGGAGGAGGAGG 540  
481 CGAGCTGAGCTGCGCCGAGCTTGTATCCAGAGCTCCAGGGGCTGCTGGGGGAGGAGGAGGAGG 540  
541 TGTCAATGAGGAGCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600  
541 TGTCAATGAGGAGCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600  
601 GAGCCCTGAGCTGCGCCGAGCTTGTATCCAGAGCTCCAGGGGCTGCTGGGGGAGGAGGAGGAG 660  
601 GAGCCCTGAGCTGCGCCGAGCTTGTATCCAGAGCTCCAGGGGCTGCTGGGGGAGGAGGAGGAG 660  
661 GAGAGCTGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720  
661 GAGAGCTGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720  
721 GAGAGCTGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780  
721 GAGAGCTGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780  
781 CTTTAACCCCAACCTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 819  
781 CTTTAACCCCAACCTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 819

## RESULT 2

US-08-988-819-4  
; Sequence 4, Application US/08988819  
; Patent No. 6054294  
; GENERAL INFORMATION:  
; APPLICANT: CHANG, MING-SHI  
; TITLE OF INVENTION: NEUROTROPHIC FACTOR NNT-1  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: AMGEN INC.  
; STREET: ONE AMGEN CENTER DRIVE  
; CITY: THOUSAND OAKS  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 91320  
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/988,819  
FILING DATE: 12-DEC-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/792,019  
FILING DATE: 03-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: COOK, ROBERT R.  
REGISTRATION NUMBER: 31,602  
REFERENCE/DOCKET NUMBER: A-442A  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 819 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 95..769  
FEATURE:  
NAME/KEY: mat peptide  
LOCATION: 176..769  
FEATURE:  
NAME/KEY: sig peptide  
LOCATION: 95..175  
US-08-988-819-4  
Query Match 100.0%; Score 819; DB 3; Length 819;  
Best Local Similarity 100.0%; Pred. No. 1.5e-205;  
Matches 819; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 TATTATTAAAGCTTGGCCGAGAGCCGAGGCTGCTCCCACTCCGCGCAGAGCTCTGGAGAGA 60  
1 TATTATTAAAGCTTGGCCGAGAGCCGAGGCTGCTCCCACTCCGCGCAGAGCTCTGGAGAGA 60  
61 GAGAGCCGCGCCGCGCGCCGCGCCGCGCCGCGCCGCGCCGCGCCGCGCCGCGCCGCGCCGCG 120  
61 GAGAGCCGCGCCGCGCGCCGCGCCGCGCCGCGCCGCGCCGCGCCGCGCCGCGCCGCGCCGCG 120  
121 GGGGATGTTAGCTTGGCTATGCAAGGCTGCTGAGCACTCTCCCTGAGAGGCTCTTAA 180  
121 GGGGATGTTAGCTTGGCTATGCAAGGCTGCTGAGCACTCTCCCTGAGAGGCTCTTAA 180  
181 TCGCAGAGAGATCCAGAGCCCTGCGCCCTCCATCCAGAAAACCTATGACCTTACCCGCTA 240  
181 TCGCAGAGAGATCCAGAGCCCTGCGCCCTCCATCCAGAAAACCTATGACCTTACCCGCTA 240  
241 CTGAGAGATCAATCCGAGAGCTTGAAGCTGAGCACTTACCTGAACTAAGGAGGAGGAGGAGG 300  
241 CTGAGAGATCAATCCGAGAGCTTGAAGCTGAGCACTTACCTGAACTAAGGAGGAGGAGGAGG 300  
301 CAACGAGCTGACCTTCAATCTCTGCTGAGCTGGGGGAGAAAATCTGCGCCAGGAGGAGGAGG 360  
301 CAACGAGCTGACCTTCAATCTCTGCTGAGCTGGGGGAGAAAATCTGCGCCAGGAGGAGGAGG 360  
361 CAACGAGCTGACCTTCAATCTCTGCTGAGCTGGGGGAGAAAATCTGCGCCAGGAGGAGGAGG 420  
361 CAACGAGCTGACCTTCAATCTCTGCTGAGCTGGGGGAGAAAATCTGCGCCAGGAGGAGGAGG 420  
421 GTACAGTCACTCTGCTGTTACTTCTGCTGAGCTGGGGGAGAAAATCTGCGCCAGGAGGAGGAG 480  
421 GTACAGTCACTCTGCTGTTACTTCTGCTGAGCTGGGGGAGAAAATCTGCGCCAGGAGGAGGAG 480  
481 CGAGCTGAGCTGCGCCGAGCTTGTATCCAGAGCTCCAGGGGCTGCTGGGGGAGGAGGAGGAGG 540  
481 CGAGCTGAGCTGCGCCGAGCTTGTATCCAGAGCTCCAGGGGCTGCTGGGGGAGGAGGAGGAGG 540

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 9, 2004, 06:10:20 ; Search time 66.8985 Seconds  
(without alignments)  
5403.600 Million cell updates/sec

Title: US-09-931-704-4

Perfect score: 819

Sequence: 1 taccataaagctcgcscg.....agccacagtcagctgtcctt 819

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 569978 segs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

Issued Patents NA: \*  
1: /cgn2\_6/prodata/2/ina/5A\_COMB.seq: \*  
2: /cgn2\_6/prodata/2/ina/5B\_COMB.seq: \*  
3: /cgn2\_6/prodata/2/ina/6A\_COMB.seq: \*  
4: /cgn2\_6/prodata/2/ina/6B\_COMB.seq: \*  
5: /cgn2\_6/prodata/2/ina/PC/US\_COMB.seq: \*  
6: /cgn2\_6/prodata/2/ina/Backfile1.seq: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	819	100.0	819	1	US-08-792-019B-4
2	819	100.0	819	3	US-08-988-819-4
3	819	100.0	819	3	US-09-016-534-4
4	669.4	81.7	797	1	US-08-792-019B-1
5	669.4	81.7	797	3	US-08-988-819-1
6	669.4	81.7	797	3	US-09-016-534-1
7	627	76.6	1710	3	US-09-106-182-1
8	429.6	52.5	5087	1	US-08-792-019B-3
9	429.6	52.5	5087	3	US-08-988-819-3
10	429.6	52.5	5087	3	US-09-016-534-3
11	52	6.3	396	3	US-09-106-182-7
12	43.2	5.3	6803	3	US-08-665-259-19
13	43.2	5.3	6803	3	US-08-762-500-19
14	42.4	5.2	1642	2	US-08-665-037-1
15	42.4	5.2	1642	2	US-08-666-067-1
16	42.4	5.2	1642	2	US-08-732-870-1
17	38.4	4.7	68750	2	US-09-335-409-1
18	38.4	4.7	68750	4	US-09-568-102-1
19	38.4	4.7	68750	4	US-09-567-969-1
20	38.4	4.7	68750	4	US-09-568-480-1
21	38.4	4.7	68750	4	US-09-568-486-1
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23	38.4	4.7	68750	4	US-09-567-899-1
24	37	4.5	789	4	US-09-252-991A-5788
25	37	4.5	957	4	US-09-252-991A-5803
26	37	4.5	1248	4	US-09-252-991A-5821
27	36.6	4.5	5263	4	US-09-060-299-31

28	36.6	4.5	5263	4	US-09-402-923A-31	Sequence 31, Appl
C 29	35.6	4.3	2045	4	US-09-620-312D-759	Sequence 759, App
C 30	35	4.3	579	4	US-09-252-991A-2876	Sequence 2876, Ap
C 31	35	4.3	1536	4	US-09-252-991A-3182	Sequence 3182, Ap
C 32	35	4.3	2070	4	US-09-252-991A-2687	Sequence 2687, Ap
C 33	34.8	4.2	537	4	US-09-252-991A-2859	Sequence 2859, Ap
C 34	34.8	4.2	1476	4	US-09-252-991A-2659	Sequence 2659, Ap
C 35	34.8	4.2	1488	4	US-09-252-991A-2759	Sequence 2759, Ap
C 36	34.8	4.2	2298	4	US-09-252-991A-3207	Sequence 3207, Ap
C 37	34.8	4.2	4403765	3	US-09-103-840A-2	Sequence 2, Appl
C 38	34.8	4.2	4411529	3	US-09-103-840A-1	Sequence 1, Appl
C 39	34.4	4.2	1225	1	US-08-197-496A-1	Sequence 1, Appl
C 40	34.4	4.2	1225	1	US-08-275-370-1	Sequence 1, Appl
C 41	34.2	4.2	1590	4	US-09-252-991A-10070	Sequence 10070, A
C 42	34.2	4.2	1878	4	US-09-252-991A-9765	Sequence 9765, Ap
C 43	34	4.2	405	4	US-09-252-991A-17	Sequence 17, Appl
C 44	34	4.2	483	4	US-09-252-991A-18	Sequence 18, Appl
C 45	33.6	4.1	1308	4	US-08-937-067-18	Sequence 18, Appl

#### ALIGNMENTS

RESULT 1  
US-08-792-019B-4  
; Sequence 4, Application US/08792019B  
; Patent No. 5741772  
GENERAL INFORMATION:  
APPLICANT: CHANG, MING-SHI  
TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: AMGEN INC.  
STREET: 1840 DEHAVILLAND DRIVE  
CITY: THOUSAND OAKS  
STATE: CA  
COUNTRY: USA  
ZIP: 91320  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/792,019B  
FILING DATE: 03-FEB-1997  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: COOK, ROBERT R.  
REGISTRATION NUMBER: 31,602  
REFERENCE/DOCKET NUMBER: A-442  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 819 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 95..769  
FEATURE:  
NAME/KEY: mat peptide  
LOCATION: 176..769  
FEATURE:  
NAME/KEY: sig peptide  
LOCATION: 95..175  
US-08-792-019B-4  
Query Match 100.0%; Score 819; DB 1; Length 819;  
Best Local Similarity 100.0%; Pred. No. 1.5e-205;  
Matches 819; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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## RESULT 13

extracellular solute-binding protein, family 5 - Deinococcus radiodurans (strain R1)

C/Species: Deinococcus radiodurans  
C/Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 17-Mar-2000  
C/Accession: B75332

R.White, O.; Eisen, J.A.; Heibelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;  
M.; Shen, M.; Vamathavan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zaleski, C.; Ma  
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

Science 286, 1571-1577, 1999

A/Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A/Reference number: A75250; PMID:20036896; PMID:10567266

A/Accession: B75332

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-520 <WHI>

A/Cross-references: GB:AE002034; GB:AE000513; NID:G6459742; PIDN:AAFI1508.1; PID:G645974

A/Experimental source: strain R1

C/Genetics:

A:Gene: DR1955

A:Map position: 1

C:Superfamily: dipeptide transport protein

Query Match

Best Local Similarity 23.3%; Pred. No. 6.1;

Matches 40; Conservative 20; Mismatches 54; Indels 58; Gaps 7;

QY 19 LNHLPVAPALNRTGDPGPGPSIQ-----FNPRILGAETLPRAVTLVLEWRSIN-DRLRLTON 63

DB 363 LMY-----PSIRNYLPTPKVFAEAIADLGAIGIKVNLKEDPDKYEDRRAGVFMQVLY 418

QY 64 YLGPPNEED-----FNPRILGAETLPRAVTLVLEWRSIN-DRLRLTON 106

DB 419 GNGGDNDNDPNFYSAFYGKSGDDIGFNP-----NLTNTLTKGRALTYA 464

QY 107 YEAVSHLCYLRGLNROQATAEELRSLAHFCTSLQG-----LLGSIAGVMTLIG 155

DB 465 QQR-----PYKQHLHLYTNANVRLPLVHSTAPAAARTYKGMITGPISIVG 511

RESULT 14

A83271

hypothetical protein PA2984 [imported] - Pseudomonas aeruginosa (strain PA01)

C/Species: Pseudomonas aeruginosa

C/Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000

C/Accession: A83271

R.Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lapidig, K.; Lim,

.; Lofy, S.; Olson, M.V.

Nature 406, 959-964, 2000

A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho

A/Reference number: A82950; PMID:20437337; PMID:10984043

A/Accession: A83271

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-741 <STO>

A/Cross-references: GB:AE004724; GB:AE004091; NID:G9949083; PIDN:AA06372.1; GSPDB:GN001

A/Experimental source: strain PA01

C/Genetics:

A:Gene: PA2984

Query Match 6.9%; Score 84; DB 2; Length 741;

Best Local Similarity 26.2%; Pred. No. 12;

Matches 64; Conservative 13; Mismatches 81; Indels 86; Gaps 13;

QY 5 AGDSW-----GMLACITVLMHLPVAPALNRTGDPGPGPSIQKYDLTRYLEHQLRSLAGT 60

DB 447 AAASVALGMLGALC-----MLAPA-----GLP-----LRLGAA 477

QY 61 YINYLGPNEEDFNPRILGAETLPRAVTLVLEWRSINLDRRLTONYEAVSHLCYLRG 119

DB 478 LL-----LPLALPSSPPVWENG-----RAEVRVIDVGGLAVLVTRTE-----HVLVYDSG 522

QY 120 LNRQAA-----TAEIRSLAHFTSLQGLSIGVAMATLGYPL-----PQ 160

DB 523 A-RQAFPMGERVYVPLVSLDLR-----LDGLLSHNDNDHAGAPVYASRPVY 573

QY 161 PLPGTEPAPAPGPAHSDFLQKDDFWLLKEQLTWLRSAKDFNRLKKKQPPAAVTLHL 220

DB 574 WIVSGEPALPPLFADSCDERSWSWDGVFQWMAWAQGDEN-----DRSCVLAV 624

QY 221 EAHG 224

DB 625 EADG 628

## RESULT 15

hypothetical protein SC5C7.24c SC5C7.24c - Streptomyces coelicolor

C/Species: Streptomyces coelicolor

C/Date: 05-Nov-1999 #sequence\_revision 05-Nov-1999 #text\_change 05-Nov-1999

C/Accession: T35231

R.Seeger, K.J.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, September 1998

A/Reference number: Z21572

A/Accession: T35231

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-272 <SEB>

A/Cross-references: EMBL:AL031515; PIDN:CAA20636.1; GSPDB:GN00070; SCOEDB:SC5C7.24c

A/Experimental source: strain A3(2)

C/Genetics:

A:Gene: SCOEDB:SC5C7.24c

Query Match

Best Local Similarity 23.9%; Pred. No. 4.2;

Matches 38; Conservative 15; Mismatches 50; Indels 56; Gaps 7;

QY 23 PAVPALN-----RTGDPGPGPSIQKYDLTRYLEHQLRSLAGTYLNYLGPEN----- 70

DB 95 PALGALREGMERLIGYEYFPALVDATRYVLAARGIMLMDGVAEHLLTPPLNAIRLT 154

QY 71 -EPDFNPRILGAETLPRAVTLVLEWRSINLDRRLTONYEAVSHLCYLRGLNROQATAE 129

DB 155 LHPDGLAPRIR-----NLREWR-----GHL-----EGM 178

QY 130 RSLA-HFCTSLQGLSIGVAMATLGYPLPPLPTEP 167

DB 179 ERQIALHRSRPLRELYDEVA-----AYPVPSVGAEP 211

Search completed: February 9, 2004, 06:17:42

Job time : 18 secs



Db 267 DDEDESADKEDDEAVKOL-----SEKDL--LKRHIE 298

## RESULT 6

G02312  
C:Species: Homo sapiens (man)  
C>Date: 21-Dec-1996 #sequence\_revision 06-Jun-1997 #text\_change 17-Jul-1998  
C/Accession: G02312  
R:Wood, W.I.  
Submitted to the EMBL Data Library, December 1995  
A:Reference number: H01035

A/Accession: G02312

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-201 <MOO>

A/Cross-references: EMBL:U43030; NID:g1151149; PID:g1151150

C/Genetics: GDB:CTF1; CT-1

A/Cross-references: GDB:567078

A/Map position: 1p22-1p22

## Query Match

Best Local Similarity 25.7%; Score 91.5; DB 2; Length 201;

Matches 45; Conservative 23; Mismatches 92; Indels 15; Gaps 5;

40 IOKTYDLTRYLEHQSLAGTYLNYGPPNEPDPNPRPGAETLPRAVTNLEWRSIAND 99

27 IRTHTSLAHLITKARQLOEYVQLOGDPGLPSFSPPLPVAGL-SAPAPSHAGLPVH 85

100 RLRLTONYEAYSHLCTYRLGNLROA-----TALRRSLAHFCTSLQGLGSIAGVWATL 154

86 RLRL--DAALALPPLDVAVCRAQLNPRARLRLRLDARQARALGAVALALAL 143

155 GV-----PLQPLGTEPAPAPGPAHSDFLQKMDFWLKLQWTWRSKADPRL 205

144 GAANRGPRAEPAPATASA--ASATGVFAKVIAGLVCGLYREWLSTRTEGDLGOL 195

Db 144 GAANRGPRAEPAPATASA--ASATGVFAKVIAGLVCGLYREWLSTRTEGDLGOL 195

Query Match 7.4%; Score 90; DB 2; Length 195;

Best Local Similarity 27.7%; Pred. No. 0.63;

Matches 52; Conservative 21; Mismatches 83; Indels 33; Gaps 10;

46 LTRYLEHQSLAGTYLNYGPPNEPDPNPRPGAETLPRAVTNLEWRSIANDRLRLTQ 105

Query Match 7.4%; Score 90; DB 2; Length 195;

Best Local Similarity 27.7%; Pred. No. 0.63;

Matches 52; Conservative 21; Mismatches 83; Indels 33; Gaps 10;

46 LTRYLEHQSLAGTYLNYGPPNEPDPNPRPGAETLPRAVTNLEWRSIANDRLRLTQ 105

Query Match 7.4%; Score 90; DB 2; Length 195;

Best Local Similarity 27.7%; Pred. No. 0.63;

Matches 52; Conservative 21; Mismatches 83; Indels 33; Gaps 10;

46 LTRYLEHQSLAGTYLNYGPPNEPDPNPRPGAETLPRAVTNLEWRSIANDRLRLTQ 105

Db 23 LARKMSDVTDLIDYVEROG-----LDASISVAADVGPPTAAV--ERNAEQTGTORLID 75

Qy 106 N--YEAYSHLCTYRLGNLROA--ATAELRSLA-----HPTSLQGLGSIAGVMA 152

Db 76 NLAAVRAEFTLAKQMEERELLGDTDAELGPAALMLQVSAFYTHLELL-----ELE 130

Qy 153 TLGYPPLQPLPGTEPAPAPGPAHSDFLQKMDFWLKLQWTWRSKADPRLKKKQPP 212

Db 131 SRGAPAE--GSEPP-AP-PRLSLEPQLRGILRVRLRLAQAQVAVRSVRRLRLQSK--HGP 183

Qy 213 AASVTIHL 220

Db 184 GSGAALGL 191

## RESULT 8

F82965  
Hypothetical protein PA5441 [imported] - Pseudomonas aeruginosa (strain PA01)

C/Species: Pseudomonas aeruginosa

C/Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000

C/Accession: F82965

R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardig, K.; Lim,

.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho

A/Reference number: A82950; MUID:20437337; PMID:10984043

A/Accession: F82965

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-733 <STO>

A/Cross-references: GB:AE004957; GB:AE004091; NID:g9951770; PIDN:AAG08826.1; GSPDB:GN001

C/Experimental source: strain PA01

C/Genetics: PA5441

## Query Match

Best Local Similarity 23.9%; Score 90; DB 2; Length 733;

Matches 48; Conservative 24; Mismatches 81; Indels 48; Gaps 8;

23 PAVPALNRTGDPGPPSIQKTYDLTRYLEHQSLAGTYLNYGPPNEPDPNPRPGAET 82

102 PALPASEAETPPAPAPSPPLAEIAR-----OMGAE 132

Qy 83 TLPRATVLEWRSIANDRLRLTONYEAYSHLCTYRLGNLROAATAELR-RSLAHPTSLQ 141

Db 133 ALPEKIAAEFEFGESRCRSDQDA--LAFRLQV-RDGLGEAETKALAN--SRL 184

Qy 142 GLGSIAGVMAATLGYPLPGTEPAPAPGPAHSDFLQKMDFWLKLQWTWRSKAD 201

Db 165 DLGACMGEBELGCVLAQ---GVES--AAGRAFTYLEAANFTSGR-----PDEAROG 234

Qy 202 ENRLKKKQPPAPASVTLHLEA 222

Db 235 FKALQDVQPMWLKETALYIQA 255

## RESULT 9

DB3588  
Conserved hypothetical protein PA0454 [imported] - Pseudomonas aeruginosa (strain PA01)

C/Species: Pseudomonas aeruginosa

C/Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000

C/Accession: DB3588

R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardig, K.; Lim,

.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho

A/Reference number: A82950; MUID:20437337; PMID:10984043

A/Accession: DB3588

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-733 <STO>





C;Genetics:

**THIS PAGE BLANK (USPTO)**

RA Iwahara T., Fujimoto J., Wen D., Cupples R., Bucay N., Arakawa T.,  
RA Mori S., Ratzkin B., Yamamoto T.;  
RT "Molecular characterization of ALK, a receptor tyrosine kinase  
RT expressed specifically in the nervous system.";  
RL Oncogene 14:439-449 (1997).  
RN [4]  
RX PARTIAL SEQUENCE FROM N.A., AND CHROMOSOMAL TRANSLOCATION.  
RX MEDLINE-94167588; PubMed-8122112;  
RA Morris S.W., Kirschen M.N., Valentine M.B., Dittner K.G.,  
RA Shapiro D.N., Salzman D.L., Look A.T.;  
RT "Fusion of a kinase gene, ALK, to a nucleolar protein gene, NPM, in  
RT non-Hodgkin's lymphoma.";  
RL Science 263:1281-1284 (1994).  
CC -1- FUNCTION: Orphan receptor with a tyrosine-protein kinase activity.  
CC Appears to play an important role in the normal development and  
CC function of the nervous system.  
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
CC tyrosine phosphate.  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -1- TISSUE SPECIFICITY: Expressed in brain and CNS. Also expressed in  
CC the small intestine and testis, but not in normal lymphoid cells.  
CC -1- PTM: N-glycosylated.  
CC -1- DISEASE: A FORM OF NON-HODGKIN'S LYMPHOMA IS CHARACTERIZED BY A  
CC CHROMOSOMAL TRANSLOCATION T(2;5) (P23;Q35) THAT INVOLVES NPM1 AND  
CC ALK.  
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. INSULIN  
CC RECEPTOR SUBFAMILY.  
CC -1- SIMILARITY: Contains 1 LDL-receptor class A domain.  
CC -1- DATABASE: NAME-Atlas Genet. Cytogenet. Oncol. Haematol.;  
CC WWW="http://www.infobiogen.fr/services/chrncancer/Genes/ALK.html".  
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CC -----  
DR EMBL: U62540; AAB71619.1; -;  
DR EMBL: U66559; AAC51104.1; -;  
DR HSPB: P08631; IAD5.  
DR Genew: HGNC:427; ALK.  
DR MIM: 105590; -;  
DR InterPro: IPR002172; LDL\_receptor\_A.  
DR InterPro: IPR000998; MAM\_domain.  
DR InterPro: IPR000719; Prot\_kinase.  
DR InterPro: IPR002011; RTKinaseII.  
DR InterPro: IPR001245; Tyr\_kinase.  
DR Pfam: PF00629; MAM\_1.  
DR Pfam: PF00069; pkinase; 1.  
DR PRINTS: PR00109; TYRKINASE.  
DR ProDom: PD000001; Prot\_kinase; 1.  
DR SMART: SM00192; Tyrc; 1.  
DR SMART: SM00219; LDla; 1.  
DR PROSITE: PS00740; MAM\_1; FALSE\_NEG.  
DR PROSITE: PS50060; MAM\_2; 2.  
DR PROSITE: PS01209; LDla\_1; FALSE\_NEG.  
DR PROSITE: PS50068; LDla\_2; FALSE\_NEG.  
DR PROSITE: PS50107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE: PS00109; PROTEIN\_KINASE\_TYR; 1.  
DR PROSITE: PS00239; RECEPTOR\_TYR\_KIN\_II; 1.  
KW Transferase; Tyrosine-protein kinase; Transmembrane; ATP-binding;  
KW phosphorylation; Receptor; Glycoprotein; Repeat; Signal;  
KW Proto-oncogene; Chromosomal translocation.  
KW SIGNAL 1 18 POTENTIAL.  
FT CHAIN 19 1620 ALK TYROSINE KINASE RECEPTOR.  
FT DOMAIN 19 1038 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 1039 1059 POTENTIAL.  
FT DOMAIN 1060 1620 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 264 427 MAM 1.

FT DOMAIN 437 473 LDL-RECEPTOR CLASS A.  
FT DOMAIN 478 636 MAM 2.  
FT DOMAIN 1116 1392 PROTEIN KINASE.  
FT DOMAIN 816 940 GLY-RICH.  
FT NP\_BIND 1122 1130 ATP (BY SIMILARITY).  
FT BINDING 1150 1150 ATP (BY SIMILARITY).  
FT ACT\_SITE 1249 1249 BY SIMILARITY.  
FT MOD\_RES 1282 1282 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
FT CARBOHYD 169 169 N-LINKED (GLCNAC...) (POTENTIAL).  
FT CARBOHYD 244 244 N-LINKED (GLCNAC...) (POTENTIAL).  
FT CARBOHYD 285 285 N-LINKED (GLCNAC...) (POTENTIAL).  
FT CARBOHYD 324 324 N-LINKED (GLCNAC...) (POTENTIAL).  
FT CARBOHYD 411 411 N-LINKED (GLCNAC...) (POTENTIAL).  
FT CARBOHYD 424 424 N-LINKED (GLCNAC...) (POTENTIAL).  
FT CARBOHYD 445 445 N-LINKED (GLCNAC...) (POTENTIAL).  
FT CARBOHYD 563 563 N-LINKED (GLCNAC...) (POTENTIAL).  
FT CARBOHYD 571 571 N-LINKED (GLCNAC...) (POTENTIAL).  
FT CARBOHYD 627 627 N-LINKED (GLCNAC...) (POTENTIAL).  
FT CARBOHYD 709 709 N-LINKED (GLCNAC...) (POTENTIAL).  
FT CARBOHYD 808 808 N-LINKED (GLCNAC...) (POTENTIAL).  
FT CARBOHYD 863 863 N-LINKED (GLCNAC...) (POTENTIAL).  
FT CARBOHYD 864 864 N-LINKED (GLCNAC...) (POTENTIAL).  
FT CARBOHYD 886 886 N-LINKED (GLCNAC...) (POTENTIAL).  
FT CARBOHYD 986 986 N-LINKED (GLCNAC...) (POTENTIAL).  
FT CONFLICT 36 36 S -> P (IN REF. 3).  
FT CONFLICT 1491 1491 K -> R (IN REF. 3).  
FT CONFLICT 1529 1529 D -> E (IN REF. 3).  
SQ SEQUENCE 1620 AA; 176417 MW; A62604B242961E1E CRC64;

Query Match 6.5%; Score 79; DB 1; Length 1620;  
Best Local Similarity 23.1%; Pred. No. 41;  
Matches 54; Conservative 15; Mismatches 77; Indels 88; Gaps 9;

QY 18 VMHLPAYVAL-----NRTGDPGPGPSIQTYDILTRLEQLSLAGTYANYLGP 67  
DB 6 LLMLLPLLSTAAVSGMGCTGRASPAGSPLOPREPLS-YSRLOKSLA----- 55  
QY 68 PNEPDPPNPRUGARTLPRAVTNLEWWSLNDRLTLQVYEAESH-LCYLGLNROAAT 126  
DB 56 ----VDFVPSL-----FRVYADLLPLSSSELKAGR 84  
QY 127 AELRSLAHFTSLQGLLSINAGWATLGYLPOLP----- 163  
DB 85 PEARSLMLDCAPIRLRLGPARVSWTAGSPAPARFTLSRVLKGSYVKLRRAQVLVE 144  
QY 164 -GTEP-----AMAPPAISDFLQKDDFWLKELOTWLMRSKADNRRLKKKQOP 211  
DB 145 LGEEAILRGCVGPPEBAAVGLIQ-----FNLSFLSWMIROGE--GRIRIRIMP 191

Search completed: February 9, 2004, 06:15:35  
Job time : 12.5 secs

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DR EMBL; 270692; CA94666.1; ALT\_TERM.  
 DR EMBL; 270692; CA94665.1; ALT\_INIT.  
 DR EMBL; AE007074; AAK46576.1; --  
 DR TIGR; MT2292; --  
 DR Tuberculin; RV2232; --  
 DR Tuberculin; RV2233; --  
 DR Interpro; IPR005834; Hydrolase.  
 DR Pfam; PF00702; Hydrolase; 1.  
 DR Hypothetical protein; Complete proteome.  
 KW SEQUENCE 291 AA; 30694 MW; 750F090FB154B65 CRC64;  
 SQ

Query Match 6.5%; Score 79; DB 1; Length 291;  
 Best Local Similarity 25.8%; Pred. No. 4.6; Mismatches 65; Indels 54; Gaps 11;  
 Matches 47; Conservative 16; Mismatches 65; Indels 54; Gaps 11;

QY 23 PAVPALNRTGDPGPGPSIQKTYDITRYLEHQLSLAGTY---LNYLGPPFNEPDP----- 74  
 DB 64 PPRABARASSRSGESPOL-VIFDLGDTLDSARGIVSFRHLNHIQAVPEGLATHIV 122  
 QY 75 NEPRIGAEPLP-----RATVNLVWRSLNDRLRLTONTYANVSHLLCYLR- 118  
 DB 123 GPPM--HETLRAMGLGESAEEBAIVAVRADYSARGM-----AMNSLFGIGIPLDLADLT- 173  
 QY 119 -GLNQQAATF---LRSLAHP-----CRSLGGLGSIAGWATLGYPLPQ--P 161  
 DB 174 AGVRLAVATSKAEPTARLIRHFGBQHEVFIAGASTDSRGSKVQVLA---HALAQLRP 230  
 QY 162 LP 163  
 DB 231 LP 232

RESULT 14  
 BAT3 HUMAN  
 ID BAT3 HUMAN STANDARD; PRT; 1132 AA.  
 AC P46379;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Large proline-rich protein BAT3 (HLA-B-associated transcript 3) (G3).  
 GN BAT3 OR G3.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=T-cell;  
 RX MEDLINE=90192810; PubMed=2156268;  
 RA Banerji J., Sande J., Strominger J.L., Spies T.;  
 RT "A gene pair from the human major histocompatibility complex encodes  
 RT large proline-rich proteins with multiple repeated motifs and a  
 RT single ubiquitin-like domain."  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:2374-2378 (1990).  
 CC -1- FUNCTION: UNKNOWN.  
 CC -1- SIMILARITY: Contains 1 ubiquitin-like domain.  
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DR EMBL; M33519; AAA35587.1; --  
 DR EMBL; M33521; AAA35588.1; --  
 DR EMBL; M33520; AAA35588.1; JOINED.  
 DR PIR; A35098; A35098.  
 DR HSSP; P02248; IUBI.  
 DR Genew; HGNC:13919; BAT3.  
 DR MIM; 142590; --  
 DR GO; GO:0003822; P:MHC-interacting protein; TAS.  
 DR Interpro; IPR000626; Ubiquitin.  
 DR Pfam; PF00240; Ubiquitin; 1.  
 DR SMART; SM00213; UBO; 1.  
 DR PROSITE; PS00299; UBIQUITIN\_1; 1.  
 DR PROSITE; PS00553; UBIQUITIN\_2; 1.  
 KW Repeat.  
 FT DOMAIN 17 77 UBIQUITIN-LIKE.  
 FT DOMAIN 202 207 POLY-PRO.  
 FT DOMAIN 242 636 4 X 29 AA APPROXIMATE REPEATS.  
 FT REPEAT 242 270 1.  
 FT REPEAT 415 443 2.  
 FT REPEAT 574 602 3.  
 FT REPEAT 608 636 4.  
 FT REPEAT 657 670 POLY-PRO.  
 FT DOMAIN 1132 AA; 119504 MW; E28C8A78C38DD18 CRC64;  
 SQ

Query Match 6.5%; Score 79; DB 1; Length 1132;  
 Best Local Similarity 26.1%; Pred. No. 26; Mismatches 67; Indels 46; Gaps 11;  
 Matches 46; Conservative 17; Mismatches 67; Indels 46; Gaps 11;

QY 23 PAVPALNRTGDPGPGPSIQKTYDITRYLEHQLSLAGTYLNYLGPPFNEPDPFRLGAE 82  
 DB 261 PA-PETNAPNHPSPAEVYEVQLQELR-LESRLQFLQGYEVLGAAAT-TYNNNHGGR 317  
 QY 83 TLPRATVNLVWRSLNDRLRLTON-YEYSHLLCYLRSLNQAAAT---AEIRSLAHP 137  
 DB 318 EDOR-LINL-----VGSRLRLGNTFVALSDRLCNL-----ACTPPRHLLVVRPMSHYT 365  
 QY 138 TSLGGLGSIAGWATLGYPL-----PQPLPGTE-PAMAPGPAHS 176  
 DB 366 TPM-----VLQQAALPIQINVGITVTMTGNGTRPPPPNMAEAPPGGQASS 412

RESULT 15  
 ALK HUMAN  
 ID ALK HUMAN STANDARD; PRT; 1620 AA.  
 AC Q9UT73; Q9Y4K6;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE ALK tyrosine kinase receptor precursor (EC 2.7.1.112) (Anaplastic  
 DE lymphoma kinase) (CD246 antigen).  
 GN ALK.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN (1)  
 RP SEQUENCE FROM N.A., SUBCELLULAR LOCATION, TISSUE SPECIFICITY, AND  
 RP GLYCOSYLATION.  
 RX MEDLINE=97316779; PubMed=9174053;  
 RA Morris S.W., Naeye C.W., Mathew P., James P.L., Kirstein M.N., Cui X.,  
 RA Witte D.P.;  
 RT "ALK, the chromosome 2 gene locus altered by the c(2;5) in non-  
 RT Hodgkin's lymphoma, encodes a novel neutral receptor tyrosine kinase  
 RT that is highly related to leukocyte tyrosine kinase (LTK).";  
 RL Oncogene 14:2175-2188 (1997).  
 CC [2]  
 CC ERRATUM.  
 RP Morris S.W., Naeye C.W., Mathew P., James P.L., Kirstein M.N., Cui X.,  
 RA Witte D.P.;  
 RL Oncogene 15:2883-2883 (1997).  
 CC [3]  
 CC SEQUENCE FROM N.A.  
 RX MEDLINE=97178863; PubMed=9053841;

GN TCIRG1 OR ATP6N1C.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 RN NCBI\_TaxID=9606;  
 RP [1]  
 RC SEQUENCE FROM N.A. (ISOFORM LONG).  
 RC TISSUE=Osteoclastoma;  
 RX MEDLINE=96158968; PubMed=8579597;  
 RA Li Y.P., Chen W., Staehenko P.;  
 RT "Molecular cloning and characterization of a putative novel human  
 RT osteoclast-specific 116-kDa vacuolar proton pump subunit.";  
 RL Biochem. Biophys. Res. Commun. 218:813-821(1996).  
 RP SEQUENCE FROM N.A. (ISOFORM SHORT).  
 RA Utku N., Heinemann T., Bulwin C.-G., Beinke S., Beato F., Randall J.,  
 RA Busconi L., Delphire E., Robertson E.R., Kojima R., Volk H.D.,  
 RA Milford E.L., Guillans S.R.;  
 RN Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
 RP SEQUENCE FROM N.A. (ISOFORM SHORT).  
 RX MEDLINE=99263502; PubMed=10329006;  
 RA Heinemann T., Bulwin G.C., Randall J., Schnieders B., Sandhoff K.,  
 RA Volk H.D., Milford E., Guillans S.R., Utku N.;  
 RT "Genomic organization of the gene coding for TIRG7, a novel membrane  
 RT protein essential for T cell activation.";  
 RL Genomics 57:398-406(1999).  
 CC -1- FUNCTION: PART OF THE PROTON CHANNEL OF V-ATPASES (BY SIMILARITY).  
 CC -1- SEEMS TO BE DIRECTLY INVOLVED IN T CELL ACTIVATION.  
 CC -1- SUBUNIT: V-ATPASE IS AN HETEROMULTIMERIC ENZYME COMPOSED OF A  
 CC PERIPHERAL CATALYTIC VI COMPLEX (MAIN COMPONENTS: SUBUNITS A, B,  
 CC C, D, E, AND F) ATTACHED TO AN INTEGRAL MEMBRANE V0 PROTON PORE  
 CC COMPLEX (MAIN COMPONENT: THE PROTEOLIPID PROTEIN).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=Long;  
 CC IsoId=Q13488-1; Sequence=displayed;  
 CC Name=Short;  
 CC IsoId=Q13488-2; Sequence=VSP\_000345;  
 CC Note=No experimental confirmation available;  
 CC -1- TISSUE SPECIFICITY: THE LONG ISOFORM IS HIGHLY EXPRESSED IN  
 CC OSTEOCLASTOMAS. THE SHORT FORM IS HIGHLY EXPRESSED IN THYMUS.  
 CC -1- SIMILARITY: BELONGS TO THE V-ATPASE 116 kDa SUBUNIT FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL: U45285; AAA97878.1;  
 CC EMBL: AF025374; AAC35742.1;  
 CC EMBL: AF030303; AAC31081.2;  
 CC DR Genew; HGNC:11647; TCIRG1.  
 CC MIM: 604592;  
 CC DR GO: GO:0005887; C: integral to plasma membrane; TAS.  
 CC DR GO: GO:0005215; P: transporter activity; TAS.  
 CC DR GO: GO:0006968; P: cellular defense response; TAS.  
 CC DR GO: GO:0008284; P: positive regulation of cell proliferation; TAS.  
 CC DR GO: GO:0015992; P: proton transport; TAS.  
 CC DR InterPro: IPR002490; V: ATPase\_sub116.  
 CC DR Pfam: PF01496; V: ATPase\_sub\_1;  
 CC DR Hydrogen ion transport; Glycoprotein;  
 CC Alternative splicing.  
 CC KW DOMAIN 1 397 EXTRACELLULAR (POTENTIAL).  
 CC FT TRANSMEM 398 418 POTENTIAL.  
 CC FT TRANSMEM 445 465 POTENTIAL.  
 CC FT TRANSMEM 504 524 POTENTIAL.  
 CC FT TRANSMEM 538 558 POTENTIAL.  
 CC FT TRANSMEM 576 596 POTENTIAL.

FT TRANSMEM 636 656 POTENTIAL.  
 FT TRANSMEM 771 791 POTENTIAL.  
 FT CARBOHYD 41 41 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 483 483 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 503 503 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT VARSPLIC 1 216 Missing (in isoform short).  
 FT CONFLICT 377 377 /FTid=VSP\_000345.  
 FT CONFLICT 603 603 A -> R (IN REF. 1).  
 SO SEQUENCE 830 AA; 92997 MW; 62EBAE9A22DC698B CRC64;  
 Query Match 6.5%; Score 79.5; DB 1; Length 830;  
 Best Local Similarity 24.3%; Pred. No. 16;  
 Matches 45; Conservative 25; Mismatches 66; Indels 49; Gaps 9;  
 QY 40 IQKTYLTYLTHQRLSLAGTYLNTGPPNPDPNPPGLGATLPRATVNLVWMSLND 99  
 DB 61 LKTF--TFLOEVRV-AGL--VLPKPKGLPAPPR-----D 93  
 QY 100 RLRLQNYEAYSHLLCYLRGNRAATAEIRSLAFTSLQGLGSIAGVM--ATLGY 156  
 DB 94 LRLQETETRLAQELRDVNG-NQALRLQHLQHLQAATVLRQHEPQLAAATDGSERT 152  
 QY 157 PLPQPLPTGEPAPAPPAHS-----FLQKMDPWLKELQTLWMSAK-----DFNRLK 207  
 DB 153 PLIQ-----ARQPHQDLRVNFVAGVAPHPKAPALERLLMRACRGFLIASPRELQ 203  
 QY 208 KNQPP 212  
 DB 204 PLEHP 208  
 RESULT 13  
 YMS2\_MYCTU STANDARD; PRT; 291 AA.  
 ID YMS2\_MYCTU  
 AC Q10515; Q10516;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Hypothetical protein Rv2232/Rv2233.  
 GN Rv2232/Rv2233 OR MT2292 OR MTCY427.13/MTCY427.14.  
 OS Mycobacterium tuberculosis.  
 OC Bacteria; Actinobacteria; Actinomycetales;  
 OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.  
 OX NCBI\_TaxID=1773;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H37RV;  
 RX MEDLINE=98295987; PubMed=9634230;  
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Church C., Harris D.,  
 RA Gordon S.V., Eiglmeier K., Gae S., Barry C.E. III, Tekala F.,  
 RA Badcock K., Baham D., Brown D., Chillingworth T., Connor R.,  
 RA Davies R., Devlin K., Feltham T., Garg S., Hamlin N., Holroyd S.,  
 RA Horsby T., Jagers K., Krogan A., McLean J., Moule S., Murphy L.,  
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,  
 RA Ruter S., Seeger K., Skelton S., Squares S., Squares R.,  
 RA Sultun J.E., Taylor K., Whitehead S., Barrall B.G.;  
 RT "Deciphering the biology of Mycobacterium tuberculosis from the  
 RT complete genome sequence.";  
 RL Nature 393:537-544(1998).  
 RL [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CDC 1551 / Oshkosh;  
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,  
 RA Peterson J., Deboy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,  
 RA Kolony J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,  
 RA Delcher A., Uterback T., Weidman J., Kouri H., Gill J., Mikula A.,  
 RA Bishai W.;  
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and  
 RT laboratory strains.";  
 RT Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE CBBY/CBBZ/GPH/YIEH FAMILY.  
 CC -----

RX MEDLINE=91177633; PubMed=2007559;  
RA Xu H.W., Wall J.D.;  
RT "Clustering of genes necessary for hydrogen oxidation in Rhodobacter  
RT capsulatus";  
RL J. Bacteriol. 173:2401-2405(1991).  
RN (2)  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 33303 / B10;  
RX MEDLINE=93268090; PubMed=8497190;  
RA Colbeau A., Richard P., Toussaint B., Caballero F.J., Elster C.,  
RA Delphin C., Smith R.U., Chabert J., Vignais P.M.;  
RT "Organization of the genes necessary for hydrogenase expression in  
RT Rhodobacter capsulatus. Sequence analysis and identification of two  
RT hyp regulatory mutants";  
RL Mol. Microbiol. 8:15-29(1993).  
CC -1- SIMILARITY: BELONGS TO THE HUPK FAMILY.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL, M55089; AAA72924.1; -  
CC DR EMBL, 215089; CAA78803.1; -  
CC DR PIR, S32947; S32947.  
CC FT CONFLICT 70 70 A -> R (IN REF. 2).  
CC SQ SEQUENCE 294 AA; 30222 MW; 2669EB870AF35EDA CRC64;  
  
Query Match 6.9%; Score 84.5; DB 1; Length 294;  
Best Local Similarity 31.2%; Pred. No. 1.4; Mismatches 38; Indels 47; Gaps 6;  
Matches 40; Conservative 3;  
  
QY 76 PPRGAEPLPRATVNLVWRSINDRLRLTONYEAAYSHLLCYLGRNQATNE---LRNS 132  
DB 36 PPGQVALLPR-----LFNLGAAQGHAAIAL-----GLPAEAAPARREILRDH 80  
QY 133 LAHFCTSLGSLGSLAGWATIGYRPPRLPRTGPRMAGPRAHSDPFLQMDPFLKLEQ 192  
DB 81 LAKLCLVWPKLGL-----APQPLP---EHMAGGA-----ALQ 111  
QY 193 TWLMRSAX 200  
DB 112 HWLMGAK 119  
  
RESULT 11  
MB2\_PIG M2B2\_PIG STANDARD; PRT; 995 AA.  
AC Q28949;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Epilidymis-specific alpha-mannosidase precursor (EC 3.2.1.24)  
DE (Mannosidase alpha class 2B member 2) (AUMAN).  
GN MAN2B2.  
OS Sue acrota (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_Taxid=9823;  
RN (1)  
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
RC TISSUE=Epilidymis;  
RX MEDLINE=96117077; PubMed=8562059;  
RA Okamura N., Tamba M., Liao H.-D., Onoe S., Sugita Y., Dacheux F.,  
RA Dacheux J.-L.;  
RT "Cloning of complementary DNA encoding a 135-kilodalton protein  
RT secreted from porcine corpus epididymis and its identification as an  
RT epididymis-specific alpha-mannosidase";  
RL Mol. Reprod. Dev. 42:141-148(1995).  
CC -1- FUNCTION: CAN DIGEST BOTH P-NITRO-PHENYL-ALPHA-D-MANNOSIDE AND

CC HIGH MANNOSE OLIGOSACCHARIDE (MAN(8)-GLCNAC(2)). MAY BE INVOLVED  
CC IN SPERM MATURATION. HAS A POSSIBLE ROLE IN SPECIFIC SPERM-EGG  
CC INTERACTION SINCE SPERM SURFACE MANNOSIDASE ACTS LIKE A RECEPTOR  
CC FOR MANNOSE-CONTAINING OLIGOSACCHARIDES LOCATED ON THE ZONA  
CC PELLUCIDA.  
CC -1- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing alpha-D-  
CC mannose residues in alpha-D-mannosides.  
CC -1- SUBCELLULAR LOCATION: SECRETED. FOUND AT THE SPERM SURFACE AS A  
CC 27 kDa FRAGMENT.  
CC -1- TISSUE SPECIFICITY: SPECIFIC TO THE CAPUT AND CORPUS OF THE  
CC EPIDIDYMIS.  
CC -1- PTM: PROCESSED INTO A 27 kDa FRAGMENT LOCALIZED ON THE EQUATORIAL  
CC SEGMENT AND THE APICAL RIM OF THE HEAD OF MATURE SPERM.  
CC -1- MISCELLANEOUS: OPTIMAL MANNOSIDASE ACTIVITY WAS FOUND AT PH 6.5.  
CC -1- SIMILARITY: BELONGS TO FAMILY 38 OF GLYCOSYL HYDROLASES.  
CC -----  
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CC -----  
CC EMBL, D28521; BAA05877.1; ALT INIT.  
CC DR InterPro: IPR000602; Glyco\_hydro\_38; 1.  
CC DR Pfam: PF01074; Glyco\_hydro\_38; 1.  
CC KM Hydrolase; Glycosidase; Signal; Glycoprotein.  
CC FT SIGNAL 21  
CC FT CHAIN 22 995 EPIDIDYMIS-SPECIFIC ALPHA-MANNOSIDASE.  
CC FT CARBOHYD 285 285 N-LINKED (GLCNAC. . .) (POTENTIAL).  
CC FT CARBOHYD 593 593 N-LINKED (GLCNAC. . .) (POTENTIAL).  
CC FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL).  
CC FT CARBOHYD 657 657 N-LINKED (GLCNAC. . .) (POTENTIAL).  
CC FT CARBOHYD 733 733 N-LINKED (GLCNAC. . .) (POTENTIAL).  
CC FT CARBOHYD 793 793 N-LINKED (GLCNAC. . .) (POTENTIAL).  
CC FT CARBOHYD 875 875 N-LINKED (GLCNAC. . .) (POTENTIAL).  
CC FT CARBOHYD 977 977 N-LINKED (GLCNAC. . .) (POTENTIAL).  
CC FT CONFLICT 945 945 D -> A (IN REF. 1; AA SEQUENCE).  
CC SQ SEQUENCE 995 AA; 114230 MW; 79D21B8CE5A6F62 CRC64;  
  
Query Match 6.6%; Score 80.5; DB 1; Length 995;  
Best Local Similarity 23.0%; Pred. No. 16; Mismatches 62; Indels 67; Gaps 9;  
Matches 45; Conservative 22;  
  
QY 50 LEHQ---LRSLAGTYLVLPDPPEPPNPRLCAETL-----PRATVNLVWRS 97  
DB 827 LQHRPVVLFRELGVQNGPGRKQEPVTLPPSLILQILSIQGWYSSNHTVHLKMLQK 886  
QY 98 NDR-----LRITONVEAYSHLLCYLGRNQATAEIRSLAFCSTLQGLLSI 147  
DB 887 HYRRAKADPRRVLLRLHLHYLNGSH---QALSRPV-----LNLQSVLNLGL 929  
QY 148 AGVATLGLYRPPRLPRTGPRMAGPRAHSDPFLQMDPFLKLEQTLWLMRSAXDEN--L 205  
DB 930 GSVAVP---EERSLTG-----MDVNSLHRMWMKEDGHHNGS 965  
QY 206 KKQAOFP--AASVTLH 219  
DB 966 SRRLPLRPLRGPNVTH 981  
  
RESULT 12  
VPP3\_HUMAN VPP3\_HUMAN STANDARD; PRT; 830 AA.  
AC Q13488; O75877;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Vacuolar proton translocating ATPase 116 kDa subunit A isoform 3 (V-  
DE ATPase 116-kDa isoform a3) (Osteoclastic proton pump 116 kDa subunit)  
DE (OC-116 kDa) (OC116) (T-cell immune regulator 1) (T cell immune  
DE response cDNA) protein) (TIRC7).

RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,  
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,  
 RA Cerretti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,  
 RA Shparovski G.V., Uesery D., Barrell B.G., Nurse P.;  
 RT "The genome sequence of *Schistosoma* *pompe*.";  
 RL Nature 415:871-880(2002)  
 CC -1- FUNCTION: BINDS TO AND FACILITATES THE FUNCTIONING OF THE MEIOTIC  
 CC REGULATOR MEI2. MAY ALSO BE INVOLVED IN CONJUGATION BY INTERACTING  
 CC WITH STE11. ESSENTIAL FOR CELL GROWTH.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- SIMILARITY: Contains 7 WD repeats.  
 CC -----  
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 CC -----  
 CC EMBL: AB032552; BAA84585.1; -  
 CC EMBL: Z95396; CAB08769.1; -  
 CC PIR: T38943; T38943.  
 CC DR GeneDB: SPombe; SPAC57A7.1; -  
 CC InterPro: IPR001680; WD40.  
 CC DR InterPro: IPR004083; Yeast176.  
 CC Pfam: PF00400; WD40; 5.  
 CC PRINTS: PR01547; YEAST176DUF.  
 CC SMART: SM00320; WD40; 6.  
 CC DR PROSITE: PS00678; WD\_REPEATS\_1; 1.  
 CC DR PROSITE: PS00682; WD\_REPEATS\_2; 2.  
 CC DR PROSITE: PS0294; WD\_REPEATS\_REGION; 1.  
 CC Meiosis; WD Repeat; Repeat.  
 CC FT REPEAT 986 1029 WD 1.  
 CC FT REPEAT 1033 1074 WD 2.  
 CC FT REPEAT 1087 1126 WD 3.  
 CC FT REPEAT 1130 1170 WD 4.  
 CC FT REPEAT 1176 1216 WD 5.  
 CC FT REPEAT 1219 1259 WD 6.  
 CC FT REPEAT 1268 1308 WD 7.  
 CC SO SEQUENCE 1313 AA; 148533 MW; C71B663B0171E7A4 CRC64;  
 Query Match 7.0%; Score 86; DB 1; Length 1313;  
 Best Local Similarity 22.2%; Pred. No. 7;  
 Matches 58; Conservative 31; Mismatches 84; Indels 88; Gaps 12;  
 QY 15 LCTVLMHLAV--PALNR-----TGDPGPGSI-----QTYDLTRYLHQLR 56  
 DB 811 LAFLQHLPALHAKASLKDITNSVTSDEKPPFVSSENKILNRSFSLRSLKGLALS 870  
 QY 57 LAG-----TYLNYL-----GPP-FNEBDPFPRLGAEITLPRATNL 91  
 DB 871 LAGSDRASLISLNGENKPAESNLNHLTSAKVGPAPAELELYQ-----SELDMLTSLYIF 926  
 QY 92 EVMRSINDRLRLTONYEAYSHLLCYLRGL--NRQATAELEKRSIAHPTS-----LOG 142  
 DB 927 DMSRKYFTPEQKRPNEDEPGSICYNQRLMRNRNKLITRRPRLAELYSTNGMNQNLMT 986  
 QY 143 LIGSLAGVATLGYPLPQLPGLTEPAMAGPAPASDPLQKMDDFWLKE---LQTLWRSA 199  
 DB 987 FNNITL-----PRKLMHFQEDQLITLGDMDIIOVMDMRN 1022  
 QY 200 KDFNRLKKKKOPPAASVTLHL 220  
 DB 1023 KCLNSFK-----TSASATNV 1038  
 RESULT 9  
 PHAC\_PSEOL STANDARD; PRT; 560 AA.  
 AC P26496;  
 DT 01-AUG-1992 (Rel. 23, Created)  
 DT 01-AUG-1992 (Rel. 23, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Poly(3-hydroxyalkanoate) polymerase 2 (EC 2.3.1.-) (PHA polymerase 2)  
 DE (PHA synthase 2) (Polyhydroxyalkanoic acid synthase 2).  
 GN PHAC.  
 OS Pseudomonas oleovorans.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Pseudomonadaceae; Pseudomonas.  
 OX NCBI\_TaxID=301;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=GP01.  
 RX MEDLINE=9115830; PubMed=1989978;  
 RA Hulsman G.W., Wontink E., Weima R., Kazemier B., Teipstra P.,  
 RA Micholt B.;  
 RT "Metabolism of poly(3-hydroxyalkanoates) (PHAs) by *Pseudomonas*  
 RT *oleovorans*. Identification and sequences of genes and function of the  
 RT encoded proteins in the synthesis and degradation of PHA.";  
 RL J. Biol. Chem. 266:2191-2198(1991).  
 CC -1- FUNCTION: P.OLEOVORANS ACCUMULATES POLY(3-HYDROXYALKANOATES) AFTER  
 CC GROWTH ON MEDIUM CHAIN LENGTH HYDROCARBONS. LARGE AMOUNTS OF THIS  
 CC POLYESTER ARE SYNTHESIZED WHEN CELLS ARE GROWN UNDER NITROGEN-  
 CC LIMITING CONDITIONS. WHEN NITROGEN IS RESUPPLIED IN THE MEDIUM,  
 CC THE ACCUMULATED PHA IS DEGRADED.  
 CC -1- SIMILARITY: BELONGS TO THE PHA/PHB SYNTHASE FAMILY.  
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 CC -----  
 CC EMBL: M58445; AAA25934.1; -  
 CC PIR: C38604; C38604.  
 CC DR InterPro: IPR000073; A/b hydrolyase.  
 CC DR Pfam: PF00561; abhydrolyase; 1.  
 CC KM PHA biosynthesis; Transferase; Acyltransferase.  
 CC FT ACT SITE 296 296 POTENTIAL.  
 CC SO SEQUENCE 560 AA; 62631 MW; E2CD844FC1616883 CRC64;  
 Query Match 7.0%; Score 85.5; DB 1; Length 560;  
 Best Local Similarity 30.2%; Pred. No. 2.6;  
 Matches 38; Conservative 16; Mismatches 43; Indels 29; Gaps 7;  
 QY 77 PRLGAEITLPRATVNEVMRSINDRLRLTONYEAYSHLLCYLRGLNRQATAELEKRSI--A 134  
 DB 5 PAKGPTPLPATSMNVQ-----NAIIGLRGR-----DLISTLRNVSROS-----LRHPLHTA 50  
 QY 135 HFCTSLGSLGSLAGVATLGYPLPQLPG-----TEPAMAPAPASDPLQKMDDFWLKE 190  
 DB 51 HHLALGGLGRV-----ILGDTPLQPNDRPDRFSDPTWSONPFRGLQA---YLAWQ 101  
 QY 191 LQTLWR 196  
 DB 102 KQTRLM 107  
 RESULT 10  
 HUPK\_RHOCA STANDARD; PRT; 294 AA.  
 ID HUPK\_RHOCA  
 AC P30757;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hydrogenase expression/formation protein hupK.  
 GN HUPK.  
 OS Rhodospirillum rubrum (Rhodospirillum rubrum).  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirales;  
 OC Rhodospirillaceae; Rhodospirillum.  
 OX NCBI\_TaxID=1061;  
 RN [1]  
 RP SEQUENCE FROM N.A.



RA Fribourg S., Braun I.C., Izaurralde E., Conti E.;  
 RT "Structural basis for the recognition of a nucleoporin FG repeat by  
 RT the NTF2-like domain of the TAP/p15 mRNA nuclear export factor.",  
 RL Mol. Cell 8:645-656(2001).  
 RP STRUCTURE BY NMR OF 551-619, AND MUTAGENESIS OF PHE-617.  
 RX MEDLINE=21912422; PubMed=11875519;  
 RA Grant R.P., Hurt E., Neuhaus D., Stewart M.;  
 RT "Structure of the C-terminal FG-nucleoporin binding domain of  
 RT Tap/Nxt1".  
 RL Nucleic. Biol. 9:247-251(2002).  
 CC -1- FUNCTION: Involved in the nuclear export of mRNA species bearing  
 CC retroviral constitutive transport elements (CTE) and in the export  
 CC of mRNA from the nucleus to the cytoplasm.  
 CC -1- SUBUNIT: Interacts with NXT1, NXT2, E1B-AP5, RAB1, the RRP  
 CC proteins and with several nucleoporins.  
 CC -1- SUBCELLULAR LOCATION: Nuclear; localized predominantly in the  
 CC nucleoplasm and at both the nucleoplasmic and cytoplasmic faces of  
 CC the nuclear pore complex. Shuttles between the nucleus and the  
 CC cytoplasm.  
 CC -1- TISSUE SPECIFICITY: Expressed ubiquitously.  
 CC -1- DOMAIN: The minimal CTE binding domain consists of an RNP-  
 CC type RNA binding domain (RBD) and leucine-rich repeats.  
 CC -1- DOMAIN: The nucleoporin binding domain consists of a NTF2-like  
 CC domain and a UBA-like domain. The NTF2 domain heterodimerizes with  
 CC NXT1 AND NXT2. The formation of NXT1/NXT1 heterodimers is required  
 CC for NXT1-mediated nuclear mRNA export. The UBA-like domain  
 CC mediates direct interactions with nucleoporin-FG-repeats and is  
 CC necessary and sufficient for localization of NXT1 to the nuclear  
 CC rim. The conserved loop 594-NMD-596 of the UBA domain has a  
 CC critical role in the interaction with nucleoporin.  
 CC -1- DOMAIN: The leucine-rich repeats and the NTF2-domain are  
 CC essential for the export of mRNA from the nucleus.  
 CC -1- MISCELLANEOUS: The RNA-binding domain is a non-canonical RNP-type  
 CC domain.  
 CC -1- SIMILARITY: BELONGS TO THE NXP FAMILY.  
 CC -1- SIMILARITY: Contains 4 leucine-rich (LRR) repeats.  
 CC -1- SIMILARITY: Contains 1 NTF2 domain.  
 CC -1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.  
 CC -1- SIMILARITY: Contains 1 UBA-like domain.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL, AJ133713; CA10753.1; -;  
 DR EMBL, AF12880; AAD39102.1; -;  
 DR EMBL, AF126246; AAD20016.1; -;  
 DR EMBL, BC004904; AAH04904.1; -;  
 DR EMBL, AK027192; -; NOT ANNOTATED\_CDS.  
 DR EMBL, U80073; AAB81111.1; -;  
 DR PDB, 1FO1; 03-NOV-00.  
 DR PDB, 1FT8; 11-DEC-00.  
 DR PDB, 1KOH; 27-FEB-02.  
 DR PDB, 1KOO; 27-FEB-02.  
 DR PDB, 1OAI; 20-FEB-03.  
 DR Genew; HGNC:8071; NXP1.  
 DR GK; Q9UBU9; -;  
 DR MIM; 602647; -;  
 DR InterPro; IPR001611; LRR.  
 DR InterPro; IPR003603; LRRcap.  
 DR InterPro; IPR002075; NTF2.  
 DR InterPro; IPR005637; TAP\_C.  
 DR PDB; 1G05; 28-MAR-02.  
 DR PDB; 1JUG; 18-DEC-02.  
 DR PDB; 1JNS; 23-JUN-01.  
 DR Pfam; PF00560; LRR; 1.  
 DR Pfam; PF02136; NTF2; 1.  
 DR Pfam; PF03943; TAP\_C; 1.

DR PRINTS; PR00019; LEURICRPT.  
 DR SMART; SM00446; LRRcap; 1.  
 DR PROSITE; PS0177; NTF2 DOMAIN; 1.  
 KW Transport; mRNA transport; Nuclear protein; RNA-binding; Repeat;  
 KW Leucine-rich repeat; Multigene family; 3D-structure.  
 FT DOMAIN 119 198 RNA-BINDING (RRM).  
 Query Match 7.0%; Score 86; DB 1; Length 619;  
 Best local similarity 25.4%; Pred. No. 2.7;  
 Matches 61; Conservative 32; Mismatches 89; Indels 58; Gaps 14;  
 QY 5 AGDSWGM-----ACICTVLMHLPAVPALNRTGDP-GRGSIQKTYDLT---RYLEHQL 54  
 DB 400 SGRDGLDAVDHAGCCSLIPFQNPASRLAEYFQDSRNKKLKPFTLRFLKQTR 459  
 QY 55 RSLACTYINLYGPPNEDRNP--PRGAE--TLPRATVN---LEWMSLNDRLR-LTON 106  
 DB 460 LNVV-AFLNEL--PTQHDVNSFVVDISAQSTLLCFSVNGVFKVDKSRDLSLAFRT 516  
 QY 107 Y---EAYSHLCTYLRG--LNRQAATAELEDRSLAHFCTSLQGLAGSIAGMATLGYPLPOP 161  
 DB 517 FIAPNPSNSGLCTVNDLEFVNMSSEIQRAFA-----MAP 553  
 QY 162 LPGETPAPAPGPASDFLOK-----MDFWLKLKQLTWL---RSANDFRLKKKQGP 212  
 DB 554 TPSSPVPFTLSPEDQEMLQARSTQSGMWLEWSQKCLQNNMDYTRSQAFTLLKAKGRIP 613  
 RESULT 8  
 MIP1\_SCHPO STANDARD; PRT; 1313 AA.  
 AC P87141;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 40, Last annotation update)  
 DE WD-repeat protein mip1.  
 GN MIP1 OR SPAC5747.11.  
 OS Schizosaccharomyces pombe (Fission yeast).  
 OC Schizosaccharomycetes; Fungi; Ascomycota; Schizosaccharomycetes;  
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
 OC Schizosaccharomycetes.  
 OX NCBI\_TaxID=4896;  
 RN [1]  
 RP SEQUENCE FROM N.A., FUNCTION, AND SUBCELLULAR LOCATION.  
 RX MEDLINE=20115869; PubMed=10648609;  
 RA Shinozaki-Yabana S., Watanabe Y., Yamamoto M.;  
 RT "Novel WD-repeat protein Mip1 facilitates function of the meiotic  
 RT regulator Mei2p in fission yeast.";  
 RL Mol. Cell. Biol. 20:1234-1242(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=972;  
 RX MEDLINE=21848401; PubMed=11859360;  
 RX Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,  
 RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Boman S.,  
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,  
 RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,  
 RA Gentles S., Goble A., Hamlin N., Harris D., Hitalso J., Hodgson G.,  
 RA Holtroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagsle J.,  
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,  
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odeh C.,  
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitch E.,  
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,  
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,  
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,  
 RA Woodward J., Volkart G., Aert R., Roben J., Grymoprez B.,  
 RA Welljens I., Vansireels E., Rieger M., Schaefer M., Mueller-Auer S.,  
 RA Gabel C., Fuchs M., Fritz C., Holzer M., Moestl D., Hilbert H.,  
 RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,  
 RA Eger P., Zimmermann W., Wedler H., Wandt R., Purnelle B.,  
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Leleau V., Motter S.,  
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,  
 RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Thode G.,

SQ SEQUENCE 1009 AA; 113987 MW; F3DB81DD06135266 CRC64;  
Query Match 7.2%; Score 88; DB 1; Length 1009;  
Best Local Similarity 23.3%; Pred. No. 3.3;  
Matches 45; Conservative 21; Mismatches 65; Indels 62; Gaps 8;  
QY 50 LEHQ-----LRSAGTYLNTYLPFPNEDFNPRLGATLPRATVEMVSLNDRRLTQ 105  
DB 842 LQHRPVVLFGDLAGTAPKLPFGPOQGEAVTLPPNHLQIL-----SIPGMYSSNHTHSQ 896  
QY 106 NYRNYHLLCYAGLNRQAATALRSIAHF-----CTSLQGLGSIAG 149  
DB 897 N-----LKKHGEAQAOLRVLLRYLHYEVGEDPVLSQPTVNLQAVLQALGS 946  
QY 150 VVATLGYPLPPLPGTEPAPAPASDFLQKMDFWLKELOTWLRSAKDFNR--LKK 207  
DB 947 VVAV-----EERSLTGT-----WDLMLRMKRWKTPGHRHDDTTS 982  
QY 208 KMGPPAAS-VTLH 219  
DB 983 PSRPPGPGPIITVH 995  
RESULT 7  
NXFL HUMAN STANDARD; PRT; 619 AA.  
AC 09UBD9; 099799; 09UOL2;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Nuclear RNA export factor 1 (Tip associating protein) (Tip-associated protein) (mRNA export factor TAP).  
OS NXFL OR TAP.  
GN Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
OX NCBI\_TaxID:9606;  
RN [1]  
RP SEQUENCE FROM N.A., AND MUTAGENESIS.  
RC TISSUE=Cervical carcinoma;  
RX MEDLINE=99219873; PubMed=10202158;  
RA Braun I.C., Rohrbach E., Schmitt C., Izaurralde E.;  
RT "TAP binds to the constitutive transport element (CTE) through a novel RNA-binding motif that is sufficient to promote CTE-dependent RNA export from the nucleus.";  
RL EMBO J. 18:1953-1965(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99257272; PubMed=10323864;  
RA Kang Y., Cullen B.R.;  
RT "The human Tap protein is a nuclear mRNA export factor that contains novel RNA-binding and nucleocytoplasmic transport sequences.";  
RL Gene Dev. 13:1126-1139(1999).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99384298; PubMed=10454577;  
RA Bear J., Tan W., Zolotukhin A.S., Tabernero C., Hudson E.A., Felber B.K.;  
RT "Identification of novel import and export signals of human TAP, the protein that binds to the constitutive transport element of the type D retrovirus mRNA.";  
RL Mol. Cell. Biol. 19:6306-6317(1999).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Placenta;  
RX MEDLINE=12477932;  
RA Straussberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schler G.D., Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., RA Vallon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., RA Fahy J., Helton E., Kettman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., RA Whiting M., Madan A., Young A.C., Green E.D., Dickson M.C., RA Blakesley R.W., Touchman J.W., Myers J., Myers R.M., RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., RA Butterfield J.S.N., Krzywicki M.I., Skalska U., Smalls D.E., RA Schercher A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [5]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RA Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K., RA Nakajima Y., Mizuno T., Morinaga M., Tanigami A., Fujimura T., Ota T., RA Yamada K., Fujii Y., Ozaki K., Hideo M., Ohmori Y., Ota T., Suzuki Y., RA Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y., RA Isogai T., Sugano S.;  
RT "NEO human cDNA sequencing project.";  
RL Submitted (FEB-2000) to the EMBL/Genbank/DBJ databases.  
RN [6]  
RP SEQUENCE OF 61-619 FROM N.A.  
RC TISSUE=Lymphocytes;  
RX MEDLINE=97318898; PubMed=9175835;  
RA Yoon D.-W., Lee H., Seol W., Demaria M., Rosenzweig M., Jung J.U.;  
RT "Tap: a novel cellular protein that interacts with tip of herpesvirus salmuri and induces lymphocyte aggregation.";  
RL Immunity 6:571-582(1997).  
RN [7]  
RP FUNCTION.  
RX MEDLINE=98325379; PubMed=9660949;  
RA Grueter P., Tabernero C., von Kobbe C., Schmitt C., Saavedra C., RA Bachl A., Wilm M., Felber B.K., Izaurralde E.;  
RT "TAP, the human homolog of Mex67p, mediates CTE-dependent RNA export from the nucleus.";  
RL Mol. Cell 1:649-659(1998).  
RN [8]  
RP CHARACTERIZATION.  
RX MEDLINE=21282872; PubMed=11259411;  
RA Braun I.C., Herold A., Rode M., Conti E., Izaurralde E.;  
RT "Overexpression of rrp1/5 heterodimers bypasses nuclear retention and stimulates nuclear mRNA export.";  
RL J. Biol. Chem. 276:20536-20543(2001).  
RN [9]  
RP CHARACTERIZATION.  
RX MEDLINE=20132240; PubMed=10668806;  
RA Bachl A., Braun I.C., Rodriguez J.P., Pante N., Ribbeck K., RA von Kobbe C., Kutay U., Wilm M., Gorlich D., Carmo-Fonseca M., RA Izaurralde E.;  
RT "The C-terminal domain of TAP interacts with the nuclear pore complex and promotes export of specific CTE-bearing RNA substrates.";  
RL RNA 6:136-158(2000).  
RN [10]  
RP MUTAGENESIS.  
RX MEDLINE=21151125; PubMed=11256625;  
RA Suyama M., Doerks T., Braun I.C., Sattler M., Izaurralde E., Bork P.;  
RT "Prediction of structural domains of TAP reveals details of its interaction with p15 and nucleoporins.";  
RL EMBO Rep. 1:53-58(2000).  
RN [11]  
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 102-372.  
RX MEDLINE=20514125; PubMed=11060011;  
RA Liker E., Fernandez E., Izaurralde E., Conti E.;  
RT "The structure of the mRNA export factor TAP reveals a cis arrangement of a non-canonical RNP domain and an LRR domain.";  
RL EMBO J. 19:5587-5598(2000).  
RN [12]  
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF COMPLEX WITH NXFL, AND X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF COMPLEX WITH NXFL-PG-REPEAT.  
RX MEDLINE=21468398; PubMed=11583626;



RT "Paranodal junction formation and spermatogenesis require  
RT sulfolipcolipids."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:4227-4232(2002).  
CC -1- FUNCTION: Catalyzes the sulfation of membrane glycolipids. Seems  
CC to prefer beta-glycosides at the nonreducing termini of sugar  
CC chains attached to a lipid moiety. Catalyzes the synthesis of  
CC HSO3-3-galactosylceramide (sulfolipid), a major lipid component of  
CC the myelin sheath and of HSO3-3-monogalactosylalkylglycerol  
CC (semioipid), present in spermatozoa. Also acts on  
CC lactosylceramide, galactosyl 1-alkyl-2-sn-glycerol and galactosyl  
CC diacylglycerol (in vitro).  
CC -1- CATALYTIC ACTIVITY: 3'-phosphoadenylylsulfate + a  
CC galactosylceramide = adenosine 3',5'-bisphosphate +  
CC galactosylceramide sulfate.  
CC -1- CATALYTIC ACTIVITY: 3'-phosphoadenylylsulfate +  
CC monogalactosylalkylglycerol = adenosine 3',5'-bisphosphate +  
CC monogalactosylalkylglycerol sulfate.  
CC -1- PATHWAY: Sphingolipid and glycerolipid biosynthesis.  
CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Golgi membrane (By  
CC similarity).  
CC -1- TISSUE SPECIFICITY: Expressed in brain, testis, kidney, stomach,  
CC muscle, and spleen.  
CC -1- MISCELLANEOUS: Mice homozygous for a null mutation of the CST gene  
CC display hindlimb weakness from week 6 of age and subsequently show  
CC a pronounced tremor and progressive ataxia. Myelin vacuolation is  
CC observed in the cerebellar white matter, diencephalon, brainstem  
CC and spinal anterior column. Male mice were infertile due to a  
CC blocked spermatogenesis.  
CC  
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CC  
CC EMBL; AB032940; BAA93009.1; -  
CC EMBL; AB032939; BAA93008.1; -  
CC EMBL; AK007645; BAA25160.1; -  
CC EMBL; BC026806; AAB26806.1; -  
CC MGD; MG1:1858277; Gcst.  
CC GO; GO:0016021; C:integral to membrane; IC.  
CC DR GO; GO:0001733; P:galactosylceramide sulfotransferase activity; IDA.  
CC DR GO; GO:0006682; P:galactosylceramide biosynthesis; IDA.  
CC DR GO; GO:0042552; P:myelination; IMP.  
CC DR GO; GO:0007283; P:spermatogenesis; IMP.  
CC KW Transferrase; Transmembrane; Glycoprotein.  
CC FT DOMAIN 1 12 CYTOPLASMIC (POTENTIAL).  
CC FT TRANSMEM 13 35 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
CC FT (POTENTIAL).  
CC FT DOMAIN 36 423 LUMENAL, CATALYTIC (POTENTIAL).  
CC FT CARBOHYD 66 66 N-LINKED (GLCNAC. ) (POTENTIAL).  
CC FT CARBOHYD 312 312 N-LINKED (GLCNAC. ) (POTENTIAL).  
CC FT CONFLICT 18 18 L -> P (IN REF. 2).  
CC FT CONFLICT 263 263 R -> Q (IN REF. 2).  
CC FT CONFLICT 271 271 E -> Q (IN REF. 2).  
CC FT CONFLICT 358 358 Q -> R (IN REF. 1).  
CC FT CONFLICT 392 392 R -> G (IN REF. 2).  
CC FT CONFLICT 398 398 I -> T (IN REF. 1).  
CC FT CONFLICT 423 423 AA; 48968 MW; FDS4ALA71FAABE46 CRC64;  
CC SQ SEQUENCE

Query Match 7.6%; Score 93; DB 1; Length 423;  
Best Local Similarity 23.1%; Pred. No. 0.37;  
Matches 55; Conservative 22; Mismatches 65; Indels 96; Gaps 11;

44 YDLTRYLEHQLSLAGTYNY---LGGP-----FNEP-----72  
Db 204 YPSSYNAHYLNKLFYDLGYSLLDPASPRVOEHLEVERRHVLLQYEDDESIVLLR 263  
73 -----DFNPPRLGAEFLPRATVNLVWMSLNDRLRLTONYEAYSHL 113

Db 264 ELLCWDLVDLYEKNARNRSDPVRISGELYRRAT-----AMNLLD--VRLYRHFNASFWR 317  
Qy 114 LCTLRGLNROA-ATAEILRS---IAFCTSLQGLGSLA-----GVMATLGYV 157  
Db 318 KVAFGRERMARVALRLROANEMRITCIDGGAVAEALQDSAMPQWPLGKSLIGV 377  
Qy 158 LPQPLDGTBPVAMPAPGASHDFLOKMDFWLKLKIQ-----TWLMSAKDFNR 204  
Db 378 LKRSI-----GQHOLGRM-----LTPEIQVLSLDGANLWTKMLKFLRDLFR 422

RESULT 4  
CTFL\_HUMAN STANDARD; PRT; 201 AA.  
ID CTFL\_HUMAN  
AC Q16619;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Cardiotrophin-1 (CT-1).  
GN CTFL.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Heart;  
RX MEDLINE=96429882; PubMed=8833032;  
RA Beatty B.G., Swanson T.A., Shaw K.U., Kuang W.-J., Gray C.L.,  
RT "Human cardiotrophin-1: protein and gene structure, biological and  
RT binding activities, and chromosomal localization."  
RL Cytokine 8:183-189(1996)  
CC -1- FUNCTION: INDUCES CARDIAC MYOCYTE HYPERROPHY IN VITRO. BINDS TO  
CC AND ACTIVATES THE LEUKEMIA INHIBITORY FACTOR RECEPTOR (LIF  
CC RECEPTOR)/GP 130 RECEPTOR COMPLEX.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART, SKELETAL MUSCLE,  
CC THYMUS, TESTIS AND OVARY. LOWER LEVELS IN LUNG, KIDNEY, PANCREAS,  
CC BRAIN, PLACENTA, LIVER, SPLEEN, COLON OR PERIPHERAL BLOOD  
CC LEUCOCYTES.  
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.  
CC  
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CC  
CC EMBL; U43033; AAD12173.1; -  
CC EMBL; U43031; AAD12173.1; JOINED.  
CC EMBL; U43032; AAD12173.1; JOINED.  
CC EMBL; U43030; AAB85229.1; -  
CC PIR; G02312; G02312.  
CC GeneW; HGNC:2499; CTFL.  
CC MIM; 600435; -  
CC DR GO; GO:0005576; C:extracellular; TAS.  
CC DR GO; GO:0005146; P:leukemia inhibitory factor receptor ligand . . . ; TAS.  
CC DR GO; GO:0008283; P:cell proliferation; TAS.  
CC DR GO; GO:0007267; P:cell-cell signaling; TAS.  
CC DR GO; GO:0007517; P:muscle development; TAS.  
CC DR GO; GO:0007399; P:neurogenesis; TAS.  
CC DR GO; GO:0008284; P:positive regulation of cell proliferation; TAS.  
CC KW Cytokine; Polymorphism.  
CC FT VARIANT 92 92 A -> T (IN dbSNP:2234933).  
CC FT  
CC SQ SEQUENCE 201 AA; 21227 MW; 0235A7B5745F675F CRC64;  
FT

Query Match 7.5%; Score 91.5; DB 1; Length 201;  
Best Local Similarity 25.7%; Pred. No. 0.2;

Db 84 -SERLR--QDAALGALPALLDAVRRROKELNPRARLRLSLSDAARQVRAALGAAYETVL 140  
OY 152 ATIGV-----PLPQPLPCTEPAPAPGPAHSDFLOKDDDFLLKEQLTWMRSKXDNRL 205  
Db 141 AALGAANGPVEPV-ATISALTNSAGVFSKAVLGLHVCGLYGEWVSRTGDLGQL 197

RESULT 2  
CTPI\_MOUSE  
ID CTPI\_MOUSE STANDARD; PRT; 203 AA.  
AC 060753;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-JUL-1998 (Rel. 36, Last annotation update)  
DE Cardiotrophin-1 (CT-1).  
GN CTPI.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95166785; PubMed=7862649;  
RA Penica D., King K.L., Shaw K.J., Luis E., Rullamae J., Luoh S.-M.,  
RA Darbonne W.C., Knutson D.S., Yen R., Chien K.R., Baker J.B.,  
RA Wood W.I.;  
RT "Expression cloning of cardiotrophin 1, a cytokine that induces  
RT cardiac myocyte hypertrophy.";  
RL Proc. Natl. Acad. Sci. U.S.A. 92:1142-1146(1995).  
CC -1- FUNCTION: INDUCES CARDIAC MYOCYTE HYPERTROPHY IN VITRO. BINDS TO  
CC RECEPTOR/GP 130 RECEPTOR COMPLEX.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART, SKELETAL MUSCLE,  
CC LIVER, LUNG AND KIDNEY. LOWER LEVELS IN TESTIS AND BRAIN. NO  
CC EXPRESSION IN SPLEEN.  
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.  
CC  
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CC  
CC EMBL; U18366; AAC52173.1; .  
CC DR PIR; I49153; I49153.  
CC DR MGI; MGI:105115; Ctf1.  
CC KW Cytokine.  
SQ SEQUENCE 203 AA; 21509 MW; 8B3D41A0B3B232F CRC64;

Query Match 9.0%; Score 110.5; DB 1; Length 203;  
Best Local Similarity 27.4%; Pred. No. 0.0034;  
Matches 49; Conservative 23; Mismatches 86; Indels 21; Gaps 6;

OY 40 IOKTDLTRYELHQLRSLAGTYLNTVIGPPRNPDPNPPPL---GAETLPRAVNELEWRS 96  
Db 27 IROTNLALLTKRYAEQLLEBYVOOGGFFGFGPSPLPLAGLSGAPASAGLPV--- 83  
OY 97 LNDRLRLTONYEAVALCYLGLNROA-----TALRLSLAHCTSLQGLGSIAGVM 151  
Db 84 -SERLR--QDAALGALPALLDAVRRROKELNPRARLRLSLSDAARQVRAALGAAYETVL 140  
OY 152 ATIGV-----PLPQPLPCTEPAPAPGPAHSDFLOKDDDFLLKEQLTWMRSKXDNRL 205  
Db 141 AALGAANGPVEPV-ATISALTNSAGVFSKAVLGLHVCGLYGEWVSRTGDLGQL 197

RESULT 3  
CST\_MOUSE  
ID CST\_MOUSE STANDARD; PRT; 423 AA.  
AC 09JHE4; Q9D8V6;

DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Galactosylceramide sulfoltransferase (EC 2.8.2.11) (GalCer  
DE sulfoltransferase) (Cerebroside sulfoltransferase) (3')-  
DE phosphadenylylsulfate:galactosylceramide 3'-sulfoltransferase)  
DE (3'-phosphadenosine-5'-phosphosulfate:GalCer sulfoltransferase).  
GN CST OR GCST.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.  
RC TISSUE=Kidney;  
RX MEDLINE=20193614; PubMed=10727929;  
RA Hirahara Y., Tsuda M., Wada Y., Honke K.;  
RT "cDNA cloning, genomic cloning, and tissue-specific regulation of  
RT mouse cerebroside sulfoltransferase.";  
RL Eur. J. Biochem. 267:1909-1917(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Pancreas;  
RX MEDLINE=21085660; PubMed=11217851;  
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,  
RA Aizawa K., Irawa M., Nishi K., Kiyosawa H., Kondo S., Yamanka I.,  
RA Saito T., Okazaki Y., Gojodori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Ballov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,  
RA Kuell P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
RA Schriml L.M., Straubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
RA Blake J., Botelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Butt C., Fletcher C., Fujita M., Gariboldi M.,  
RA Guestinch S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazarelli J., Mombere P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,  
RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,  
RA Hayashizaki Y.;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:665-690(2001).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Colon;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shermen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Schetz T.B.,  
RA Brownstein M.J., Usdin T.B., Toshlyuk S., Carinini P., Prange C.,  
RA Raha S.S., Loguella N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,  
RA Villalon D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettelman M., Madan A.C., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A.C., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmitt J., Myers R.M.,  
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Matra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
RT human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [4]  
RP FUNCTION.  
RX MEDLINE=21927584; PubMed=11917099;  
RA Honke K., Hirahara Y., Dupree J., Suzuki K., Popko B., Fukushima K.,  
RA Fukushima J., Nagasawa T., Yoshida N., Wada Y., Taniguchi N.;

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OM protein - protein search, using sw model

Run on: February 9, 2004, 06:14:57 ; Search time 10.5 Seconds

(Without alignments)  
1007.715 Million cell updates/sec

Title: US-09-931-704-5

Perfect score: 1224

Sequence: 1 MDLRAGDSWGMALACTVLM.....KKKMPAASVTLHEAHGF 225

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	118.5	9.7	203	CTP1_RAT	Q63086 ratuys novy
2	110.5	9.0	203	CTP1_MOUSE	Q60753 mus musculus
3	93	7.6	423	CST_MOUSE	Q9jhe4 m galactosy
4	91.5	7.5	201	CTP1_HUMAN	Q16619 homo sapien
5	90	7.4	195	CNTF_CHICK	Q02011 gallus gall
6	88	7.2	1009	M2B2_HUMAN	Q9y2es homo sapien
7	86	7.0	619	NKX1_HUMAN	Q9ub99 homo sapien
8	85.5	7.0	1313	MIPI_SCHPO	P87141 schizosacch
9	85.5	7.0	560	PHAC_PSEOL	P26496 pseudomonas
10	84.5	6.9	294	HUPK_RHOCA	P30797 rhodobacter
11	80.5	6.6	995	M2B2_PIG	Q28649 sus scrofa
12	79.5	6.5	830	VPB3_HUMAN	Q13488 h vacuolar
13	79	6.5	291	YM32_MYCTU	Q10515 mycobacteri
14	79	6.5	1332	ATK1_HUMAN	P46379 homo sapien
15	79	6.5	1620	ATK1_HUMAN	Q9um73 homo sapien
16	78.5	6.4	571	ATK1_MYCTU	P96371 mycobacteri
17	78.5	6.4	1473	NAL1_HUMAN	Q9c000 homo sapien
18	78.5	6.4	1844	POLR_TTMV	P10358 turpiti yell
19	78	6.4	422	Y140_HUMAN	Q14533 homo sapien
20	78	6.4	427	RT65_MYXXA	P23071 myxococcus
21	78	6.4	515	YBL1_SCHPO	Q10340 schizosacch
22	78	6.4	917	SYI_STAUV	P41972 staphylococ
23	77.5	6.3	572	SYM_AEPP	Q94y3 aeropyrum p
24	77.5	6.3	1182	HAIR_MOUSE	Q61645 mus musculu
25	76.5	6.3	2261	RRLP_MUMPM	P30929 mumps virus
26	76.5	6.2	870	BCA1_HUMAN	P56945 homo sapien
27	76.5	6.2	2390	SPCP_HUMAN	Q15020 homo sapien
28	76	6.2	372	CD14_RABIT	Q28680 cryotolagus
29	76	6.2	508	EGRI_RAT	P08154 rattus norv
30	76	6.2	1137	MSB1_YEAST	P21339 saccharomyc
31	75.5	6.2	334	BC12_HUMAN	Q9h009 homo sapien
32	75.5	6.2	346	YG20_YEAST	P53359 saccharomyc
33	75.5	6.2	390	YL28_STRCO	P40181 streptomyce

34	75	6.1	296	1	RECO_ANASP	Q89D19 anabaena sp
35	75	6.1	343	1	DEFA_SYNY3	P73212 synchocyst
36	75	6.1	452	1	TIL_DROME	P18102 drosophila
37	75	6.1	552	1	MP2_MOUSE	Q9w734 mus musculu
38	75	6.1	715	1	PERE_HUMAN	P16578 homo sapien
39	74.5	6.1	346	1	CNA1_SCHPO	P36599 schizosacch
40	74.5	6.1	1009	1	FAK2_HUMAN	Q14289 h protein t
41	74.5	6.1	1941	1	YRM8_CAEEL	Q09417 caenorhabdi
42	74.5	6.1	2388	1	SPCP_RAT	Q9gwn8 rattus norv
43	74	6.0	388	1	YINB_BCOLI	P76223 escherichia
44	74	6.0	421	1	PTB2_HUMAN	P49753 homo sapien
45	74	6.0	618	1	NKX1_RAT	Q88984 rattus norv

## ALIGNMENTS

RESULT 1	CTP1_RAT	STANDARD	PRT	203 AA
ID	CTP1_RAT			
AC	063086			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	15-JUL-1998 (Rel. 36, Last annotation update)			
DE	Cardiotrophin-1 (CT-1).			
GN	CTP1.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
RP	(1)			
RC	SEQUENCE FROM N.A.			
RC	STRAIN=WiStar; TISSUE=Heart;			
RA	MEDLINE=96193659; PubMed=8604995;			
RA	Ishikawa M., Saito Y., Miyamoto Y., Kuwahara K., Ogawa E.,			
RA	Nakagawa O., Harada M., Masuda I., Nakao K.;			
RT	"CDNA cloning of rat cardiotrophin-1 (CT-1): augmented expression of			
RT	CT-1 gene in ventricle of genetically hypertensive rats."			
RL	Biochem. Biophys. Res. Commun. 219:377-381(1996).			
CC	- FUNCTION: INDUCES CARDIAC MYOCYTE HYPERTROPHY IN VITRO. BINDS TO			
CC	AND ACTIVATES THE LEUKEMIA INHIBITORY FACTOR RECEPTOR (LIF			
CC	RECEPTOR)/GP 130 RECEPTOR COMPLEX.			
CC	- SUBCELLULAR LOCATION: Secreted (By similarity).			
CC	- TISSUE SPECIFICITY: EXPRESSED IN THE VENTRICLE AND ATRIUM OF ADULT			
CC	RATS. ALSO DETECTED IN THE LUNG, KIDNEY, LIVER, SKELETAL MUSCLE,			
CC	SPLEEN AND URINARY BLADDER. NOT DETECTED IN BRAIN, COLON, TESTIS,			
CC	HYPERTENSION AND HYPERTROPHY.			
CC	- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.			
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CC	or send an email to <a href="mailto:license@sib-sib.ch">license@sib-sib.ch</a> ).			
DR	EMBL; D78591; BA011427.1; -			
DR	PIR; JC4645; JC4645.			
KW	Cytokine.			
SC	SEQUENCE 203 AA, 21439 MW, DFB8921A2FA1C832 CRC64;			
QY	Query Match	9.7%; Score 118.5; DB 1; Length 203;		
DB	Best Local Similarity	27.5%; Pred. No. 0.0061;		
QY	Matches	49; Conservative 26; Mismatches 84; Indels 19; Gaps 6;		
DB	40 IOKTDIRRYLEHQRSLAGTYLNLGPPFNEPDPNPRLL--GATLPRAVNLFWRS 96			
DB	27 IROTNLRLRLTKVADQLEEVYQGGSPFGLGSPSPRLPLAGLSGAPSLAGLPV--- 83			
QY	97 LNDRLRLTQNEAVYSHLTCYLRGLNRQAA-----TAEIRSLAHRCSTSLQGLGSIAGVM 151			

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Qy	61	YNYIGPPN-----EPDFNPRLGAEITLPRATVNLFWRSINDRLTLTONYEASH	112
Db	71	YLSLKNKLSGAMRRSQPGVSP---GPE-----TOPEEKRVRELETEQAYVARLH	122
Qy	113	LL--CYLRGLNRQATAELRSLAHFCTSLQGLGSIAGVMA-TLGYPLPQPLPGTEPAW	169
Db	123	LIDQVFFQELREAG-----RSKAPFEDVVKLIFSNISSIYRPHAQFLPE-LQRRVDM	176
Qy	170	APGPAHSDFLOKMDDFWL-----KELOTWLRSAKDFNRLKKKQOPPAASVT	217
Db	177	AATPRIGDVIQKLAFLKMYSEYVKNFERAAELLATMDKS-QPQEVVTRIQCSAASSS	235
Qy	218	LHLEAH 223	
Db	236	LTLQHH 241	

Search completed: February 9, 2004, 06:19:06  
 Job time : 37 secs



DT 01-OCT-2002 (TRENBLrel. 22, Created)  
 DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)  
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)  
 DE IL-27 p28 subunit.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Pflanz S., Timane J., Cheung J., Robales R., Kanzler H., Gilbert J.,  
 RA Hibbert L., Churakova T., Travis M., Valberg E., Blumenschein W.,  
 RA Macdon J., Wagner J., To W., Zurawski S., McClanahan T., Gorman D.,  
 RA Bazan F., de Waal Malefyt R., Rennick D., Kastlein R.;  
 RT "IL-27 p28 subunit sequences.";  
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY09296; AAM34498.1;  
 SQ SEQUENCE 243 AA; 27476 MW; 2FA0A8B6CF61A8 CRC64;

Query Match 7.6%; Score 92.5; DB 4; Length 243;  
 Best Local Similarity 23.3%; Pred. No. 1; Matches 57; Conservative 26; Mismatches 105; Indels 57; Gaps 9;

QY 1 MDLRAGD-SWGMILACTVL-----MHLPAVALNRTPGPGPSIQK-----TYDL 46  
 DB 1 MCGTAGDGLMRSLSLPLLVQAGVWGRPRPG-----RQSLQGLREFTVSLHL 53  
 QY 47 TRYLEHQLSLAGTYLN-----YLGPPNEPDPNPRGLAETLPRAVNLVWRSIN 98  
 DB 54 AKLSEVVGQAHRAESHLPVNLVLP-----LG-EQLPDLSTFQAMRRIS 101  
 QY 99 DDLRLTQNVAYSHLVCYRGLNRQAATLRLR-SLAHFTSLQGLSIAQVMTLQVP 157  
 DB 102 DDERLCFSTTQPPHAPLGLGTQGRWTNEMQMLAMRLDRDQRLRPQVLAAGN 161  
 QY 158 LEPQ-----LPCTEPAMAPASDPLQMDPDLKELQTLWMSAKDF 202  
 DB 162 LPREBEEREBEERKGLPGALGSLQGPAGVSPQLSYRLHSLVLSAVNEL 221  
 QY 203 NLKK 207  
 DB 222 LLSK 226

## RESULT 14

ID Q9MAU1 PRELIMINARY; PRT; 332 AA.  
 AC Q9MAU1;  
 DT 01-OCT-2000 (TRENBLrel. 15, Created)  
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)  
 DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)  
 DE F13M7.8 protein (Hypothetical protein).  
 GN F13M7.8.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC Eursids II; Brassicales; Brassicaceae; Arabidopsie.  
 NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV, Columbia;  
 RA Violette V.S., Schwartz J.R., Tortum M., Yu G., Kwan A., Liu, S.,  
 RA Li J., Kremenetskaia I., Luros J., Araujo R., Au M., Bredel V.,  
 RA Buehler E., Conway A., Dewar K., Feng J., Kim C., Kurtz D., Li Y.,  
 RA Palm C., Shinn P., Sun H., Davis R., Ecker J., Federjfel N.,  
 RA Theologis A.;  
 RT "The sequence of BAC F13M7 from Arabidopsis thaliana chromosome 1.";  
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV, Columbia;  
 RA Theologis A.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N.,  
 RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;  
 RT "Full-length messenger RNA sequences greatly improve genome  
 RT annotation.";  
 RL Genome Biol. 0:0-0(2002).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,  
 RA Feldmann K.;  
 RT "Full-length cDNA from Arabidopsis thaliana.";  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AC004809; AAF4044.1;  
 DR EMBL; AY085490; AAM62716.1;  
 DR InterPro; IPR002965; P-rich\_exten.  
 DR PRINTS; PR01217; PRICHEXTEN.  
 KW Hypothetical protein.  
 SQ SEQUENCE 332 AA; 36793 MW; 10B86871A1A070F4 CRC64;

Query Match 7.5%; Score 92; DB 10; Length 332;  
 Best Local Similarity 25.9%; Pred. No. 1.7; Matches 57; Conservative 24; Mismatches 73; Indels 66; Gaps 12;

QY 23 PAVPALNRTPGPGPSIQKTYDRLTRYLEHQLSLAGTYLN----- 64  
 DB 113 PSVTGNLSGTP-PPSP--TYDPGYHQRMESLQOFIERNDQIRPLRLGSGFVG 169  
 QY 65 LQPPNEPDPNPRGLAETLPRAVNLVWRSINLDRRLTQNVAYSHLVCYRGLNRQA 124  
 DB 170 LGPIRASQFQIPRA-----PPPSILDTSNRRKRSK-----DCALAVNG--RKV 215  
 QY 125 ATAELRSL-----AHFCTSLQGLSIAQVMTLQVP--GTEPMA 170  
 DB 216 RITBSSSLVLSGRSWMNGAHV-----GIPOBSGIMK--PLKPLPVDLTITTSVP 266  
 QY 171 PPAHSDPLQMDPDLKELQTLWMSAKDFNLKCKKQ 210  
 DB 267 DDPDEBSADEKDEBAVKQL-----SEKL--LKRIIE 298

## RESULT 15

ID Q8BY35 PRELIMINARY; PRT; 655 AA.  
 AC Q8BY35;  
 DT 01-MAR-2003 (TRENBLrel. 23, Created)  
 DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)  
 DE Faciogential dysplasia homolog 2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Thymus;  
 RX MEDLINE=22354683; PubMed=12465651;  
 RA The FANTOM Consortium,  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs.";  
 RL Nature 420:563-573(2002).  
 DR EMBL; AK042260; BAC31206.1;  
 SQ SEQUENCE 655 AA; 74634 MW; F5272F107A29BDBE CRC64;

Query Match 7.5%; Score 92; DB 11; Length 655;

Best Local Similarity 24.8%; Pred. No. 4.1; Matches 61; Conservative 32; Mismatches 93; Indels 60; Gaps 11;

QY 21 HLPVALNRTPGPGPSIQKTYDRLTRYLEHQL-----RSLAGT 60  
 DB 13 NLVAVFENNR--PGEAPGSHLEDQPHSPHQSLSPPEWADPPVKALKSEFRPVSRT 70

DR InterPro; IPR000219; RhGEF.  
 DR InterPro; IPR000306; Znf\_FYVE.  
 DR Pfam; PF01363; FYVE; 1.  
 DR Pfam; PF00169; PH; 1.  
 DR Pfam; PF00621; RhGEF; 1.  
 DR SMART; SM00064; FYVE; 1.  
 DR SMART; SM00233; PH; 1.  
 DR SMART; SM00325; RhGEF; 1.  
 DR PROSITE; PS50010; PH\_2; 1.  
 DR PROSITE; PS50003; PH\_DOMAIN; 1.  
 DR PROSITE; PS50178; ZF\_FYVE; 1.  
 SQ SEQUENCE 727 AA; E2093 MW; 5CD0FBFB905C5FC5 CRC64;

Query Match 7.6%; Score 93; DB 11; Length 727;  
 Best Local Similarity 24.8%; Pred. No. 3.7;  
 Matches 61; Conservative 32; Mismatches 93; Indels 60; Gaps 11;

QY 21 HLPVAVPALNRGTGDPGPGSIQKTYDLTRYLEHQL-----RSLAGT 60  
 DB 13 NLVAVFENNRT--PGEAPGSHLEDPHLPHEQLSLSPPEWAPVKEALKSEFRVPSRT 70  
 QY 61 YANYLGPPFN-----EPDENPRLGAEITLPRAVNLVWRSINDRLRLTONYEAYSH 112  
 DB 71 YLSLKNKLSSGAMRSCQPGVSP--GPE-----IQEBEKKVVELLETEQAVYARLH 122  
 QY 113 LH--CYLRGLNRQATAEILRRSLAHFCTSLQGLGSIAGVMA-TLGYPLPOLPGTEPPAW 169  
 DB 123 LLDQVFFQGLNRAG-----RSKAFPEVDVVKLIFSNISSIRPHAQFLPE-LQRVVDW 176  
 QY 170 APGPASDPLQKMDFWLL-----KELQTLWRSKDFNRLKKQPPASV 217  
 DB 177 AATPRIGDVIQKLAFLPKMYSEYVKNFERAEELATWMDKS-QPQEVVTRIQCSBAS 235  
 QY 218 LHLFAH 223  
 DB 236 LTLQHH 241

## RESULT 11

QYBBI PRELIMINARY; PRT; 200 AA.  
 AC QYBBI;  
 DT 01-MAR-2002 (TREMBlrel. 20, Created)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE Hypothetical protein BMEI10989.  
 GN BMEI10989.  
 OS Brucella melitensis.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Brucellaceae; Brucella.  
 OX NCBI\_TaxID=29459;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=16M / ATCC 23456 / Biotype 1;  
 RX MEDLINE=20020109; PubMed=1175668;  
 RA DelVecchio V.G., Kapralic V., Redkar R.J., Patra G., Mijer C., Los T.,  
 RA Ivanova N., Anderson I., Bhatnagar A., Lykidis A., Renik G.,  
 RA Jabloncki L., Larsen N., D'Souza M., Bernal A., Mazur M., Goldsman E.,  
 RA Selkov E., Elser P.H., Hagius S., O'Callaghan D., Letesson J.-J.,  
 RA Haselkorn R., Kyriades N., Overbeek R.;  
 RT "The genome sequence of the facultative intracellular pathogen  
 RT Brucella melitensis";  
 RT Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).  
 RL EMBL; AE009732; AAL54231.1; -.  
 DR InterPro; IPR000734; Lipase.  
 DR PROSITE; PS00120; LIPASE\_SER; 1.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 200 AA; 21513 MW; BAA8596707B67617 CRC64;

Query Match 7.6%; Score 92.5; DB 16; Length 200;  
 Best Local Similarity 23.9%; Pred. No. 0.78;  
 Matches 55; Conservative 21; Mismatches 89; Indels 65; Gaps 11;

QY 10 GMLACLCTVLMHLPVAVPALNRGTGDPGPGSIQKTYDLTRYLEHQLSLAGTYLNYLGPPF 69  
 DB 2 GILAGAAV---LPSPAPAKTQQAAMPNATSPHQADVYL---LRGFADISTGI----- 51  
 QY 70 NEBDNPPRLGAEITLPRAVNLVWRSINDRLRLTONYEAYSHLCTLRGLNRQA 124  
 DB 52 -----DEIGAE-LQAAGVNAHVQGHAMRLVNLRIADQKNGHLPVLLIGHSLGANA 103  
 QY 125 A---TAELRRSLAHFCTSLQGLGSIAGVMAITGYPLPOLPGT-----EPAW-- 169  
 DB 104 ALIYIAEELRR-----GLAVDYMATFAATGPPPLDGNVRRVYVNFYKQHGKGL 151  
 QY 170 --APGPASDPLQKMDFWLLKELQTLWRSKDFNRLK-KKQPPASV 216  
 DB 152 PLVPGRRFRIHLEND-----FSNKKDVGHFNIEKQRLQAEV 189

## RESULT 12

QYBBI PRELIMINARY; PRT; 232 AA.  
 AC QYBBI;  
 DT 01-MAR-2003 (TREMBlrel. 23, Created)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Hypothetical protein.  
 GN BRA0258.  
 OS Brucella suis.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Brucellaceae; Brucella.  
 OX NCBI\_TaxID=29461;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=1330 / Biovar 1;  
 RX MEDLINE=22247741; PubMed=12271122;  
 RA Paulsen I.T., Sehnadi R., Nelson K.E., Eisen J.A., Heidelberg J.F.,  
 RA Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Beanan M.J.,  
 RA Daugherty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R.,  
 RA Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J., Van Aken S.E.,  
 RA Riedmuller S., Tettelin H., Gill S.R., White O., Salzberg S.L.,  
 RA Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Frazer C.M.;  
 RT The Brucella suis genome reveals fundamental similarities between  
 RT animal and plant pathogens and symbionts.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).  
 DR EMBL; AE014526; AAN33460.1; -.  
 DR TIGR; BRA0258; -.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 232 AA; 24810 MW; 612CB963D7A56E18 CRC64;

Query Match 7.6%; Score 92.5; DB 16; Length 232;  
 Best Local Similarity 23.9%; Pred. No. 0.95;  
 Matches 55; Conservative 21; Mismatches 89; Indels 65; Gaps 11;

QY 10 GMLACLCTVLMHLPVAVPALNRGTGDPGPGSIQKTYDLTRYLEHQLSLAGTYLNYLGPPF 69  
 DB 34 GILAGAAV---LPSPAPAKTQQAAMPNATSPHQADVYL---LRGFADISTGI----- 83  
 QY 70 NEBDNPPRLGAEITLPRAVNLVWRSINDRLRLTONYEAYSHLCTLRGLNRQA 124  
 DB 84 -----DEIGAE-LQAAGVNAHVQGHAMRLVNLRIADQKNGHLPVLLIGHSLGANA 135  
 QY 125 A---TAELRRSLAHFCTSLQGLGSIAGVMAITGYPLPOLPGT-----EPAW-- 169  
 DB 136 ALIYIAEELRR-----GLAVDYMATFAATGPPPLDGNVRRVYVNFYKQHGKGL 183  
 QY 170 --APGPASDPLQKMDFWLLKELQTLWRSKDFNRLK-KKQPPASV 216  
 DB 184 PLVPGRRFRIHLEND-----FSNKKDVGHFNIEKQRLQAEV 221

## RESULT 13

QYBBI PRELIMINARY; PRT; 243 AA.  
 AC QYBBI;  
 DT 01-MAR-2003 (TREMBlrel. 23, Created)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Hypothetical protein.  
 GN BRA0258.  
 OS Brucella suis.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Brucellaceae; Brucella.  
 OX NCBI\_TaxID=29461;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=1330 / Biovar 1;  
 RX MEDLINE=22247741; PubMed=12271122;  
 RA Paulsen I.T., Sehnadi R., Nelson K.E., Eisen J.A., Heidelberg J.F.,  
 RA Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Beanan M.J.,  
 RA Daugherty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R.,  
 RA Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J., Van Aken S.E.,  
 RA Riedmuller S., Tettelin H., Gill S.R., White O., Salzberg S.L.,  
 RA Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Frazer C.M.;  
 RT The Brucella suis genome reveals fundamental similarities between  
 RT animal and plant pathogens and symbionts.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).  
 DR EMBL; AE014526; AAN33460.1; -.  
 DR TIGR; BRA0258; -.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 243 AA; 25810 MW; 612CB963D7A56E18 CRC64;

Q8G87 PRELIMINARY: PRT: 8601 AA.  
 ID Q8G87  
 AC Q8G87  
 DT 01-MAR-2003 (TREMBLrel. 23, Created)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Mixed type I polyketide synthase/nonribosomal peptide synthetase.  
 GN PEDF.  
 OS symbiotic bacterium of *Paederus fuscipes*.  
 OC Bacteria.  
 OX NCBI\_TaxID=176282;  
 RN [1]  
 RP - SEQUENCE FROM N.A.  
 RX MEDLINE=22294974; PubMed=12381784;  
 RA Piel J.;  
 RT "A polyketide synthase-peptide synthetase gene cluster from an uncultured bacterial symbiont of *Paederus* beetles.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 99:14002-14007(2002).  
 DR EMBL; AY059471; AAL27851.1;  
 SQ SEQUENCE 8601 AA; 948046 MW; C498AC8B0860827 CRC64;  
 Query Match 7.7%; Score 94; DB 2; Length 8601;  
 Best Local Similarity 26.1%; Pred. No. 74;  
 Matches 52; Conservative 33; Mismatches 72; Indels 42; Gaps 11;  
 QY 58 AGTYLNYGPPNPEDPFPRLGAETLPRAVTNLEWMSLNDRLRLTONYEAYSHLQYL 117  
 DB 5078 SGTNHLVVEEVRNSDEPRVLDVSSSTAPRL-ILSTKDAEKLSEVTLNLAHFV 5133  
 QY 118 RGLNQAATTAELRSLAHCSTSLQ-----LGSIGVATL----- 154  
 DB 5134 RQAQNPADLE-RLSLADLAVTLQVGRAMEGRVALLVGDLAGLEALSALREPRCPVS 5192  
 QY 155 ---GTPLPQPLPPTERPAWAPGASDFLQKMDPWL---LKEI-QTWMRSACKPFRNLK 206  
 DB 5193 VWSGVVEGPPSGASTVADQPA-AELLQRIPO-WLAEGALDELQAWVAGAPIDMCQR 5250  
 QY 207 KKMOPPAASVTLLEAHGF 225  
 DB 5251 RR-RPPR---RVHLPSYFP 5265  
 RESULT 9  
 ID 054153 PRELIMINARY: PRT: 640 AA.  
 AC 054153  
 DT 01-JUN-1998 (TREMBLrel. 06, Created)  
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Transferrase.  
 GN SCOS890 OR SCJF7.10.  
 OS Streptomyces coelicolor.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Streptomycineae; Streptomycetaceae; Streptomyces.  
 OX NCBI\_TaxID=1902;  
 RN [1]  
 RP - SEQUENCE FROM N.A.  
 RC STRAIN=A3(2);  
 RA Oliver K., Harris D.;  
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP - SEQUENCE FROM N.A.  
 RC STRAIN=A3(2);  
 RA Parkhill J., Barrell B.G., Rajandream M.A.;  
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP - SEQUENCE FROM N.A.  
 RC STRAIN=A3(2);  
 RX MEDLINE=97000351; PubMed=8643436;  
 RA Redenbach M., Kleiser H.M., Denaplatte D., Eichner A., Cullum J.,  
 RA Kinoshita H., Hopwood D.A.;  
 RT "A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";

RL Mol. Microbiol. 21:77-96(1996).  
 RN [4]  
 RP - SEQUENCE FROM N.A.  
 RC STRAIN=A3(2) / M145;  
 RX MEDLINE=21996410; PubMed=12000953;  
 RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,  
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleiser H.,  
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,  
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,  
 RA Huang C.-H., Kleiser H., Larke L., Murphy L., Oliver K., O'Neill S.,  
 RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,  
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,  
 RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,  
 RA Hopwood D.A.;  
 RT "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";  
 RT Nature 417:141-147(2002).  
 DR EMBL; AL939125; CNA16181.1;  
 DR HSSP; P12998; 1BS0.  
 DR InterPro; IPR004839; Aminoacyl-tRNA synthetase/2.  
 DR InterPro; IPR006163; PP. bind.  
 DR Pfam; PF00135; aminocyclase\_1; 1.  
 DR Pfam; PF00550; PP-binding; 2.  
 DR PROSITE; PS50075; ACP DOMAIN; 1.  
 KW Phosphopantetheine; Complete proteome.  
 SQ SEQUENCE 640 AA; 68061 MW; E519FB555A613P CRC64;  
 Query Match 7.6%; Score 93.5; DB 16; Length 640;  
 Best Local Similarity 28.3%; Pred. No. 2.8;  
 Matches 52; Conservative 12; Mismatches 63; Indels 57; Gaps 9;  
 QY 22 LPAPALNRDTPGPGPSIQTYDLTRYLHQ-----RLAGTYLNYGPPNPEDPFPNR 78  
 DB 100 LPAPPA-BGTDPPTAVAAAMRQYQKHQGLADLEG-----E 140  
 QY 79 LGAEITPRATVNLFWMSLNDRLRLTONYEAYSHLQYLRLNQAATTAELRSLAHCST 138  
 DB 141 LGVDSVLTSSVAE-----TERLGLT-----GAAPDAAGATTLRALA-----D 179  
 QY 139 SLQGLGSIAGVATLGYPLPQPLPPTERPAWAPGASDFLQKMDPWLLEQTLWLR 198  
 DB 180 ALRGL-----VAAAPGTAPEAAPATGAA-APAGRSGNAP-----ARGADGMDHRS 225  
 QY 199 AKDF 202  
 DB 226 MKDF 229  
 RESULT 10  
 ID 088841 PRELIMINARY: PRT: 727 AA.  
 AC 088841  
 DT 01-NOV-1998 (TREMBLrel. 08, Created)  
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Faciogenital dysplasia protein 2.  
 GN FG2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP - SEQUENCE FROM N.A.  
 RX MEDLINE=99389726; PubMed=10458911;  
 RA Pastoris N.G., Gorski J.L.;  
 RT "Isolation, characterization, and mapping of the mouse and human fg2 genes, faciogenital dysplasia (FGD1; aarskog syndrome) gene homologues.";  
 RT Genomics 50:57-66(1999).  
 CC -I- SIMILARITY: CONTAINS 1 PH DOMAIN.  
 DR EMBL; AF017368; AAC35430.1;  
 DR MGD; MGI:1347084; Fgd2.  
 DR InterPro; IPR001849; PH.

Query Match 11.8%; Score 144.5; DB 13; Length 215;  
Best Local Similarity 26.5%; Pred. No. 9.6e-06;  
Matches 44; Conservative 34; Mismatches 73; Indels 15; Gaps 4;

QY 56 SLAGTYLNTLGGPFNPDENPPRLGAETLPRATVNLVWRSINDRLRLTQNTYEAYSHLIC 115  
DB 55 SLPTFLSFGAPLSDPDYQLPHIKVNLPTAMVDYTFIRQDDETRLKNLIFYSAIVE 114  
QY 116 YLR-----GLN--RQATAEIRSLAHFCTSLQGLSIGAVMATLGYPLPGTEPAMA 166  
DB 115 FLKEAMTEQEDLNPAELSLKAKEEAMANSNTLISKISIMTQMGMSVITLTP--K 168  
QY 167 PAMAPGPAHSDFLQKMDFWLKELOTWLRSAKDFNRLKKKQPP 212  
DB 169 PLVVPFKGSAYFSKJLRGAVCKEYKERVFLTRKDFMLAEKYQGP 214

RESULT 5  
Q9PU2 PRELIMINARY; PRT; 215 AA.

AC Q9PU2; 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
DE 01-MAY-2000 (Tremblrel. 13, Last annotation update)  
GN Receptivity factor isoform 1 precursor.  
OS Plethodon jordani (Salamander).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Caudata; Salamandroidea; Plethodontidae;  
OC Plethodon.  
ON NCBI\_TaxID=8336;  
RN [1]  
RX MEDLINE=99420364; PubMed=10489368;  
RA Rollman S.M., Houck L.D., Feldhoff R.C.;  
RT "Proteinaceous pheromone affecting female receptivity in a terrestrial  
salamander";  
RL Science 285:1907-1909(1999).  
DR EMBL; AF181480; AAF01025.1; -.  
KM Signal.  
FT SIGNAL. 1 23 POTENTIAL.  
SQ SEQUENCE 215 AA; 24138 MW; B1906BB6635738 CRC64;

Query Match 11.8%; Score 144.5; DB 13; Length 215;  
Best Local Similarity 25.6%; Pred. No. 9.6e-06;  
Matches 41; Conservative 31; Mismatches 81; Indels 7; Gaps 3;

QY 56 SLAGTYLNTLGGPFNPDENPPRLGAETLPRATVNLVWRSINDRLRLTQNTYEAYSHLIC 115  
DB 55 SLPTFLSFGAPLSDPDYQLPHIKVNLPTAMVDYTFIRQDDETRLKNLIFYSAIVE 114  
QY 116 YLR-----AATAELRSLAHFCTSLQGLSIGAVMATLGYPLPGTEPAMA 170  
DB 115 FLKEAMTEQEDLNPAELSLKAKEEAMANSNTLISKISIMTQMGMSVITLTP--KPLVV 172  
QY 171 PGPASDPLQKMDFWLKELOTWLRSAKDFNRLKKKQ 210  
DB 173 PREGSAYFRKKJLRGAVCKEYKERVFLTRKDFMLAEKYQGP 212

RESULT 6  
Q9PU9 PRELIMINARY; PRT; 215 AA.

AC Q9PU9; 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
DE 01-MAY-2000 (Tremblrel. 13, Last annotation update)  
GN Receptivity factor isoform 4 precursor.  
OS Plethodon jordani (Salamander).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Caudata; Salamandroidea; Plethodontidae;  
OC Plethodon.

OX NCBI\_TaxID=8336;  
RN [1]  
RX MEDLINE=99420364; PubMed=10489368;  
RA Rollman S.M., Houck L.D., Feldhoff R.C.;  
RT "Proteinaceous pheromone affecting female receptivity in a terrestrial  
salamander";  
RL Science 285:1907-1909(1999).  
DR EMBL; AF181483; AAF01028.1; -.  
KM Signal.  
FT SIGNAL. 1 23 POTENTIAL.  
SQ SEQUENCE 215 AA; 24054 MW; A4A412135FPA4E7F CRC64;

Query Match 11.6%; Score 142.5; DB 13; Length 215;  
Best Local Similarity 25.3%; Pred. No. 1.5e-05;  
Matches 41; Conservative 33; Mismatches 81; Indels 7; Gaps 3;

QY 56 SLAGTYLNTLGGPFNPDENPPRLGAETLPRATVNLVWRSINDRLRLTQNTYEAYSHLIC 115  
DB 55 SLPTFLSFGAPLSDPDYRLPHIKVNLPTAMVDYTFIRQDDETRLKNLIFYSAIVE 114  
QY 116 YLR-----AATAELRSLAHFCTSLQGLSIGAVMATLGYPLPGTEPAMA 170  
DB 115 FLKEAMTEQEDLNPAELSLKAKEEAMANSNTLISKISIMTQMGMSVITLTP--KPLVV 172  
QY 171 PGPASDPLQKMDFWLKELOTWLRSAKDFNRLKKKQPP 212  
DB 173 PFGSAYFSKJLRGAVCKEYKERVFLTRKDFMLAEKYQGP 214

RESULT 7  
Q8N358 PRELIMINARY; PRT; 287 AA.

AC Q8N358; 01-OCT-2002 (Tremblrel. 22, Created)  
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)  
DE 01-OCT-2002 (Tremblrel. 22, Last annotation update)  
GN Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
ON NCBI\_TaxID=9606;  
RN [1]  
RX MEDLINE=99420364; PubMed=10489368;  
RA Rollman S.M., Houck L.D., Feldhoff R.C.;  
RT "Proteinaceous pheromone affecting female receptivity in a terrestrial  
salamander";  
RL Science 285:1907-1909(1999).  
DR EMBL; BC028076; AAH28076.1; -.  
KM Hypothetical protein.  
FT SIGNAL. 1 23 POTENTIAL.  
SQ SEQUENCE 287 AA; 32156 MW; 6E571BCA0328E74E CRC64;

Query Match 7.7%; Score 94; DB 4; Length 287;  
Best Local Similarity 22.3%; Pred. No. 0.9;  
Matches 47; Conservative 18; Mismatches 62; Indels 84; Gaps 9;

QY 15 LCTVLMHLPAVALNRITGPGGPGPSIQKTYD-----LTRY---LEHQL--RSLAG 59  
DB 132 LPLVWLRP-----PDGPTLNTLQCPGSRQSPGVLRFHNOQLMHVLTGFAFTN 181  
QY 60 TYLNTY-----LGPFPNPDENPPRLGAETLPRATVNLVWRSINDRLRLTQNTYEAYSHLIC 115  
DB 182 TYLFGAIVRGV-----ESSVSYSIRLA 204  
QY 116 YLR-----AATAELRSLAHFCTSLQGLSIGAVMATLGYPLPGTEPAMA 169  
DB 205 YL-----LSPLACLILCFGTLHQLSTLSPGAGGPAWPAHWPACPLPGIRLQ 256  
QY 170 ACPASDPLQKMDFWLKELOTWLRSAKDFNRLKKKQPP 212  
DB 257 LPPPHAOVLRAGAGGADTWGRSFLPFGW 287

RESULT 8

Db 121 NROAATAEIRSLAFCSTLGLGSIAGVWATTCYPLPQPLGTEBPAPAPASDFLQ 180

Qy 181 KMDDFWLKELQTLWLRSAKDFNRLKKKQPPAAVTLHLAHGF 225

Db 181 KMDDFWLKELQTLWLRSAKDFNRLKKKQPPAAVTLHLAHGF 225

# RESULT 2

ID Q9UBD9 PRELIMINARY; PRT; 225 AA.

AC Q9UBD9; 01-MAY-2000 (TRENBLrel. 13, Created)

DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)

DE Neurotrophin-1/B-cell stimulating factor-3 (Cardiotrophin-like cytokine) (Similar to cardiotrophin-like cytokine, neurotrophin-1/B-cell stimulating factor-3).

GN CLC.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

NCBI\_TaxID=9606;

RP SEQUENCE FROM N.A.

RA MEDLINE=99432254; PubMed=10500198; Senaldi G., Varnum B.C., Sarmiento U., Starnes C., Lile J., Scully S., Guo J., Elliott G., McNinch J., Shaklee C.L., Freeman D., Mann F., Simonet W.S., Boone T., Chang M.-S., "Novel neurotrophin-1/B cell-stimulating factor-3: A cytokine of the IL-6 family."

RT Proc. Natl. Acad. Sci. U.S.A. 96:11458-11463(1999).

RL Biochem. Biophys. Res. Commun. 262:132-138(1999).

RN SEQUENCE FROM N.A.

RA MEDLINE=99382254; PubMed=10448081; Shi Y., Wang W., Yourey P.A., Gohari S., Zukauskas D., Zhang J., Ruben S., Alderson R.F., "Computational EST database analysis identifies a novel member of the neurotrophic cytokine family."

RT Biochem. Biophys. Res. Commun. 262:132-138(1999).

RL SEQUENCE FROM N.A.

RA Hu X., Xu Y., Zhang B., Peng X., Yuan J., Qiang B., Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

RN SEQUENCE FROM N.A.

RC TISSUE=Kidney;

RA Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL, AF176912; AAF00992.1; -

DR EMBL, AF176911; AAF00991.1; -

DR EMBL, AY049779; AAL15436.1; -

DR EMBL, BC012939; AAL12939.1; -

SEQUENCE 225 AA; 25176 MW; E2DD4B628083B55 CRC64;

Query Match 97.5%; Score 1193; DB 4; Length 225;

Best Local Similarity 96.5%; Pred. No. 1.6e-105;

Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MDLRAGDSKGMACCTVLMHLPAYPALNRTGDPGSPISQTYDLTRYLHQSLAGT 60

Db 1 MDLRAGDSKGMACCTVLMHLPAYPALNRTGDPGSPISQTYDLTRYLHQSLAGT 60

Qy 61 YLVYIGPPNEBDFNPRLGAEITLPATVNEVWSLNDRLRLTONYEAYSHLLCYLRL 120

Db 61 YLVYIGPPNEBDFNPRLGAEITLPATVNEVWSLNDRLRLTONYEAYSHLLCYLRL 120

Qy 121 NROAATAEIRSLAFCSTLGLGSIAGVWATTCYPLPQPLGTEBPAPAPASDFLQ 180

Db 121 NROAATAEIRSLAFCSTLGLGSIAGVWATTCYPLPQPLGTEBPAPAPASDFLQ 180

Db 181 KMDDFWLKELQTLWLRSAKDFNRLKKKQPPAAVTLHLAHGF 225

Qy 181 KMDDFWLKELQTLWLRSAKDFNRLKKKQPPAAVTLHLAHGF 225

Db 181 KMDDFWLKELQTLWLRSAKDFNRLKKKQPPAAVTLHLAHGF 225

# RESULT 3

ID Q9PUJ1 PRELIMINARY; PRT; 215 AA.

AC Q9PUJ1; 01-MAY-2000 (TRENBLrel. 13, Created)

DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)

DE Receptivity factor isoform 2 precursor.

GN PRF.

OS Plethodon jordan (Salamander).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Caudata; Salamandridae; Plethodontidae;

NCBI\_TaxID=8336;

RP SEQUENCE FROM N.A.

RA MEDLINE=99420364; PubMed=10489368; Rollmann S.M., Houck L.D., Feldhoff R.C., "Proteinaceous pheromone affecting female receptivity in a terrestrial

RL Science 285:1907-1909(1999).

DR EMBL, AF181481; AAF01026.1; -

KW Signal.

FT SIGNAL.

SEQUENCE 215 AA; 24080 MW; B341B8B784E28438 CRC64;

Query Match 11.8%; Score 144.5; DB 13; Length 215;

Best Local Similarity 25.6%; Pred. No. 9.6e-06;

Matches 41; Conservative 31; Mismatches 81; Indels 7; Gaps 3;

Qy 56 SLAFTYLVYIGPPNEBDFNPRLGAEITLPATVNEVWSLNDRLRLTONYEAYSHLLC 115

Db 56 SLAFTYLVYIGPPNEBDFNPRLGAEITLPATVNEVWSLNDRLRLTONYEAYSHLLC 115

Qy 116 YLR-GLNQ---AATAEIRSLAFCSTLGLGSIAGVWATTCYPLPQPLGTEBPAPMA 170

Db 116 YLR-GLNQ---AATAEIRSLAFCSTLGLGSIAGVWATTCYPLPQPLGTEBPAPMA 170

Qy 173 PFGSAYPRKTLRGVCKEYKERVLTJKRDFEFLAKKQ 212

Db 173 PFGSAYPRKTLRGVCKEYKERVLTJKRDFEFLAKKQ 212

# RESULT 4

ID Q9PUJ0 PRELIMINARY; PRT; 215 AA.

AC Q9PUJ0; 01-MAY-2000 (TRENBLrel. 13, Created)

DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)

DE Receptivity factor isoform 3 precursor.

GN PRF.

OS Plethodon jordan (Salamander).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Caudata; Salamandridae; Plethodontidae;

NCBI\_TaxID=8336;

RP SEQUENCE FROM N.A.

RA MEDLINE=99420364; PubMed=10489368; Rollmann S.M., Houck L.D., Feldhoff R.C., "Proteinaceous pheromone affecting female receptivity in a terrestrial

RL Science 285:1907-1909(1999).

DR EMBL, AF181482; AAF01027.1; -

KW Signal.

FT SIGNAL.

SEQUENCE 215 AA; 24024 MW; 6EB6E4AD93A1343 CRC64;

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 9, 2004, 06:14:57 ; Search time 36 Seconds

(without alignments)  
1612.823 Million cell updates/sec

Title: US-09-931-704-5

Perfect score: 1224  
Sequence: 1 MDLRAGDSWGMCLACTVLM.....KKMKPPASVTLHLRNGR 225

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_23:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_oraganelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertedrate:\*  
14: sp\_unclassified:\*  
15: sp\_rv1rus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1234	100.0	225	11	O9QZM3
2	1193	97.5	225	4	O9QZM3
3	144.5	11.8	215	13	O9PUJ1
4	144.5	11.8	215	13	O9PUJ0
5	144.5	11.8	215	13	O9PUJ2
6	142.5	11.6	215	13	O9PUJ9
7	94	7.7	287	4	O8N358
8	94	7.7	8601	2	O8GM87
9	93.5	7.6	640	16	O54153
10	93	7.6	727	11	O88841
11	92.5	7.6	200	16	O8YB81
12	92.5	7.6	232	16	O8FX31
13	92.5	7.6	243	10	O8NEV9
14	92	7.5	332	4	O8NAU1
15	92	7.5	655	11	O8BY35
16	91.5	7.5	455	11	O9CWM7

17	90	7.4	733	16	O9HTC5	O9htc5 pseudomonas
18	89.5	7.3	379	2	O8KRX4	O8kxr4 streptococ
19	89.5	7.3	530	3	O8XOE9	O8xoe9 neuropept
20	89	7.3	733	16	O91664	O91664 pseudomonas
21	88	7.2	222	2	O91584	O91584 streptococ
22	87	7.1	332	2	O8KNP2	O8knt2 micromonsp
23	86.5	7.1	318	4	O961S2	O961s2 homo sapien
24	85.5	7.0	389	17	O9YA71	O9ya71 aeropyrum p
25	85.5	7.0	522	7	O8HWH4	O8hwh4 mus musculu
26	85.5	7.0	1122	10	O8GVC8	O8gvc8 oryza sativ
27	85.5	7.0	1154	11	O921R2	O921r2 mus musculu
28	85	6.9	332	11	O8B1I3	O8b1i3 mus musculu
29	85	6.9	422	11	O8BGR5	O8bgr5 mus musculu
30	85	6.9	476	11	O8R363	O8r363 mus musculu
31	85	6.9	520	16	O9RT14	O9rt14 deinococcus
32	85	6.9	585	5	O9VNR6	O9vnr6 drosophila
33	85	6.9	1024	16	O8FRH1	O8frh1 corynedace
34	84.5	6.9	716	16	O8PT99	O8pt99 xanthomonas
35	84	6.9	468	16	O8DHQ5	O8dhq5 synchococ
36	84	6.9	741	16	O9H2M0	O9h2m0 pseudomonas
37	83	6.8	272	16	O86721	O86721 streptococ
38	83	6.8	396	2	O9AR00	O9arf0 frankia sp.
39	83	6.8	456	13	O8AYL4	O8ayl4 oncorhynch
40	83	6.8	955	11	O88287	O88287 mus musculu
41	83	6.8	1561	11	O88286	O88286 mus musculu
42	82.5	6.7	213	2	O8GNS7	O8gns7 streptococ
43	82.5	6.7	1098	11	O9WTN8	O9wtn8 rattus norv
44	82.5	6.7	5990	2	O9RLP6	O9rlp6 mycobacteri
45	81.5	6.7	209	2	O91593	O91593 streptococ

## ALIGNMENTS

RESULT 1	ID	Q9QZM3	PRELIMINARY	PRT	225 AA.
AC	O9QZM3				
DT	01-MAY-2000	(T-REMBLrel. 13, Created)			
DT	01-MAY-2000	(T-REMBLrel. 13, Last sequence update)			
DT	01-UTN-2001	(T-REMBLrel. 17, Last annotation update)			
DE	Neurotrophin-1/B-cell stimulating factor-3.				
GN	BSF3.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxId=10090;				
RP	SEQUENCE FROM N.A.				
RX	SENDELIN-99432254; PubMed-10500198;				
RA	Senaldi G., Varnum B.C., Sarmiento U., Starnes C., Lile J., Scully S.,				
RA	Guo J., Elliott G., McNinch J., Shaklee C.L., Freeman D., Mann F.,				
RA	Simonet W.S., Boone T., Chang M.-S.,				
RT	"Novel neurotrophin-1/B cell-stimulating factor-3: a cytokine of the				
RT	IL-6 family."				
RL	Proc. Natl. Acad. Sci. U.S.A. 96:11458-11463 (1999).				
DR	EMBL; AF176913; AAF00993.1; -				
DR	MGI; MGI:1930088; Bsf3.				
SQ	SEQUENCE 225 AA; 25261 MW; 68B1FEAAB7F1A950 CRC64;				
Query Match	100.0%; Score 1224; DB 11; Length 225;				
Best Local Similarity	100.0%; Pred. No. 1.8e-108;				
Matches	225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1 MDLRAGDSWGMCLACTVLMHLPVAVPALNRTGDPGSPSIQKTYDLTRYLEHQLSLACT 60				
DB	1 MDLRAGDSWGMCLACTVLMHLPVAVPALNRTGDPGSPSIQKTYDLTRYLEHQLSLACT 60				
QY	61 YANYIGPPFNEDPDPNPRGATLPRATYNLEWMSLNDRLALNTQYEAYSHLCTLRGL 120				
DB	61 YANYIGPPFNEDPDPNPRGATLPRATYNLEWMSLNDRLALNTQYEAYSHLCTLRGL 120				
QY	121 NRGATPAELRSLRHFCTSLGGLSISGVMTLGVPLPQPLPGRTPAAPGPHSDPLQ 180				

Query Match 95.7%; Score 1171; DB 22; Length 321;  
 Best Local Similarity 96.0%; Pred. No. 1.9e-115;  
 Matches 214; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 3 LRAGSWGMLACTLVMLPAVPALNRGDPGPGSIQKTYDLTRYLEHQRSLAGTYL 62  
 DB 99 LFTGSGWGLACTLVMLPAVPALNRGDPGPGSIQKTYDLTRYLEHQRSLAGTYL 158  
 QY 63 NYLGPPPEPDNPRLGAETLPRAVNLVWRSINDRLRLTONYEAYSHLLCYLRGLNR 122  
 DB 159 NYLGPPPEPDNPRLGAETLPRAVNLVWRSINDRLRLTONYEAYSHLLCYLRGLNR 218  
 QY 123 QATAELRSLAHFCTSLQGLLSIAGVWATLGYPLPGLPCTEPAMAPGPAHSDFLQKM 182  
 DB 219 QATAELRSLAHFCTSLQGLLSIAGVWATLGYPLPGLPCTEPAMAPGPAHSDFLQKM 278  
 QY 163 DDFPFLKEIQTWLRSAKDFNRLKKMOPPAASVTLHLEAHGF 225  
 DB 279 DDFPFLKEIQTWLRSAKDFNRLKKMOPPAASVTLHLEAHGF 321

RESULT 15  
 AAB19587  
 ID AAB19587 standard; Protein; 215 AA.  
 AC AAB19587;  
 XX 22-JAN-2001 (first entry)  
 DT Mouse Interleukin-B60 (IL-B60).  
 DE Interleukin-B60; IL-B60; mouse; cytokine; cytokine-like factor-1;  
 KW haematopoietic; inflammation; antiinflammatory; autoimmune disease;  
 KM therapy.  
 OS Mus musculus.  
 XX Key Location/Qualifiers  
 FH 1..17  
 FT Peptide /label= Signal\_peptide  
 FT Protein /label= Mature-protein  
 PN WO200053631-A1.  
 XX 14-SEP-2000.  
 PD 09-MAR-2000; 2000WO-US06182.  
 PF 11-MAR-1999; 99US-0267901.  
 PR (SCHE) SCHERING CORP.  
 PA Opmann B, Tlman JC, Kastelein RA, Bazan JF;  
 PI WPI; 2000-587426/55.  
 DR N-PSDB; AAA89547.  
 XX Cytokine-like factor 1 (CLF-1) and interleukin (IL)-B60 complexes,  
 PT polypeptides, and nucleic acids, useful in research, diagnosis and for  
 PT treating inflammatory and autoimmune disorders -  
 XX Claim 1; Page 17; 97pp; English.

CC The present sequence is that of mouse interleukin-B60 (IL-B60), a  
 CC novel, small soluble cytokine-like protein that exhibits structural  
 CC motifs characteristic of a member of the long-chain cytokines, and  
 CC which shows homology to granulocyte colony stimulating factor and  
 CC interleukin-6. IL-608 may have either stimulatory or inhibitory  
 CC effects on haematopoietic cells, including e.g. lymphoid cells,  
 CC such as T-cells, B-cells, natural killer cells, macrophages,  
 CC dendritic cells, haematopoietic progenitors, etc. Methods are  
 CC provided for modulating the physiology or development of a cell or

CC tissue culture cells by contacting the cell with an agonist or  
 CC antagonist of IL-B60 or an agonist of antagonist of a complex of  
 CC mature IL-B60 and its partner, cytokine-like factor-1 (CLF-1, see  
 CC AAB19588). The IL-B60/CLF-1 cytokine serves as a key physiological  
 CC factor in motor neuron development and regeneration. IL-608, its  
 CC agonists and antagonists may be used to treat inflammatory or  
 CC autoimmune disorders and also for drug screening.

CC Sequence 215 AA;  
 SQ

Query Match 95.3%; Score 1167; DB 21; Length 215;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-115;  
 Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 MLAGCTVLMHLPAPVAPALNRGDPGPGSIQKTYDLTRYLEHQRSLAGTYLNYLGPPPN 70  
 DB 1 MLAGCTVLMHLPAPVAPALNRGDPGPGSIQKTYDLTRYLEHQRSLAGTYLNYLGPPPN 60  
 QY 71 EPDFNPRLGAETLPRAVNLVWRSINDRLRLTONYEAYSHLLCYLRGLNRQAATAELR 130  
 DB 61 EPDFNPRLGAETLPRAVNLVWRSINDRLRLTONYEAYSHLLCYLRGLNRQAATAELR 120  
 QY 131 RSLAHFCTSLQGLLSIAGVWATLGYPLPGLPCTEPAMAPGPAHSDFLQKMDFWLLKE 190  
 DB 121 RSLAHFCTSLQGLLSIAGVWATLGYPLPGLPCTEPAMAPGPAHSDFLQKMDFWLLKE 180  
 QY 191 LOTWLRSAKDFNRLKKMOPPAASVTLHLEAHGF 225  
 DB 181 LOTWLRSAKDFNRLKKMOPPAASVTLHLEAHGF 215

Search completed: February 9, 2004, 06:16:54  
 Job time : 35.5 secs

PN WO200157188-A2.  
 XX 09-AUG-2001.  
 PD 05-FEB-2001; 2001WO-US03800.  
 XX 03-FEB-2000; 2000US-0496914.  
 PR 27-APR-2000; 2000US-0560875.  
 XX (HYSE-) HYSEQ INC.  
 PA Tang YT, Liu C, Drmanac RT;  
 PI WPI; 2001-457740/49.  
 DR N-PSDB; ABA09140.  
 XX Human proteins and DNA encoding sequences useful for preventing,  
 PT treating or ameliorating a medical condition in a mammalian subject  
 PT e.g. arthritis and cancer -  
 XX Claim 20; Page 273; 1963pp; English.  
 XX Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and  
 CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The  
 CC invention also relates to vectors and recombinant host cells comprising a  
 CC nucleotide of the invention, methods of producing the novel polypeptides,  
 CC antibodies against the polypeptides, methods of detecting the nucleotides  
 CC or polypeptides in a sample, and methods of identifying compounds which  
 CC bind to polypeptides of the invention. Although novel, many of the  
 CC polypeptides of the invention have homology to known proteins, thereby  
 CC giving an insight into their probable biological activities, and hence  
 CC potential therapeutic applications. The polypeptides of the invention may  
 CC have various activities, including cytokine, cell proliferation or cell  
 CC differentiation activities; stem cell growth factor activity;  
 CC haematopoiesis regulatory activity; tissue growth activity;  
 CC immunomodulatory activity; activin- or inhibin-related activities;  
 CC chemotactic or chemokinetic activities; haemostatic, thrombotic or  
 CC thrombolytic activities; receptor or ligand activities; or may be  
 CC involved in oncogenesis, cancer cell proliferation or metastasis.  
 CC Depending on their biological activities, polypeptides and nucleotides of  
 CC the invention are useful for preventing, treating or ameliorating medical  
 CC conditions, e.g., by protein or gene therapy. Such conditions include  
 CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell  
 CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),  
 CC proliferative retinopathy, atherosclerosis, coronary heart disease,  
 CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal  
 CC vascular growth. Polypeptides involved with tissue regeneration and  
 CC repair (or nucleic acids encoding them) may be used to promote wound  
 CC healing (e.g., of burns, incisions and ulcers), while those with  
 CC immunomodulatory activities may be used in the treatment of viral,  
 CC bacterial and fungal infections in addition to immune disorders.  
 CC Polypeptides with growth factor activity may be used in cell cultures to  
 CC promote cell growth. For example, such polypeptides may be used to  
 CC manipulate stem cells in culture to give rise to neuroepithelial cells  
 CC that can be used to augment or replace cells damaged by illness,  
 CC autoimmune disease or accidental damage. The polypeptides and nucleotides  
 CC may also be used in the diagnosis of the above conditions, and in drug  
 CC screening techniques. The present sequence represents a novel human  
 CC polypeptide of the invention.  
 XX Sequence 321 AA;  
 SQ

QY 123 QATATLRRSLAHFCTSLQGLGSIAGWATLGYPLPQPLPCTBPAMAPPAHSDFLQRM 182  
 DB 219 QATATLRRSLAHFCTSLQGLGSIAGWAAALGYPLPQPLPCTBPMTWTPGPAHSDFLQRM 278  
 QY 183 DDFWLKELQTLWLRSAKDPPNRLKKKMPAASVTLHLEAHGF 225  
 DB 279 DDFWLKELQTLWLRSAKDPPNRLKKKMPAASVTLHLEAHGF 321  
 RESULT 14  
 AAM79399  
 ID AAM79399 standard; Protein; 321 AA.  
 AC AAM79399;  
 XX  
 DT 06-NOV-2001 (first entry)  
 XX  
 DE Human protein SEQ ID NO 3045.  
 XX  
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;  
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;  
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;  
 KW nervous system disorder; arthritis; inflammation.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200157190-A2.  
 PD 09-AUG-2001.  
 XX  
 PF 05-FEB-2001; 2001WO-US04098.  
 XX  
 PR 03-FEB-2000; 2000US-0496914.  
 PR 27-APR-2000; 2000US-0560875.  
 PR 20-JUN-2000; 2000US-0598075.  
 PR 19-JUL-2000; 2000US-0620325.  
 PR 01-SEP-2000; 2000US-0654936.  
 PR 15-SEP-2000; 2000US-0663561.  
 PR 20-OCT-2000; 2000US-0693325.  
 PR 30-NOV-2000; 2000US-0728422.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Gao Y, Ma Y;  
 PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZM;  
 PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;  
 DR WPI; 2001-476283/51.  
 DR N-PSDB; AAK52532.  
 XX  
 PT Nucleic acids encoding polypeptides with cytokine-like activities,  
 PT useful in diagnosis and gene therapy -  
 XX  
 XX Claim 20; Page 237; 6221pp; English.  
 XX The invention relates to polynucleotides (AAK51456-AAK53435) and the  
 CC encoded polypeptides (AAM78323-AAK80302) that exhibit activity elating to  
 CC cytokine, cell proliferation or cell differentiation which may induce  
 CC production of other cytokines in other cell populations. The  
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or  
 CC peptide therapy. The polypeptides have various cytokine-like activities,  
 CC e.g. stem cell growth factor activity, haematopoiesis regulating  
 CC activity, tissue growth factor activity, immunomodulatory activity and  
 CC activin/inhibin activity and may be useful in the diagnosis and/or  
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and  
 CC inflammation.  
 CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666  
 CC (AAM80020) are omitted as the relevant pages from the sequence listing  
 CC were missing at the time of publication.  
 XX Sequence 321 AA;  
 SQ



CC cells they are expressed in, such as: antiinflammatory; antineumatic;  
 CC antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant;  
 CC central nervous system; vitruicide; anti-HIV; fungicide; antimutagen;  
 CC cardiovascular; antianaemic; antiaggregant; haemostatic; vulnery;  
 CC antituber; osteopathic; dermatologic; antiallergic; antiaesthetic;  
 CC antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;  
 CC antiparkinsonian; and immunostimulant. The proteins and polynucleotides  
 CC encoding them can be used in gene therapy, antitense therapy and vaccine  
 CC production. The proteins and polynucleotides are useful for screening for  
 CC agonists or antagonists of a protein and for the treatment and diagnosis  
 CC of disorders associated with the activity of a protein e.g. inflammation,  
 CC rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,  
 CC neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal  
 CC infections, autoimmunity, genetic diseases, haematopoietic disorders,  
 CC anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,  
 CC osteoporosis, severe combined immunodeficiency, eczema, allergic  
 CC rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,  
 CC Alzheimer's disease, Parkinson's disease, neurodegenerative and  
 CC neurological disorders.

CC Sequence 253 AA;

Query Match 97.5%; Score 1193; DB 22; Length 253;  
 Best Local Similarity 96.9%; Pred. No. 6.3e-118;  
 Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDLRAGDSWGMACICTVLMHLPVAVPALNRGDPGPGPSIOKTYDITRYLEHQRLSLAGT 60  
 DB 29 MDLRAGDSWGMACICTVLMHLPVAVPALNRGDPGPGPSIOKTYDITRYLEHQRLSLAGT 88  
 QY 61 YLNTYGPPNPEDFPNPRPGAETLPRAVTNLEWMSLNDRLRLTONYAYSHLLCYLNGL 120  
 DB 89 YLNTYGPPNPEDFPNPRPGAETLPRAVTNLEWMSLNDRLRLTONYAYSHLLCYLNGL 148  
 QY 121 NROAATABLRSLAFCTSLGGLGSLGAGWATLGYPLPGTBPAPAPGPAHSDFLQ 180  
 DB 149 NROAATABLRSLAFCTSLGGLGSLGAGWATLGYPLPGTBPAPAPGPAHSDFLQ 208  
 QY 181 KMDDFWLKEQLQTMWRSKADFNRLKKMKOPPAASVTTLHLGAHF 225  
 DB 209 KMDDFWLKEQLQTMWRSKADFNRLKKMKOPPAASVTTLHLGAHF 253

# RESULT 12

AAE00828  
 ID AAE00828 standard; Protein; 223 AA.

AC AAE00828;

DT 02-JUL-2001 (first entry)

DE Human cardiotrophin-like cytokine (CLC) protein.

KM Human; biologically active complex; haemopoietin receptor; NR6;  
 KM cardiotrophin-like cytokine; CLC; therapy; prophylaxis; proliferation;  
 KM differentiation; cell survival; neurotrophic activity.

OS Homo sapiens.

FX Key Location/Qualifiers  
 FX Peptide 1..27  
 FX PT /label= Signal\_peptide  
 FX PT 28..223  
 FX PT /label= Human\_mature\_CLC\_protein  
 FX PT /note= "Cardiotrophin-like cytokine"

WO200127157-A1.

PN 19-APR-2001.

PD 06-OCT-2000; 2000WO-AU01216.

PR 08-OCT-1999; 99AU-0003327.

PR 12-MAY-2000; 2000AU-0007489.

XX (AMRA) AMRAD OPERATIONS PTY LTD.

PI Naah A, Jachno KM, Fabri LJ, Reid K, Bartlett PF, Hilton DJ;

PI Nakata Y, Hasegawa M;

DR WPI; 2001-281978/29.

DR N-PSDB; AAD04201.

PT New biologically active complex comprising NR6 and  
 PT cardiotrophin-like-cytokine, for facilitating proliferation,  
 PT differentiation and/or survival of a cell -

PS Claim 32; Page 114-115; 123pp; English.

CC The present invention relates to a biologically active complex comprising  
 CC a haemopoietin receptor, NR6 and cardiotrophin-like cytokine (CLC).

CC The complex is useful in the manufacture of a medicament for the  
 CC treatment and/or prophylaxis of a subject, as it is involved in  
 CC facilitating proliferation, differentiation and/or survival of a cell.

CC The complex or its components have neurotrophic activity. The present  
 CC sequence is human cardiotrophin-like cytokine (CLC) protein.

CC Sequence 223 AA;

Query Match 96.5%; Score 1181; DB 22; Length 223;  
 Best Local Similarity 96.9%; Pred. No. 9.8e-117;  
 Matches 216; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDLRAGDSWGMACICTVLMHLPVAVPALNRGDPGPGPSIOKTYDITRYLEHQRLSLAGT 60  
 DB 1 MDLRAGDSWGMACICTVLMHLPVAVPALNRGDPGPGPSIOKTYDITRYLEHQRLSLAGT 60

QY 61 YLNTYGPPNPEDFPNPRPGAETLPRAVTNLEWMSLNDRLRLTONYAYSHLLCYLNGL 120  
 DB 61 YLNTYGPPNPEDFPNPRPGAETLPRAVTNLEWMSLNDRLRLTONYAYSHLLCYLNGL 120

QY 121 NROAATABLRSLAFCTSLGGLGSLGAGWATLGYPLPGTBPAPAPGPAHSDFLQ 180  
 DB 121 NROAATABLRSLAFCTSLGGLGSLGAGWATLGYPLPGTBPAPAPGPAHSDFLQ 180

QY 181 KMDDFWLKEQLQTMWRSKADFNRLKKMKOPPAASVTTLHLGAH 223  
 DB 181 KMDDFWLKEQLQTMWRSKADFNRLKKMKOPPAASVTTLHLGAH 223

# RESULT 13

ABBI1896  
 ID ABBI1896 standard; peptide; 321 AA.

AC ABBI1896;

DT 11-JAN-2002 (first entry)

DE Human cardiotrophin-like cytokine homologue, SEQ ID NO:2266.

KM Human; cytokine; cell proliferation; cell differentiation; growth factor;  
 KM haematopoiesis regulation; tissue growth; immunomodulator; activin;  
 KM inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;  
 KM proliferation; metastasis; cancer; tumour; haematopoietic disorder;  
 KM myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;  
 KM chronic inflammatory condition; proliferative retinopathy;  
 KM atherosclerosis; coronary heart disease; arterial ischaemia;  
 KM bone disorder; osteoporosis; vascular growth disorder;  
 KM tissue regeneration; wound healing; infection; immune disorder;  
 KM cell culture; drug screening; gene therapy; antiinflammatory;  
 KM antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;  
 KM cyostatic; osteopathic; vasotropic; cardiant; vitruicide; antibacterial;  
 KM antifungal; vulnery; antituber.

OS Homo sapiens.

RESULT 10  
AAU78176  
ID AAU78176 standard; Protein; 225 AA.  
XX AAU78176;  
XX  
XX 05-JUN-2002 (first entry)  
XX  
XX Human novel neurotrophic factor NNT1.  
DE  
XX Human; NNT1; neurotrophic factor; IGF-related disease;  
KW Type I allergic disease; allergic rhinitis; eczema; dermatitis;  
KW pollinosis; asthma; immune disease; cancer; arteriosclerosis;  
KW vascular restenosis; rheumatoid arthritis; psoriatic arthritis;  
KW inflammatory arthritis; osteoarthritis; inflammatory joint disease;  
KW autoimmune disease; multiple sclerosis; lupus; diabetes; endometriosis;  
KW inflammatory bowel disease; transplant rejection; reproductive disorder;  
KW graft versus host disease; infertility; miscarriage; preterm labour.  
XX  
XX Homo sapiens.  
XX  
XX WO200215977-A2.  
XX  
XX 28-FEB-2002.  
XX  
XX 17-AUG-2001; 2001WO-US25906.  
XX  
XX 18-AUG-2000; 2000US-226436P.  
XX 16-AUG-2001; 2001US-0931704.  
XX  
XX (AMGE-) AMGEN INC.  
XX  
XX Senaldi G;  
XX  
XX WPI; 2002-280867/32.  
XX N-PSDB; ABK11647.  
XX  
XX Treating Immunoglobulin E-related disease, modulating IGE levels in a  
PT patient, preventing IGE-related disease and treating allergic diseases,  
PT involves administering NNT-1 inhibitor to a patient  
PT  
PS Claim 2; Fig 3; 63pp; English.  
XX  
XX The invention relates to treating Immunoglobulin E (IGE)-related disease,  
CC modulating IGE levels in a patient, preventing an IGE-related disease,  
CC and treating allergic diseases, comprising administering a  
CC therapeutically effective amount of novel neurotrophic factor (NNT)-1  
CC inhibitor to a patient. Also included are a method of diagnosing, by  
CC IGE-related disease or susceptibility to an IGE-related disease, by  
CC determining the presence or amount of expression of an NNT1 polypeptide  
CC encoded by a NNT1 nucleotide sequence, its fragment or naturally  
CC occurring variant, and diagnosing an IGE-related disease or  
CC susceptibility of an IGE-related disease based on the presence or amount  
CC of expression of the polypeptide and a pharmaceutical composition for use  
CC in treating IGE-related disease, comprising the NNT1 inhibitor.  
CC The NNT1 inhibitor is useful for preventing and treating IGE-related  
CC disease, modulating IGE levels, and treating allergic diseases e.g.  
CC Type I allergic disease, allergic rhinitis, eczema, dermatitis,  
CC pollinosis, asthma, immune diseases and disorders, diseases involving  
CC abnormal cell proliferation including cancer, arteriosclerosis and  
CC vascular restenosis, diseases and conditions relating to dysfunction of  
CC immune system including rheumatoid arthritis, psoriatic arthritis,  
CC inflammatory arthritis, osteoarthritis, inflammatory joint disease,  
CC autoimmune disease, multiple sclerosis, lupus, diabetes, inflammatory  
CC bowel disease, transplant rejection, and graft versus host disease, and  
CC reproductive diseases and disorders including infertility, miscarriage,  
CC preterm labour and delivery, and endometriosis. The present sequence  
CC represents human NNT1.  
XX  
XX Sequence 225 AA;  
SQ

Query Match 97.5%; Score 1193; DB 23; Length 225;  
Best Local Similarity 96.9%; Pred. No. 5.3e-118;  
Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
QY 1 MDLRAGDSWGMALACTTVIMHLPAVPALNRGTGPGGPGPSIQKTYDITRYLEHQLRLAGT 60  
DB 1 MDLRAGDSWGMALACTTVIMHLPAVPALNRGTGPGGPGPSIQKTYDITRYLEHQLRLAGT 60  
QY 61 YLNYLGPFPNEPDNPRI GAETLPRAVTYNLEWRSLSNRLRLTONYEAYSHLLCYLRGL 120  
DB 61 YLNYLGPFPNEPDNPRI GAETLPRAVTYNLEWRSLSNRLRLTONYEAYSHLLCYLRGL 120  
QY 121 NRQATATAEILRRSLAHPCTSLQGLGSIAGVMAATLGYPLPOUPGTEPPAAMPGBHSDPLQ 180  
DB 121 NRQATATAEILRRSLAHPCTSLQGLGSIAGVMAATLGYPLPOUPGTEPPAAMPGBHSDPLQ 180  
QY 181 KMDDFWLKLKELQTLWRSKADNRRLKKKQPPAASVTLHLGAHGF 225  
DB 181 KMDDFWLKLKELQTLWRSKADNRRLKKKQPPAASVTLHLGAHGF 225  
RESULT 11  
AAM25831  
ID AAM25831 standard; Protein; 253 AA.  
XX  
XX AAM25831;  
XX  
XX 16-OCT-2001 (first entry)  
XX  
XX Human protein sequence SEQ ID NO:1346.  
DE  
XX  
XX Human; cancer; HIV infection; human immunodeficiency virus;  
KW antineoplastic; antineoplastic; antineoplastic; immunosuppressive;  
KW antibacterial; endocrine; cardiac; central nervous system; vitamin;  
KW anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia;  
KW antiaggregant; haemostatic; vulnery; antitumor; osteopathic; eczema;  
KW dermatological; antiallergic; antistatic; antidiabetic; cytostatic;  
KW neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;  
KW immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;  
KW antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;  
KW cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;  
KW genetic disease; haematopoietic disorder; platelet disorder; asthma;  
KW thrombocytopaenia; osteoporosis; severe combined immunodeficiency;  
KW allergic rhinitis; diabetes; multiple sclerosis; depression;  
KW Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;  
KW neurological disorder.  
XX  
XX Homo sapiens.  
XX  
XX WO200153455-A2.  
XX  
XX 26-JUL-2001.  
XX  
XX 22-DEC-2000; 2000WO-US35017.  
XX  
XX 23-DEC-1999; 99US-0471275.  
XX 21-JAN-2000; 2000US-0488725.  
XX 25-APR-2000; 2000US-0552317.  
XX  
XX (HYSE-) HYSEQ INC.  
XX  
XX Tang YT, Liu C, Drmanac RT;  
PI WPI; 2001-457603/49.  
XX N-PSDB; AAH99772.  
XX  
XX Isolated human polynucleotides encoding polypeptides, useful for the  
PT treatment and diagnosis of e.g. cancer, ulcers and HIV infection -  
PT  
XX  
XX Claim 20; Page 278; 1217pp; English.  
XX  
XX AAH99166 to AAH99904 encode the human proteins given in AAM25225 to  
CC AAM25963. The proteins can have activities based on the tissues and

PR 03-FEB-1997; 97US-0792019.  
XX (AMGE-) AMGEN INC.  
XX Chang M,  
PI WPI; 2000-338492/29.  
DR N-PSDB; AAA39481.  
XX  
PT New nucleic acids encoding neurotrophic factors useful for stimulating  
PT growth of motor or sympathetic neurons for treating neuron cell damage  
XX  
XX  
PS Claim 1c; Fig 3; 42pp; English.  
XX  
CC This invention describes a novel nucleic acid molecule (I) encoding a  
CC novel neurotrophic factor (NNT-1) (II) which has neurotrophic,  
CC neuroprotective, anticonvulsant, antiparkinsonian, antidiabetic and  
CC ophthalmological activity. (I) is useful for producing NNT-1  
CC polypeptides which are useful for treating patients in whom various  
CC cells of the central, autonomic, or peripheral nervous system have  
CC degenerated and/or have been damaged by congenital disease, trauma,  
CC mechanical damage, surgery, stroke, ischemia, infection, metabolic  
CC disease, nutritional deficiency, malignancy and/or toxic agents. NNT-1  
CC proteins are used to treat diseases like Alzheimer's, Parkinson's,  
CC amyotrophic lateral sclerosis, Charcot-Marie-Tooth syndrome, Huntington's  
CC disease, peripheral neuropathy induced by diabetes or other metabolic  
CC disorders, and/or dystrophies or degeneration of the neural retina such  
CC as retinitis pigmentosa, drug-induced retinopathies, stationary forms of  
CC night blindness, progressive cone-rod degeneration, immune disorders and  
CC hematoepietic disorders. (I) is effective in treating neurological  
CC conditions and promotes neuron regeneration. Neural functions are  
CC effectively restored in patients suffering from various neurological  
CC disorders. This sequence represents the human NNT-1 protein described in  
CC the method of the invention.  
XX  
SQ Sequence 225 AA;  
Query Match 97.5%; Score 1193; DB 21; Length 225;  
Best Local Similarity 96.9%; Pred. No. 5.3e-118;  
Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
QY 1 MDLRAGDSWGMGLACCTVLMHLPAVPALNRTGDPGPGSIQKTYDLYRLEHQSLAGT 60  
DB 1 MDLRAGDSWGMGLACCTVLMHLPAVPALNRTGDPGPGSIQKTYDLYRLEHQSLAGT 60  
QY 61 YLNTYLGPPNEPDPNPPRLGAEITLPRAVTNLEWRSLSNDRLRLTONYEAYSHLCYLNGL 120  
DB 61 YLNTYLGPPNEPDPNPPRLGAEITLPRAVTNLEWRSLSNDRLRLTONYEAYSHLCYLNGL 120  
QY 121 NROAATAELRSLAFCSTLSQGLGSIAGWATLGYPLPOPAPGEPAPAPASDFLQ 180  
DB 121 NROAATAELRSLAFCSTLSQGLGSIAGWATLGYPLPOPAPGEPAPAPASDFLQ 180  
QY 161 KMDDFWLKELQTMWRSAKDFNRLKKKQPPAASVTLLHLEAHGF 225  
DB 161 KMDDFWLKELQTMWRSAKDFNRLKKKQPPAASVTLLHLEAHGF 225  
RESULT 9  
AAG63543  
ID AAG63543 standard; Protein; 225 AA.  
XX  
AC AAG63543;  
XX  
DT 15-OCT-2001 (fixed entry)  
XX  
DE Amino acid sequence of a human NNT-1 protein.  
XX  
KM NNT-1; CLF-1; sCNTFRalpha; nervous system; neuron; nervous system;  
KM neuro-muscular function; tumour; immune system; haematopoietic system;  
KM reproductive system; liver; skeletal muscle; neurodegenerative disease;  
KM amyotrophic lateral sclerosis; Parkinson's disease; Huntington's disease;

KM muscular mass; paralysis; cancer; obesity; fertility; endometriosis;  
KM blastocyst implantation; thrombosis; retinal disease;  
KM retinal pigmentosis.  
XX  
OS Homo sapiens.  
XX  
PN WO200155172-A2.  
XX  
PD 02-AUG-2001.  
XX  
PF 26-JAN-2001; 2001WO-FR00253.  
XX  
PR 27-JAN-2000; 2000FR-0001035.  
PR 12-OCT-2000; 2000FR-0013089.  
XX  
PA (FABR) FABRE MEDICAMENT SA PIERRE.  
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.  
PI Elson G, Gauchat J, Plun-Favreau H, Chevallier S, Gascan H;  
DR WPI; 2001-488773/53.  
DR N-PSDB; AAH74484.  
PT A complex comprising a NNT-1 protein and a CLF-1 and/or sCNTFRalpha  
PT protein useful to treat neurodegenerative disease including Parkinson's  
PT and Huntington's, obesity and cancer  
XX  
PS Claim 2; Page 58; 67pp; French.  
XX  
XX  
CC The present sequence represents a human NNT-1 protein. The specification  
CC describes a complex comprising a NNT-1 protein and a CLF-1 and/or  
CC sCNTFRalpha protein. The NNT-1/CLF-1 complex is used to modulate  
CC activity of the sCNTFRalpha/gp130/LIFRbeta receptor complex, or to  
CC induce phosphorylation of the tyrosine of gp130 and LIFRbeta.  
CC particularly where cells expressing the receptor complex are in the  
CC central or peripheral nervous system, in neurons implicated in  
CC neuro-muscular function or in skeletal muscle. The complex or  
CC antibodies are also used to decrease the survival, growth or  
CC proliferation of tumour cells or to facilitate the proliferation and/or  
CC inhibit differentiation of cells stocks. The complex is also used to  
CC modulate activity of the gp130/LIFRbeta receptor or cells expressing  
CC that receptor, particularly those cells implicated in the immune,  
CC haematopoietic, nervous or reproductive system, the liver or skeletal  
CC muscle. Molecules of the invention may be used to prevent or treat  
CC neurodegenerative diseases including amyotrophic lateral sclerosis,  
CC Parkinson's and Huntington's disease, to repair or regenerate nervous  
CC or muscular tissue or to maintain muscular mass in paralysis patients.  
CC They may also be used to treat cancer, obesity and associated diseases,  
CC and to improve fertility, particularly to avoid endometriosis and/or  
CC assist blastocyst implantation, thrombosis, or retinal disease,  
CC particular retinal pigmentosis.  
XX  
SQ Sequence 225 AA;  
Query Match 97.5%; Score 1193; DB 22; Length 225;  
Best Local Similarity 96.9%; Pred. No. 5.3e-118;  
Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
QY 1 MDLRAGDSWGMGLACCTVLMHLPAVPALNRTGDPGPGSIQKTYDLYRLEHQSLAGT 60  
DB 1 MDLRAGDSWGMGLACCTVLMHLPAVPALNRTGDPGPGSIQKTYDLYRLEHQSLAGT 60  
QY 61 YLNTYLGPPNEPDPNPPRLGAEITLPRAVTNLEWRSLSNDRLRLTONYEAYSHLCYLNGL 120  
DB 61 YLNTYLGPPNEPDPNPPRLGAEITLPRAVTNLEWRSLSNDRLRLTONYEAYSHLCYLNGL 120  
QY 121 NROAATAELRSLAFCSTLSQGLGSIAGWATLGYPLPOPAPGEPAPAPASDFLQ 180  
DB 121 NROAATAELRSLAFCSTLSQGLGSIAGWATLGYPLPOPAPGEPAPAPASDFLQ 180  
QY 161 KMDDFWLKELQTMWRSAKDFNRLKKKQPPAASVTLLHLEAHGF 225  
DB 161 KMDDFWLKELQTMWRSAKDFNRLKKKQPPAASVTLLHLEAHGF 225

XX Claim 1, Fig 3, 41pp; English.

PS The present sequence represents a human neurotrophic factor, designated  
XX NNT-1, which is capable of stimulating growth of motor or sympathetic  
CC neurons. The NNT-1 protein is useful in the treatment of neurological  
CC diseases characterised by the degeneration and death of particular  
CC classes of neurons. These diseases specifically include Parkinson's  
CC disease, amyotrophic lateral sclerosis (ALS), Alzheimer's disease,  
CC stroke and various degenerative disorders affecting vision.

XX Sequence 225 AA:

Query Match 97.5%; Score 1193; DB 19; Length 225;

Best Local Similarity 96.9%; Pred. No. 5.3e-118;

Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDLRAGDSWGMACCTCTVLMHLPAPVAPALNRGTGDPGPGPSIQKTYDITRYLEHQLRLAGT 60

DB 1 MDLRAGDSWGMACCTCTVLMHLPAPVAPALNRGTGDPGPGPSIQKTYDITRYLEHQLRLAGT 60

QY 61 YNLYGPPNEPDPNPRLGAETLPRAVTNLEWWSLNDRLRLTONYEAYSHLLCYLRGL 120

DB 61 YNLYGPPNEPDPNPRLGAETLPRAVTNLEWWSLNDRLRLTONYEAYSHLLCYLRGL 120

QY 121 NRQATAEIRRSIAHFCSTLSQGLGSIAGVMAITGYPLPQPLPTEPPAPAPGPAHSDFIQ 180

DB 121 NRQATAEIRRSIAHFCSTLSQGLGSIAGVMAITGYPLPQPLPTEPPAPAPGPAHSDFIQ 180

QY 181 KMDDFWLKELQTWLWRSKADFNRLKKKQPPAAVTLHLGAHGF 225

DB 181 KMDDFWLKELQTWLWRSKADFNRLKKKQPPAAVTLHLGAHGF 225

RESULT 7

AAW94466 ID AAW94466 standard; Protein; 225 AA.

AC AAW94466;

DT 22-APR-1999 (first entry)

DE Human cardiotrophin-like cytokine protein.

XX Human; cardiotrophin-like cytokine; interleukin 6 cytokine family;

KM CLC; IL-6; diagnosis; detection; immune system-related disorder;

KW cancer; cardiac disorder; heart failure; hypertension; cancer;

XX autoimmune disorder; infection.

XX Homo sapiens.

OS Location/Qualifiers

FT Key 1..27

FT Peptide /label= signal

FT Protein 28..225

FT Domain /label= Cardiotrophin-like\_cytokine

FT /label= CD-1

FT /note= "conserved domain"

FT /label= CD-II

FT /note= "conserved domain"

FT /label= CD-III

FT /note= "conserved domain"

MO9900415-A1.

XX (HUMA-) HUMAN GENOME SCI INC.

PA Ruben SM, Shi Y;

XX WPI; 1999-095678/08.

DR N-PSDB; AAX16161.

XX New isolated cardiotrophin-like cytokine nucleic acid - used to

PT develop products for treating cardiac and immune system disorders,

PT e.g. heart failure, hypertension, cancers, autoimmune disorders and

PT infections

XX Claim 1, Fig 1, 103pp; English.

CC The present invention relates to a novel cardiotrophin-like cytokine

CC (CLC) protein which is a member of the interleukin 6 (IL-6) cytokine

CC family. The present sequence represents the human CLC protein. The

CC present invention also describes screening methods for identifying

CC agonists and antagonists of CLC activity, as well as methods for

CC detecting cardiac and immune system-related disorders and

CC therapeutic methods for treating cardiac and immune system-related

CC disorders, e.g. heart failure, hypertension, cancers, autoimmune

CC disorders and infections.

XX Sequence 225 AA:

Query Match 97.5%; Score 1193; DB 20; Length 225;

Best Local Similarity 96.9%; Pred. No. 5.3e-118;

Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDLRAGDSWGMACCTCTVLMHLPAPVAPALNRGTGDPGPGPSIQKTYDITRYLEHQLRLAGT 60

DB 1 MDLRAGDSWGMACCTCTVLMHLPAPVAPALNRGTGDPGPGPSIQKTYDITRYLEHQLRLAGT 60

QY 61 YNLYGPPNEPDPNPRLGAETLPRAVTNLEWWSLNDRLRLTONYEAYSHLLCYLRGL 120

DB 61 YNLYGPPNEPDPNPRLGAETLPRAVTNLEWWSLNDRLRLTONYEAYSHLLCYLRGL 120

QY 121 NRQATAEIRRSIAHFCSTLSQGLGSIAGVMAITGYPLPQPLPTEPPAPAPGPAHSDFIQ 180

DB 121 NRQATAEIRRSIAHFCSTLSQGLGSIAGVMAITGYPLPQPLPTEPPAPAPGPAHSDFIQ 180

QY 181 KMDDFWLKELQTWLWRSKADFNRLKKKQPPAAVTLHLGAHGF 225

DB 181 KMDDFWLKELQTWLWRSKADFNRLKKKQPPAAVTLHLGAHGF 225

RESULT 8

AAW94466 ID AAW94466 standard; Protein; 225 AA.

AC AAW94466;

DT 24-AUG-2000 (first entry)

DE Human NNT-1 protein.

XX NNT-1; human; neurotrophic factor; neurotrophic; neuroprotective; treatment;

KM anticonvulsant; antiparkinsonian; antidiabetic; ophthalmological;

KW nervous system degeneration; Alzheimer's disease; Parkinson's disease;

```

Db      1 MDLRAGDSMGMLACICTYLMHLPAVPALNRTGDPGPGSIQKTYDLTRYLHQRLSLAGT 60
Qy      61 YLNTLGPPFPNPDNPPLRGAETLPRAVTVNLEWRSINDRLRLTONYEAYSHLLCYLRGL 120
Db      61 YLNTLGPPFPNPDNPPLRGAETLPRAVTVNLEWRSINDRLRLTONYEAYSHLLCYLRGL 120
Qy      121 NROAATLRLSLAHFCTSLQGLSAGVWATLGYPLPOPLPGTEPAMAPGPAHSDFLQ 180
Db      121 NROAATLRLSLAHFCTSLQGLSAGVWATLGYPLPOPLPGTEPAMAPGPAHSDFLQ 180
Qy      181 KMDDFWLKLKELQTVLMRSKQDFNRLKKKQPPAASVTTLHLBAHG 225
Db      181 KMDDFWLKLKELQTVLMRSKQDFNRLKKKQPPAASVTTLHLBAHG 225

RESULT 5
AAM29715
ID      AAM29715 standard; Protein; 225 AA.
AC      AAM29715;
DT      09-NOV-1998 (first entry)
DE      Human neurotrophic factor NNT-1.
XX      NNT-1; neurotrophic factor; human; antiinflammatory; adjuvant;
KW      Alzheimer's disease; Parkinson's disease; Huntington's disease;
KW      amyotrophic lateral sclerosis; Charcot-Marie-Tooth syndrome;
KW      peripheral neuropathy; dystrophy; neural retina degeneration;
KW      common variable immunodeficiency; CVID; selective IGA deficiency;
KW      hypogammaglobulinemia; X-linked agammaglobulinemia; antiseptic;
KW      therapy.
OS      Homo sapiens.
XX      Key      Location/Qualifiers
FH      Peptide      1..27
FT      /label= Sig_peptide
FT      Protein      28..225
FT      /label= Mat_protein
XX      WO9833922-A1.
XX      06-AUG-1998.
XX      02-FEB-1998; 98WO-US02363.
XX      30-JAN-1998; 98US-0016534.
XX      03-FEB-1997; 97US-0792019.
XX      (AMGE-) AMGEN INC.
XX      Chang M, Elliot GS, Sarmiento U, Senaldi G;
XX      MPI: 1998-437475/37.
XX      N-PSDB; AAV47510, AAV47511.
XX      Newly isolated nucleic acid encoding human or murine neurotrophic
XX      factor NNT-1 - useful for treatment of neurological and
XX      immunological diseases or inflammation, also as vaccine adjuvant
XX      Claim 12; Fig 3; 120pp; English.
XX      This is the amino acid sequence of a novel neurotrophic factor,
XX      designated NNT-1, that is a growth factor for neurons and for B or
XX      T cells. It was deduced from isolated cDNA (see AAV47510) and
XX      genomic DNA (see AAV47511) clones. Vectors containing the cDNA or
XX      genomic DNA and host cells are provided for use in the production
XX      of NNT-1 polypeptides. These are used to treat: (1) neurological
XX      or immunological diseases, specifically Alzheimer's, Parkinson's
XX      or Huntington's diseases, amyotrophic lateral sclerosis,
XX      Charcot-Marie-Tooth syndrome, peripheral neuropathy, dystrophy and

```

```

CC      degeneration of the neural retina, or conditions characterised by T
CC      or B cell defects, e.g. common variable immunodeficiency (CVID),
CC      selective Iga deficiency, hypogammaglobulinemia and X-linked
CC      agammaglobulinemia (Clained), but many others disclosed; and (ii)
CC      inflammation. NNT-1 is also able to boost immunoreactivity and
CC      antibody production following vaccination, and, since it inhibits
CC      tumour necrosis factor production, it may also be useful for
CC      treating sepsis. In addition, cells that have been engineered to
CC      express NNT-1 can be implanted, or nucleic acids are delivered in
CC      gene therapy vectors.
XX      SQ      Sequence      225 AA;
XX      Query Match      97.5%; Score 1193; DB 19; Length 225;
XX      Best Local Similarity 96.9%; Pred. No. 5.3e-118;
XX      Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
Qy      1 MDLRAGDSMGMLACICTYLMHLPAVPALNRTGDPGPGSIQKTYDLTRYLHQRLSLAGT 60
Db      1 MDLRAGDSMGMLACICTYLMHLPAVPALNRTGDPGPGSIQKTYDLTRYLHQRLSLAGT 60
Qy      61 YLNTLGPPFPNPDNPPLRGAETLPRAVTVNLEWRSINDRLRLTONYEAYSHLLCYLRGL 120
Db      61 YLNTLGPPFPNPDNPPLRGAETLPRAVTVNLEWRSINDRLRLTONYEAYSHLLCYLRGL 120
Qy      121 NROAATLRLSLAHFCTSLQGLSAGVWATLGYPLPOPLPGTEPAMAPGPAHSDFLQ 180
Db      121 NROAATLRLSLAHFCTSLQGLSAGVWATLGYPLPOPLPGTEPAMAPGPAHSDFLQ 180
Qy      181 KMDDFWLKLKELQTVLMRSKQDFNRLKKKQPPAASVTTLHLBAHG 225
Db      181 KMDDFWLKLKELQTVLMRSKQDFNRLKKKQPPAASVTTLHLBAHG 225

RESULT 6
AAM56141
ID      AAM56141 standard; Protein; 225 AA.
AC      AAM56141;
DT      13-JUL-1998 (first entry)
DE      Amino acid sequence of human neurotrophic factor NNT-1.
XX      Human; neurotrophic factor; NNT-1; growth; motor; sympathetic; neuron;
KW      treatment; neurological disease; degeneration; Parkinson's disease;
KW      amyotrophic lateral sclerosis; ALS; Alzheimers's disease; stroke.
XX      Homo sapiens.
XX      Key      Location/Qualifiers
FH      Peptide      1..27
FT      /note= "signal peptide"
FT      Protein      28..225
FT      /note= "mature protein"
XX      US5741772-A.
XX      21-APR-1998.
XX      03-FEB-1997; 97US-0792019.
XX      03-FEB-1997; 97US-0792019.
XX      (AMGE-) AMGEN INC.
XX      Chang M;
XX      MPI: 1998-260526/23.
XX      N-PSDB; AAV22652.
XX      Neurotrophic factor NNT-1 polypeptide and related nucleic acids -
XX      useful for stimulating growth of motor and sympathetic neurons

```

KW Huntington's disease; peripheral neuropathy; neural retina degeneration;  
 XX retinopathy; immune disorder; hematopoietic disorder.  
 XX  
 OS Mus sp.  
 XX  
 PN US6054294-A.  
 XX  
 PD 25-APR-2000.  
 XX  
 PF 12-DEC-1997; 97US-0988819.  
 XX  
 PR 03-FEB-1997; 97US-0792019.  
 XX  
 PA (AMGE-) AMGEN INC.  
 XX  
 PI Chang M;  
 XX  
 DR WPI; 2000-338492/29.  
 DR N-PSDB; AAA39483.  
 XX  
 PT New nucleic acids encoding neurotrophic factors useful for stimulating  
 PT growth of motor or sympathetic neurons for treating neuron cell damage  
 PT

Claim 2b; Fig 5; 42pp; English.

This invention describes a novel nucleic acid molecule (I) encoding a  
 CC novel neurotrophic factor (NNT-1) (II) which has neurotrophic,  
 CC neuroprotective, anticonvulsant, antiparkinsonian, antidiabetic and  
 CC ophthalmological activity. (I) is useful for producing NNT-1  
 CC polypeptides which are useful for treating patients in whom various  
 CC cells of the central, autonomic, or peripheral nervous system have  
 CC degenerated and/or have been damaged by congenital disease, trauma,  
 CC mechanical damage, surgery, stroke, ischemia, infection, metabolic  
 CC disease, nutritional deficiency, malignancy and/or toxic agents. NNT-1  
 CC proteins are used to treat diseases like Alzheimer's, Parkinson's,  
 CC amyotrophic lateral sclerosis, Charcot-Marie-Tooth syndrome, Huntington's  
 CC disease, peripheral neuropathy induced by diabetes or other metabolic  
 CC disorders, and/or dystrophies or degeneration of the neural retina such  
 CC as retinitis pigmentosa, drug-induced retinopathies, stationary forms of  
 CC night blindness, progressive cone-rod degeneration, immune disorders and  
 CC hematopoietic disorders. (II) is effective in treating neurological  
 CC conditions and promotes neuron regeneration. Neural functions are  
 CC effectively restored in patients suffering from various neurological  
 CC disorders. This sequence represents the murine NNT-1 protein described in  
 CC the method of the invention.

XX Sequence 225 AA;  
 XX

Query Match 100.0%; Score 1224; DB 21; Length 225;  
 Best Local Similarity 100.0%; Pred. No. 2,7e-121;  
 Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLRAGDSWGMGLACTCTVLMHLPVAVPALNRTGDPGPGSIQKTYDTRYLEHQSLAGT 60  
 DB 1 MDLRAGDSWGMGLACTCTVLMHLPVAVPALNRTGDPGPGSIQKTYDTRYLEHQSLAGT 60  
 QY 61 YANYLGPPNEPDPNPRGAEPLPRAATNLEWMSLNDRALKTQNYEAYSHILCTYKGL 120  
 DB 61 YANYLGPPNEPDPNPRGAEPLPRAATNLEWMSLNDRALKTQNYEAYSHILCTYKGL 120  
 QY 121 NROQATAEELRRSLAHCCTSLQGLGSIAGVMATLIGVPLPOPLPGTEPPAAPGPAHSDFLQ 180  
 DB 121 NROQATAEELRRSLAHCCTSLQGLGSIAGVMATLIGVPLPOPLPGTEPPAAPGPAHSDFLQ 180  
 QY 181 KMDDFWLKELQTLWLRSAKDFNRLKKKQPPAASVTLLEAHGF 225  
 DB 181 KMDDFWLKELQTLWLRSAKDFNRLKKKQPPAASVTLLEAHGF 225

RESULT 4  
 AAU78177  
 ID AAU78177 standard; Protein; 225 AA.

XX AAU78177;  
 AC  
 XX  
 DT 05-JUN-2002 (first entry)  
 XX  
 DE Mouse novel neurotrophic factor NNT1.  
 XX  
 XX Mouse; NNT1; neurotrophic factor; IGF-related disease;  
 XX Type I allergic disease; allergic rhinitis; eczema; dermatitis;  
 XX pollinosis; asthma; immune disease; cancer; arteriosclerosis;  
 XX vascular stenosis; rheumatoid arthritis; psoriatic arthritis;  
 XX inflammatory arthritis; osteoarthritis; inflammatory joint disease;  
 XX autoimmune disease; multiple sclerosis; lupus; diabetes; endometriosis;  
 XX inflammatory bowel disease; transplant rejection; reproductive disorder;  
 XX graft versus host disease; infertility; miscarriage; preterm labour.  
 XX  
 OS Mus sp.  
 XX  
 PN WO200215977-A2.  
 XX  
 PD 26-FEB-2002.  
 XX  
 PF 17-AUG-2001; 2001WO-US25906.  
 XX  
 PR 18-AUG-2000; 2000US-226436P.  
 PR 16-AUG-2001; 2001US-0931704.  
 XX  
 PA (AMGE-) AMGEN INC.  
 XX  
 PI Senaldi G;  
 XX  
 DR WPI; 2002-280867/32.  
 DR N-PSDB; ABK11649.  
 XX  
 PT Treating Immunoglobulin E-related disease, modulating Ige levels in a  
 PT patient, preventing IGE-related disease and treating allergic diseases,  
 PT involves administering NNT-1 inhibitor to a patient

Claim 2; Fig 5; 63pp; English.

The invention relates to treating Immunoglobulin E (IGE)-related disease,  
 CC modulating IGE levels in a patient, preventing an IGE-related disease,  
 CC and treating allergic diseases, comprising administering a  
 CC therapeutically effective amount of novel neurotrophic factor (NNT)-1  
 CC inhibitor to a patient. Also included are a method of diagnosing an  
 CC IGE-related disease or susceptibility to an IGE-related disease, by  
 CC determining the presence or amount of expression of an NNT1 polypeptide  
 CC encoded by a NNT1 nucleotide sequence, its fragment or naturally  
 CC occurring variant, and diagnosing an IGE-related disease or  
 CC susceptibility of an IGE-related disease based on the presence or amount  
 CC of expression of the polypeptide and a pharmaceutical composition for use  
 CC in treating IGE-related disease, comprising the NNT1 inhibitor.  
 CC The NNT1 inhibitor is useful for preventing and treating IGE-related  
 CC disease, modulating IGE levels, and treating allergic diseases e.g.  
 CC Type I allergic disease, allergic rhinitis, eczema, dermatitis,  
 CC pollinosis, asthma, immune diseases and disorders, diseases involving  
 CC abnormal cell proliferation including cancer, arteriosclerosis and  
 CC vascular stenosis, diseases and conditions relating to dysfunction of  
 CC immune system including rheumatoid arthritis, psoriatic arthritis,  
 CC inflammatory arthritis, osteoarthritis, inflammatory joint disease,  
 CC autoimmune disease, multiple sclerosis, lupus, diabetes, inflammatory  
 CC bowel disease, transplant rejection, and graft versus host disease, and  
 CC reproductive diseases and disorders including infertility, miscarriage,  
 CC preterm labour and delivery, and endometriosis. The present sequence  
 CC represents Mouse NNT1.  
 XX

XX Sequence 225 AA;  
 XX

Query Match 100.0%; Score 1224; DB 23; Length 225;  
 Best Local Similarity 100.0%; Pred. No. 2,7e-121;  
 Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLRAGDSWGMGLACTCTVLMHLPVAVPALNRTGDPGPGSIQKTYDTRYLEHQSLAGT 60

PR 30-JAN-1998; 98US-0016534.  
 PR 03-FEB-1997; 97US-0792019.  
 XX  
 XX (AMGE-) AMGEN INC.  
 XX  
 XX Chang M, Elliot GS, Sarmiento U, Senaldi G;  
 PI WPI, 1998-437475/37.  
 DR N-PSDB; AAV47512.  
 XX

PT Newly isolated nucleic acid encoding human or murine neurotrophic  
 PT factor NNT-1 - useful for treatment of neurological and  
 PT immunological diseases or inflammation, also as vaccine adjuvant  
 XX  
 XX Claim 13; Fig 5; 120pp; English.

CC This is the amino acid sequence of a murine neurotrophic factor,  
 CC designated NNT-1, that is a growth factor for neurons and for B or  
 CC T cells. It was deduced from isolated NNT-1 cDNA (see AAV47512).  
 CC Human NNT-1 (see AAW29715) is also provided. Vectors and host cells  
 CC for use in the production of human murine recombinant NNT-1.  
 CC polypeptides. These are used to treat: (i) neurological or  
 CC immunological diseases, specifically Alzheimer's, Parkinson's  
 CC or Huntington's diseases, amyotrophic lateral sclerosis,  
 CC Charcot-Marie-Tooth syndrome, peripheral neuropathy, dystrophy and  
 CC degeneration of the neural retina, or conditions characterized by T  
 CC or B cell defects, e.g. common variable immunodeficiency (CVID),  
 CC selective IgA deficiency, hypogammaglobulinemia and X-linked  
 CC agammaglobulinemia (claimed), but many others disclosed; and (ii)  
 CC inflammation. NNT-1 is also able to boost immunoreactivity and  
 CC antibody production following vaccination, and, since it inhibits  
 CC tumour necrosis factor production, and, since it inhibits  
 CC treating sepsis. In addition, cells that have been engineered to  
 CC express NNT-1 can be implanted, or nucleic acids are delivered in  
 CC gene therapy vectors.

SQ Sequence 225 AA;

Query Match 100.0%; Score 1224; DB 19; Length 225;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-121;  
 Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLRAGDSWGMALACTCTVLMHLPAYPALNRTGDPGPGPSIOKTYDLYRLEHQLSLAGT 60  
 DB 1 MDLRAGDSWGMALACTCTVLMHLPAYPALNRTGDPGPGPSIOKTYDLYRLEHQLSLAGT 60  
 QY 61 YLNYLGPPNPEDFPNPRLAGETLPRAVNLVWRSLSNDRRLRLQNYEAYSHLLCYLRGL 120  
 DB 61 YLNYLGPPNPEDFPNPRLAGETLPRAVNLVWRSLSNDRRLRLQNYEAYSHLLCYLRGL 120  
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 DB 121 NRQATATLRSLAIFCTSLGSLGSLGSLGSLGSLGSLGSLGSLGSLGSLGSLGSLGSL 180  
 QY 181 KMDDFWLKELQTMWLRSAKDFNRLKKKQPPAASVTTLHLBAHGF 225  
 DB 181 KMDDFWLKELQTMWLRSAKDFNRLKKKQPPAASVTTLHLBAHGF 225

RESULT 2  
 AAW56142  
 ID AAW56142 standard; Protein; 225 AA.  
 XX  
 AC AAW56142;  
 XX  
 DT 13-JUL-1998 (first entry)  
 XX  
 DE Amino acid sequence of murine neurotrophic factor NNT-1.

XX Mouse, neurotrophic factor; NNT-1; growth; motor; sympathetic; neuron;  
 KW treatment; neurological disease; degeneration; Parkinson's disease;  
 KW amyotrophic lateral sclerosis; ALS; Alzheimer's disease; stroke.

OS Mus sp.

XX Key Location/Qualifiers  
 XX Peptide 1..27  
 FT /note= "signal peptide"  
 FT 28..225  
 FT Protein  
 XX /note= "mature peptide"

PN US741772-A.

PD 21-APR-1998.

XX 03-FEB-1997; 97US-0792019.

PR 03-FEB-1997; 97US-0792019.

XX (AMGE-) AMGEN INC.

XX Chang M;

DR WPI, 1998-260526/23.

DR N-PSDB; AAV22654.

PT Neurotrophic factor NNT-1 polypeptide and related nucleic acids -  
 PT useful for stimulating growth of motor and sympathetic neurons  
 XX  
 XX Claim 2; Fig 5; 41pp; English.

CC The present sequence represents a murine neurotrophic factor, designated  
 CC NNT-1, which is capable of stimulating growth of motor or sympathetic  
 CC neurons. The NNT-1 protein is useful in the treatment of neurological  
 CC diseases characterized by the degeneration and death of particular  
 CC classes of neurons. These diseases specifically include Parkinson's  
 CC disease, amyotrophic lateral sclerosis (ALS), Alzheimer's disease,  
 CC stroke and various degenerative disorders affecting vision.

SQ Sequence 225 AA;

Query Match 100.0%; Score 1224; DB 19; Length 225;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-121;  
 Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLRAGDSWGMALACTCTVLMHLPAYPALNRTGDPGPGPSIOKTYDLYRLEHQLSLAGT 60  
 DB 1 MDLRAGDSWGMALACTCTVLMHLPAYPALNRTGDPGPGPSIOKTYDLYRLEHQLSLAGT 60  
 QY 61 YLNYLGPPNPEDFPNPRLAGETLPRAVNLVWRSLSNDRRLRLQNYEAYSHLLCYLRGL 120  
 DB 61 YLNYLGPPNPEDFPNPRLAGETLPRAVNLVWRSLSNDRRLRLQNYEAYSHLLCYLRGL 120  
 QY 121 NRQATATLRSLAIFCTSLGSLGSLGSLGSLGSLGSLGSLGSLGSLGSLGSLGSLGSLGSL 180  
 DB 121 NRQATATLRSLAIFCTSLGSLGSLGSLGSLGSLGSLGSLGSLGSLGSLGSLGSLGSL 180  
 QY 181 KMDDFWLKELQTMWLRSAKDFNRLKKKQPPAASVTTLHLBAHGF 225  
 DB 181 KMDDFWLKELQTMWLRSAKDFNRLKKKQPPAASVTTLHLBAHGF 225

RESULT 3  
 AAY87814  
 ID AAY87814 standard; Protein; 225 AA.  
 XX  
 AC AAY87814;  
 XX  
 DT 24-AUG-2000 (first entry)  
 XX  
 DE Murine NNT-1 protein.

XX NNT-1; neurotrophic factor; neurotrophic; neuroprotective; treatment;  
 KW anticonvulsant; antiparkinsonian; antidiabetic; ophthalmological;  
 KW nervous system degeneration; Alzheimer's disease; Parkinson's disease;  
 KW amyotrophic lateral sclerosis; Charcot-Marie-Tooth syndrome; murine;

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 9, 2004, 06:14:57 ; Search time 35.5 Seconds  
(without alignments)  
1006.013 Million cell updates/sec

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Perfect score: 1224  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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24: /SIDSI/gcgcdata/geneSeq/geneSeq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1224	100.0	225	19	AAW29716
2	1224	100.0	225	19	AAW56142
3	1224	100.0	225	21	AAV78177
4	1224	100.0	225	23	AAW78177
5	1193	97.5	225	19	AAW29715
6	1193	97.5	225	19	AAW56141
7	1193	97.5	225	20	AAW94466
8	1193	97.5	225	21	AAV78173
9	1193	97.5	225	22	AAW63543

10	1193	97.5	225	23	AAU78176	Human novel neurotrophin
11	1193	97.5	225	22	AAW25831	Human protein sequ
12	1181	96.5	223	22	AAE00828	Human cardiotroph
13	1171	95.7	321	22	ABH1896	Human cardiotroph
14	1171	95.7	321	22	AAW79399	Human cardiotroph
15	1167	95.3	215	21	AAH19587	Human protein SEQ
16	1164	95.1	260	22	AAW78415	Human interleukin
17	1136	92.8	215	21	AAH19586	Human interleukin
18	852	69.6	164	22	ABG55577	Human liver peptid
19	852	69.6	164	22	ABH40317	Peptide #7823 enco
20	852	69.6	164	22	ABH24716	Protein #6715 enco
21	852	69.6	164	22	AAW61118	Human brain expres
22	852	69.6	164	22	AAW73827	Human bone marrow
23	852	69.6	164	22	AAW20115	Peptide #6549 enco
24	852	69.6	164	22	AAW34012	Peptide #8049 enco
25	852	69.6	164	23	ABG43716	Human peptid enco
26	156.5	12.8	208	20	AAH09197	Human DNAX interle
27	154	12.6	208	20	AAV09196	Human DNAX interle
28	110.5	9.0	203	16	AAH83965	Human cardiac hype
29	110.5	9.0	203	17	AAH88204	Human cardiotroph
30	110.5	9.0	203	18	AAW29237	Human cardiotroph
31	92.5	7.6	243	22	AAU09153	Human cytokine zal
32	92.5	7.6	243	22	AAH20277	Human interleukin
33	92.5	7.6	243	23	ABG32291	Human IL-D80 prote
34	92.5	7.6	243	23	AAU76375	Human helical prot
35	92.5	7.5	243	24	ABG75877	Human cytokine IL-
36	92	7.5	332	21	AAW22132	Arabidopsis thalia
37	92	7.5	332	21	AAW40321	Arabidopsis thalia
38	91.5	7.5	201	16	AAH83967	Human cardiac hype
39	91.5	7.5	201	18	AAW29238	Human cardiac hype
40	91.5	7.5	201	20	AAV06490	Human tumour-assoc
41	91.5	7.5	201	21	AAH27662	Human protein PRO8
42	91.5	7.5	201	21	AAH13004	Human cardiotroph
43	91.5	7.5	201	21	AAV93697	Human cardiotroph
44	91.5	7.5	201	21	AAH7818	Amino acid sequenc
45	91.5	7.5	201	22	AAH50994	Human cardiotroph

## ALIGNMENTS

AAW29716	standard; Protein; 225 AA.
AAW29716	
09-NOV-1998	(first entry)
Mouse neurotrophic factor NNT-1.	
NNT-1; neurotrophic factor; mouse; antiinflammatory; adjuvant; Alzheimer's disease; Parkinson's disease; Huntington's disease; amyotrophic lateral sclerosis; Charcot-Marie-Tooth syndrome; peripheral neuropathy; dystrophy; neural retina degeneration; common variable immunodeficiency; CVID; selective IGA deficiency; hypogammaglobulinaemia; X-linked agammaglobulinaemia; antisepic; therapy.	
Mus sp.	
Key	Location/Qualifiers
Peptide	1..27
Protein	/label= Sig_peptide 28..225 /label= Mat_protein
W09833922-A1.	
06-AUG-1998.	
02-FEB-1998;	98WO-US02363.



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Job time : 34 secs

Search completed: February 9, 2004, 06:26:17  
Job time : 34 secs



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APPLICANT: Zernhusen, Bryan D.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-216
CURRENT APPLICATION NUMBER: US/10/231,913
CURRENT FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: 60/251,660
PRIOR FILING DATE: 2000-12-06
PRIOR APPLICATION NUMBER: 60/255,029
PRIOR FILING DATE: 2000-12-12
PRIOR APPLICATION NUMBER: 60/260,326
PRIOR FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 60/263,800
PRIOR FILING DATE: 2001-01-24
PRIOR APPLICATION NUMBER: 60/269,942
PRIOR FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 60/286,183
PRIOR FILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: 60/313,627
PRIOR FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: 60/318,712
PRIOR FILING DATE: 2001-09-12
NUMBER OF SEQ ID NOS: 292
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 98
LENGTH: 727
TYPE: PRT
ORGANISM: Mus musculus
US-10-231-913-98
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Best Local Similarity 24.8%; Pred. No. 2.2;
Matches 61; Conservative 32; Mismatches 93; Indels 60; Gaps 11;
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113 LL--CYLRGLNRQAATAEIRSLAHFCTSLQGLSIGVMA-TLGYPLPQPLPTEPAM 169
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170 AEGPASPDLQKMDDFWL-----KELQWIRSAADFVRLKKKQPPASVT 217
177 AATPRIGDVIQKLAPLKMYSEYVKNPERAAELIATWMDK--OPQEVVTRIQSEASS 235
QY 218 LMLEAH 223
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RESULT 10
US-09-810-052-5
Sequence 5; Application US/09810052
Patent No. US2002009975A1
GENERAL INFORMATION:
APPLICANT: Conklin, Darrell C.
APPLICANT: Presnell, Scott R.
TITLE OF INVENTION: HELICAL PROTEIN ZALPHA51
FILE REFERENCE: 00-24
CURRENT APPLICATION NUMBER: US/09/810,052
CURRENT FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/190,410
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: 60/199,443
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 5
LENGTH: 243
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TYPE: PRT
ORGANISM: Homo sapiens
US-09-810-052-5
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Matches 57; Conservative 26; Mismatches 105; Indels 57; Gaps 9;
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QY 47 TRYLEHQLSLAGTYLN-----YLGPFPNEPDPNPRLGAEITLPRATVNLVWMSLN 98
DB 54 ARKLSEVRGQAHRAFSHLPGVNLYLP-----LG-EQLPDVSLTFQAWRRLS 101
QY 99 DRLRLTONYEAASHLCYLRGLNRQAATAEIR-SLAHCTSLQGLSIGVMAATLGY 157
DB 102 DPERLCFISTTLQPFHAPLGLGTQGRWTNMRMQLMARLDRLQRLRFQVLAAGFN 161
QY 158 LPOP-----LPGTEPAMAPPAHSDFLQKMDDFWLKELQWIMRSAXDF 202
DB 162 LPREEREEEREEERKGLLPGLSGALQGPVQVSWPQLISTYRLHSLVLSRAVRL 221
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RESULT 11
US-09-791-497-8
Sequence 8; Application US/09791497
Publication No. US20030008343A1
GENERAL INFORMATION:
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APPLICANT: Timans, Jacqueline C.
APPLICANT: Kastelein, Robert A.
APPLICANT: Bazan, J. Fernando
APPLICANT: Peltanz, Stefan
TITLE OF INVENTION: Mammalian Cytokines; Related Reagents
FILE REFERENCE: DX01040K2
CURRENT APPLICATION NUMBER: US/09/791,497
CURRENT FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: 09/627,897
PRIOR FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: 60/146,581
PRIOR FILING DATE: 1999-07-30
PRIOR APPLICATION NUMBER: 60/147,763
PRIOR FILING DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 243
TYPE: PRT
ORGANISM: primate; surmised Homo sapiens
US-09-791-497-8
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Query Match 7.6%; Score 92.5; DB 11; Length 243;
Best Local Similarity 23.3%; Pred. No. 0.6;
Matches 57; Conservative 26; Mismatches 105; Indels 57; Gaps 9;
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DB 102 DPERLCFISTTLQPFHAPLGLGTQGRWTNMRMQLMARLDRLQRLRFQVLAAGFN 161
QY 158 LPOP-----LPGTEPAMAPPAHSDFLQKMDDFWLKELQWIMRSAXDF 202
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Db 141 AALGAARAG--PGPEPVATLFTANSTAGIFSAAVGLGFHVCGLXGEWVSRTGDLGQL 197

RESULT 7

US-10-407-303-3

Sequence 3, Application US/10407303

Publication No. US20040006018A1

GENERAL INFORMATION:

APPLICANT: Baker, Joffere

APPLICANT: Chien, Kenneth

APPLICANT: King, Kathleen

APPLICANT: Pennica, Diane

APPLICANT: Wood, William

TITLE OF INVENTION: Methods of Stimulating the Proliferation and

TITLE OF INVENTION: Differentiation of Satellite Cells Inco Myoblasts by

TITLE OF INVENTION: Contact with CT-1

FILE REFERENCE: P0994RID2C1

CURRENT APPLICATION NUMBER: US/10/407,303

CURRENT FILING DATE: 2003-04-03

PRIOR APPLICATION NUMBER: US 09/724,772

PRIOR FILING DATE: 2000-11-28

PRIOR APPLICATION NUMBER: US 08/797,014

PRIOR FILING DATE: 1997-02-07

PRIOR APPLICATION NUMBER: US 60/049,998

PRIOR FILING DATE: 1996-02-14

NUMBER OF SEQ ID NOS: 8

SEQ ID NO: 3

LENGTH: 203

TYPE: PRT

ORGANISM: Mus musculus

FEATURE:

NAME/KEY: Amino Acid

LOCATION: Pull

OTHER INFORMATION:

US-10-407-303-3

Query Match 9.0%; Score 110.5; DB 12; Length 203;

Best Local Similarity 27.4%; Pred. No. 0.0077;

Matches 49; Conservative 23; Mismatches 86; Indels 21; Gaps 6;

Qy 40 IOKTYDLTRYLHQLSLAGTYLNTYLGPPFNPDPNPRLL--GATTLPRATVNLVWRS 96

Db 27 IROTHNLARLLTKYAEQLBEYVOQGEPFGLPSPSPRLPLAGISGPAASHAGLPV--- 83

Qy 97 LNDRLRLQNTYEAHSHLCLYRGUNROA-----TAELRSLAHCTSLQGLGSIAGYM 151

Db 84 -SERLR--QDAALSVLPALLDAVRRROELNPPAPRLRLSLLEDAARQVRALGAAVETVL 140

Qy 152 ATLGYPPLQPLPGTEPA-----WAPGPAHSDFLQKMDDFWLKELQTLWLMRSAXDPNRL 205

Db 141 AALGAARAG--PGPEPVATLFTANSTAGIFSAAVGLGFHVCGLXGEWVSRTGDLGQL 197

RESULT 8

US-10-107-931-3

Sequence 3, Application US/10107931

Publication No. US20030054550A1

GENERAL INFORMATION:

APPLICANT: Baker, Joffere

APPLICANT: Chien, Kenneth

APPLICANT: King, Kathleen

APPLICANT: Pennica, Diane

APPLICANT: Wood, William

TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESSES:

ADDRESS: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patin (genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/107,931

FILING DATE: 26-Mar-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/364,187

FILING DATE: 30-Jul-1999

APPLICATION NUMBER: 08/286,304

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Hasat, Janet E.

REGISTRATION NUMBER: 28,616

REFERENCE/DOCKET NUMBER: 894P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-1896

TELEFAX: 415/952-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 203 amino acids

TYPE: amino acid

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-10-107-931-3

Query Match 9.0%; Score 110.5; DB 15; Length 203;

Best Local Similarity 27.4%; Pred. No. 0.0077;

Matches 49; Conservative 23; Mismatches 86; Indels 21; Gaps 6;

Qy 40 IOKTYDLTRYLHQLSLAGTYLNTYLGPPFNPDPNPRLL--GATTLPRATVNLVWRS 96

Db 27 IROTHNLARLLTKYAEQLBEYVOQGEPFGLPSPSPRLPLAGISGPAASHAGLPV--- 83

Qy 97 LNDRLRLQNTYEAHSHLCLYRGUNROA-----TAELRSLAHCTSLQGLGSIAGYM 151

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Db 141 AALGAARAG--PGPEPVATLFTANSTAGIFSAAVGLGFHVCGLXGEWVSRTGDLGQL 197

RESULT 9

US-10-231-913-98

Sequence 98, Application US/10231913

Publication No. US20040005576A1

GENERAL INFORMATION:

APPLICANT: Guo, Xiaojia S.

APPLICANT: Li, Li

APPLICANT: Patuturajan, Meera

APPLICANT: Shimkets, Richard A.

APPLICANT: Casman, Stacie J.

APPLICANT: Malyankar, Uriel M.

APPLICANT: Tchernev, Velizar T.

APPLICANT: Vernet, Corine A.

APPLICANT: Spytek, Kimberly A.

APPLICANT: Shenoy, Suresh G.

APPLICANT: Aliebrook II, John P.

APPLICANT: Edinger, Schlowitz

APPLICANT: Peyman, John A.

APPLICANT: Stone, David J.

APPLICANT: Ellerman, Karen

APPLICANT: Gangolli, Esma A.

APPLICANT: Boldog, Ference L.

APPLICANT: Colman, Steven D.

APPLICANT: Eissen, Andrew J.

APPLICANT: Liu, Xiaohong

APPLICANT: Padigaru, Muralidhara

APPLICANT: Spaderma, Steven K.



DB 181 KMDDFWLKELOTWLMRSKDFNRLKKKQPPAAVTLHLGAHGF 225

RESULT 2  
US-09-931-704-2

/ Sequence 2, Application US/09931704  
/ Patent No. US20020041873A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Senaldi, Giorgio  
/ TITLE OF INVENTION: Methods and Compositions for Treating IGE-Related Disease Using N  
/ FILE REFERENCE: A-695  
/ CURRENT APPLICATION NUMBER: US/09/931,704  
/ PRIOR FILING DATE: 2001-08-16  
/ PRIOR APPLICATION NUMBER: US 60/226,436  
/ NUMBER OF SEQ ID NOS: 5  
/ SOFTWARE: Patent version 3.1  
/ SEQ ID NO 2  
/ LENGTH: 225  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
US-09-931-704-2

Query Match 97.5%; Score 1193; DB 9; Length 225;  
Best Local Similarity 96.9%; Pred. No. 2,2e-110;  
Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDLRAGDSWGMACICTVLMHLPAVPALNRGDPGPGPSIQKTYDLTRYLEHQSLAGT 60  
DB 1 MDLRAGDSWGMACICTVLMHLPAVPALNRGDPGPGPSIQKTYDLTRYLEHQSLAGT 60  
QY 61 YLNYIGPPENPDFFNPRLGAETLPRAVNLVWMSLNDRLRLTONYEAYSHLLCYLRL 120  
DB 61 YLNYIGPPENPDFFNPRLGAETLPRAVNLVWMSLNDRLRLTONYEAYSHLLCYLRL 120  
QY 121 NROAATALRSLAHFCTSLGSLGSLAGVMAALGYPLPQPGTEPTWTPGPAHSDFLQ 180  
DB 121 NROAATALRSLAHFCTSLGSLGSLAGVMAALGYPLPQPGTEPTWTPGPAHSDFLQ 180  
QY 181 KMDDFWLKELOTWLMRSKDFNRLKKKQPPAAVTLHLGAHGF 225  
DB 181 KMDDFWLKELOTWLMRSKDFNRLKKKQPPAAVTLHLGAHGF 225

RESULT 3  
US-10-212-793-2

/ Sequence 2, Application US/10212793  
/ Publication No. US20030087395A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Shi et al.  
/ TITLE OF INVENTION: Cardiotrophin-Like Cytokine  
/ FILE REFERENCE: PF385DICI  
/ CURRENT APPLICATION NUMBER: US/10/212,793  
/ PRIOR FILING DATE: 2002-08-07  
/ PRIOR APPLICATION NUMBER: US 09/438,299  
/ PRIOR FILING DATE: 1999-11-12  
/ PRIOR APPLICATION NUMBER: US 09/106,182  
/ PRIOR FILING DATE: 1998-06-29  
/ PRIOR APPLICATION NUMBER: US 60/051,311  
/ PRIOR FILING DATE: 1997-06-30  
/ NUMBER OF SEQ ID NOS: 24  
/ SEQ ID NO 2  
/ LENGTH: 225  
/ TYPE: PRT  
/ ORGANISM: homo sapiens  
/ FEATURE:  
/ NAME/KEY: signal  
/ LOCATION: (-27)..(-1)  
/ FEATURE:  
/ NAME/KEY: peptide  
/ LOCATION: (1)..(198)

US-10-212-793-2

Query Match 97.5%; Score 1193; DB 15; Length 225;  
Best Local Similarity 96.9%; Pred. No. 2,2e-110;  
Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDLRAGDSWGMACICTVLMHLPAVPALNRGDPGPGPSIQKTYDLTRYLEHQSLAGT 60  
DB 1 MDLRAGDSWGMACICTVLMHLPAVPALNRGDPGPGPSIQKTYDLTRYLEHQSLAGT 60  
QY 61 YLNYIGPPENPDFFNPRLGAETLPRAVNLVWMSLNDRLRLTONYEAYSHLLCYLRL 120  
DB 61 YLNYIGPPENPDFFNPRLGAETLPRAVNLVWMSLNDRLRLTONYEAYSHLLCYLRL 120  
QY 121 NROAATALRSLAHFCTSLGSLGSLAGVMAALGYPLPQPGTEPTWTPGPAHSDFLQ 180  
DB 121 NROAATALRSLAHFCTSLGSLGSLAGVMAALGYPLPQPGTEPTWTPGPAHSDFLQ 180  
QY 181 KMDDFWLKELOTWLMRSKDFNRLKKKQPPAAVTLHLGAHGF 225  
DB 181 KMDDFWLKELOTWLMRSKDFNRLKKKQPPAAVTLHLGAHGF 225

RESULT 4  
US-09-864-761-40014

/ Sequence 40014, Application US/09864761  
/ Patent No. US20020048763A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Penn, Sharon G.  
/ APPLICANT: Rank, David R.  
/ APPLICANT: Hanzel, David K.  
/ APPLICANT: Chen, Wenheng  
/ TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
/ FILE REFERENCE: Aecmica-X-1  
/ CURRENT APPLICATION NUMBER: US/09/864,761  
/ PRIOR FILING DATE: 2001-05-23  
/ PRIOR APPLICATION NUMBER: US 60/180,312  
/ PRIOR FILING DATE: 2000-02-04  
/ PRIOR APPLICATION NUMBER: US 60/207,456  
/ PRIOR FILING DATE: 2000-05-26  
/ PRIOR APPLICATION NUMBER: US 09/632,366  
/ PRIOR FILING DATE: 2000-08-03  
/ PRIOR APPLICATION NUMBER: GB 24263.6  
/ PRIOR FILING DATE: 2000-10-04  
/ PRIOR APPLICATION NUMBER: US 60/236,359  
/ PRIOR FILING DATE: 2000-09-27  
/ PRIOR APPLICATION NUMBER: PCT/US01/00666  
/ PRIOR FILING DATE: 2001-01-30  
/ PRIOR APPLICATION NUMBER: PCT/US01/00667  
/ PRIOR FILING DATE: 2001-01-30  
/ PRIOR APPLICATION NUMBER: PCT/US01/00664  
/ PRIOR FILING DATE: 2001-01-30  
/ PRIOR APPLICATION NUMBER: PCT/US01/00669  
/ PRIOR FILING DATE: 2001-01-30  
/ PRIOR APPLICATION NUMBER: PCT/US01/00665  
/ PRIOR FILING DATE: 2001-01-30  
/ PRIOR APPLICATION NUMBER: PCT/US01/00668  
/ PRIOR FILING DATE: 2001-01-30  
/ PRIOR APPLICATION NUMBER: PCT/US01/00663  
/ PRIOR FILING DATE: 2001-01-30  
/ PRIOR APPLICATION NUMBER: PCT/US01/00662  
/ PRIOR FILING DATE: 2001-01-30  
/ PRIOR APPLICATION NUMBER: PCT/US01/00661  
/ PRIOR FILING DATE: 2001-01-30  
/ PRIOR APPLICATION NUMBER: PCT/US01/00670  
/ PRIOR FILING DATE: 2001-01-30  
/ PRIOR APPLICATION NUMBER: US 60/234,687  
/ PRIOR FILING DATE: 2000-09-21  
/ PRIOR APPLICATION NUMBER: US 09/608,408  
/ PRIOR FILING DATE: 2000-06-30  
/ PRIOR APPLICATION NUMBER: US 09/774,203  
/ PRIOR FILING DATE: 2001-01-29





US-08-443-130-3

Query Match 9.0%; Score 110.5; DB 1; Length 203;  
Best Local Similarity 27.4%; Pred. No. 0.00067;  
Matches 49; Conservative 23; Mismatches 86; Indels 21; Gaps 6;

Qy	40	IQKTYDLTRYLEHQLRSILAGTYLNYLGPPFNEPDPNPRLL---GATTLPRATVNLVWRS	96
Db	27	IRQTNINLALRLTKVAEQULEEYVQOGEPFGLPGFSPRLPLAGLSGPAPSHAGLPV---	83
Qy	97	LNDRLRLTONVEAYSHLCTYLRGLNRQAA----TAELRSLAHFCTSIQGLLSIAGVM	151
Db	84	-SERLR--QDAALSVLPALDVAVRRRQAEINPRAPRLLRSLEDARQVRALGAAVETVL	140
Qy	152	ATLGYPPLPQPLRGTEPA-----WAPGPAHSDPLQKMDPFWLKELOTWLMRSAXDENRL	205
Db	141	AALGPAARG--PGPEPVTVATLFTANSTAGIPSAKVGFHVCGLYGEWVSRTEGDLGOL	197

Search completed: February 9, 2004, 06:25:00  
Job time : 15 secs

ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: 894PID2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-4874  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 203 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-443-129-5

Query Match	9.0%;	Score 110.5;	DB 1,	Length 203;
Best Local Similarity	27.4%;	Pred. No. 0.00067;		
Matches 49;	Conservative 23;	Mismatches 86;	Indels 21;	Gaps 6;

QY 40 IOKYDRLRYRYLHQRSLAGTYLANTLGPFPNDPNPRL---GAETLPRAVLNLEWRS 96  
Db 27 IROTHNLARLLTKVAEQLEEVVQGGSEFGLRGSFPRRLPLAGLSGAPSHAGLPV--- 83  
QY 97 LNDLRPLRNTQEAAYSHLLCYLRGLNRQA-----TAELRSLAHCTSLQGLIGSIAGV 151  
Db 84 -SERLR--QDAANAISVLPALIDAVYRRQKEINPRAPRLRSLIEDARVRAALGAAYEVTL 140

QY 152 ATLGFLPQLPDLTEPA----NAPGPAHSDFLOKMDFWLLKELQTLWMSAKDENRL 205  
 141 AALGAARG--PGPEPTVATLELTANSTAGIFSAKVLGFHYCGLYGEWVSRTEGDLGQL 197

RESULT 14  
US-08-443-952-3

? Patent No 5679545  
 ?  
 ? GENERAL INFORMATION:  
 ?  
 ? APPLICANT: Baker, Joffre  
 ?  
 ? APPLICANT: Chien, Kenneth  
 ?  
 ? APPLICANT: King, Kathleen  
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 ? APPLICANT: Pennica, Diane  
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 ? APPLICANT: Wood, William  
 ?  
 ? TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor  
 ?  
 ? NUMBER OF SEQUENCES: 8  
 ?  
 ? CORRESPONDENCE ADDRESS: ?

ADDRESS: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:

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; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

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APPLICATION NUMBER: 08/233609  
FILING DATE: 25-APR-1994

;; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/286304

;; FILING DATE: 05-AUG-1994  
;; ATTORNEY/AGENT INFORMATION:

NAME: Torchia, Timothy E.  
REGISTRATION NUMBER: 36,700

REFERENCE/DOCKET NUMBER: 894P1D4  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-86  
TELEFAX: 415/952-9861

```

;          TELEX: 910/371-7168
;          INFORMATION FOR SEQ ID NO: 3
;          SEQUENCE CHARACTERISTICS:
;             LENGTH: 203 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;
US-08-443-952-3

```

Query Match	9.0%;	Score 110.5;	DB 1;	Length 203;
Best Local Similarity	27.4%;	Pred. No. 0.00067;		
Matches 49;	Conservative 23;	Mismatches 86;	Indels 21;	Gaps 6

QY 40 IOKYDSTRYEHQSLRSLAGTYLNYLPENFENPNPRL---CAETLPRTVNLNWRMS 96  
Db 27 IROHNHARLLTKYAEGLLEETVYQQGEFPCLPSPSPRLPLAGISGAPRHAGLPV--- 83  
QY 97 LNPDLRLTONYEASHLLCTYRGINRQA-----TAELRRSLAHFCTSLQGLSISAGYM 151  
Db 84 -SESLR---QDAALSTVPLALDDAARRKQAEINPAPRLRSLLEDAROVRLGAAVEFVL 140

```
OY      152 ATTCGYLPDPLPGTEPA-----WAPGPAHSDTLQKMDFWLLKEQLQTWLMSAKCPNRL 205
        |||   |||   :   |   :   :   :   :   :   :   :   :   :
DB      141 AALCAARG--PGPEVTVAATLFANSTAGISAKVLGFHVCGLYGEWTSRTEDGGQL 197
```

RESULT 15  
US-08-443-130-3

Patent No. 5723585  
GENERAL INFORMATION:  
APPLICANT: Baker, Joffre  
APPLICANT: Chen, Kenneth  
APPLICANT: King, Kathleen  
APPLICANT: Penicka, Diane  
APPLICANT: Wood, William  
TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses  
TITLE OF INVENTION: Therefor  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:

ADDRESS: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA

```

;      ZIP:  94080
;
;      COMPUTER READABLE FORM:
;
;      VENDOR:  BUREAU OF THE U.S. DEPARTMENT OF JUSTICE
;
;      DATE:  1988-08-01
;
;      TIME:  11:11

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MEDIUM TYPE: 5.25 inch, 360  
COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/M...
; SOFTWARE: patin (Genentech)
; ...
```

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/443,130
; FILING DATE: 12 MAR 2008

```

FILING DATE: 17-MAY-1995  
 CLASSIFICATION: 435

;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/233609  
;; FILING DATE: 05/13/2004

; FILING DATE: 25-APR-1994  
 ; PRIOR APPLICATION DATA:  
 ;

APPLCATION NUMBER: 08/286304  
FILING DATE: 05-AUG-1994

ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, Timothy E.  
REGISTRATION NUMBER: 35700

REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: 894P1D3

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-8674  
FAX: 415/225-8674

TELEFAX: 415/952-9881  
TELEX: 910/371-7168

3 INFORMATION FOR SEQ ID NO: 3  
SEQUENCE CHARACTERISTICS:

```

; LENGTH: 203 amino acids
; TYPE: amino acid

```

; TOPOLOGY: Linear

GENERAL INFORMATION:

APPLICANT: Baker, Joffree

APPLICANT: Chien, Kenneth

APPLICANT: King, Kathleen

APPLICANT: Pennica, Diane

APPLICANT: Wood, William

TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: dalin (Genentech).

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/443,129

FILING DATE: 17-MAY-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/233609

FILING DATE: 25-APR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/286

FILING DATE: 05-AUG-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 304

FILING DATE: (null)

```

; Patent No. 5534615
; GENERAL INFORMATION:
; APPLICANT: Baker, Joffe
; APPLICANT: Chien, Kenneth
; APPLICANT: King, Kathleen
; APPLICANT: Pennica, Diane
; APPLICANT: Wood, William
; TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/233, 609
; FILING DATE: 25-APR-1994
; CLASSIFICATION: A35
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 894
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 203 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
;
US-08-233-609-3

Query Match          9.0%; Score 110.5; DB 1; Length 203;
Best Local Similarity 27.4%; Pred. No. 0.00067;
Matches 49; Conservative 23; Mismatches 86; Indels 21; Gaps 6

QY      40 IOKTYDRLRYLEHQRLSLAGTLYLNTLGPFENEDFNPRPL---GATTLPRATVNLIEWMS 96
       ||::|||:|||||:|||||:|||||:|||||:|||||:|
DB      27 IRQTINLLARLLTKVAEQULEERTVOQGGEFFGLPGSPPLPLAGSGPAPSHAGLPV-- 83
       ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY      97 INDRILRTONTVEAYSHILCYLRGLNRQA-----TAELRSLSIAHFCTSSLOGLSIAGVM 151
       :|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB      84 -SERIR--QDAALASVLPAALLAVARRROALENPPRRILRSLEDAROVRLGAAYETVL 140
       ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY      152 ATLVGYLPQLPUGTEPA-----WADGPASHDFLOKWDDEFWMLKEIQTWLMRSAKDNRL 205
       |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB      141 AALGAARG--GGPPPVTVATLFTANSTAGIFSAKVLGHVCGVGCEWVSRTGEDIGOL 197
       |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 10
US-08-444-083-3
; Sequence 3, Application US/08444083
; Patent No. 5571675
; GENERAL INFORMATION:
; APPLICANT: Baker, Joffe
; APPLICANT: Chien, Kenneth
; APPLICANT: King, Kathleen
; APPLICANT: Pennica, Diane
; APPLICANT: Wood, William
; TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:

```

```

ADDRESS: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,083
FILING DATE: 17-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/233609
FILING DATE: 25-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/286304
FILING DATE: 05-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 894PIDS
TELEPHONE: 415/225-8674
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 203 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-444-083-3

Query Match          9.0%; Score 110.5; DB 1; Length 203;
Best Local Similarity 27.4%; Pred. No. 0.00067;
Matches 49; Conservative 23; Mismatches 86; Indels 21; Gaps 6;

QY  I Q K T Y D L T R Y E H Q L R S L A G T Y L N Y L G P P E N E P D F N P R L --- G A E T L P R A T V N L E V R S 96
   | : : : : : | : : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db  27 I R Q H N L A R L I T T K A B O L L E E Y V Q O G E P F G L P G S P P R L L A G S G A P S H A G L P V --- 83
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY  97 L N D R L R L T O N Y E A V S H L L C Y L R G L N R O A A --- T A E I R S L A H F C T S L O G I L G S I A G V M 151
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db  84 - S E R L R --- Q D A A L S V L P A L L D A V R R R Q G A E L N P R A P R L R S L E D N A Q V R L L G A V E Y V L 140
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY  152 A T L G P L P Q P L R G T E P A --- W A P G A H S D F L Q K M D F W L K E L Q T W L M S A D F N R L 205
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db  141 A A L G A A A R G - P G D E P Y V A T L P F A N S T A G I F S A K V L G F H V C G L Y G E W V S R T E D L G Q L 197
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 11
US-08-286-304-3
; Sequence 3, Application US/08286304
; Patent No. 5571893
; GENERAL INFORMATION:
; APPLICANT: Baker, Joffre
; APPLICANT: Chien, Kenneth
; APPLICANT: King, Kathleen
; APPLICANT: Pennica, Diane
; APPLICANT: Wood, William
; TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:

```

Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDLRAGDSWGMCLACTVLMHLPAVPALNRITGDPGPGPSIQKTYDLTRYLHQLSLAGT 60  
DB 1 MDLRAGDSWGMCLACTVLMHLPAVPALNRITGDPGPGPSIQKTYDLTRYLHQLSLAGT 60

QY 61 YLNYLGPPNPBPDPFPPRLGAGTLPRAVTNLEVMRSLNDRLLTONYEAASHLCTYLRGL 120  
DB 61 YLNYLGPPNPBPDPFPPRLGAGTLPRAVTNLEVMRSLNDRLLTONYEAASHLCTYLRGL 120

QY 121 NRQAATAEIRSLAHFCTSLQGLGSIAGWATLGYLPQPLPGTEPMAAPGPAHSDFLQ 180  
DB 121 NRQAATAEIRSLAHFCTSLQGLGSIAGWATLGYLPQPLPGTEPMTWGPASDFLQ 180

QY 181 KMDDFWLKEIQTLWLRSAKDFNRLKKMKOPPAASVTLHLEAHGF 225  
DB 181 KMDDFWLKEIQTLWLRSAKDFNRLKKMKOPPAASVTLHLEAHGF 225

## RESULT 7

US-09-016-534-2  
; Sequence 2, Application US/09016534  
; Patent No. 6143874  
; GENERAL INFORMATION:  
; APPLICANT: CHANG, MING-SHI  
; APPLICANT: ELLIOTT, GARY S.  
; APPLICANT: SARMIENTO, ULLA  
; APPLICANT: SENALDI, GIORGIO  
; TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: AMGEN INC.  
; STREET: ONE AMGEN CENTER  
; CITY: THOUSAND OAKS  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 91320  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/016,534  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/792,019  
; FILING DATE: 03-FEB-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: COOK, ROBERT R.  
; REGISTRATION NUMBER: 31,602  
; REFERENCE/DOCKET NUMBER: A-442B  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 225 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-016-534-2

Query Match 97.5%; Score 1193; DB 3; Length 225;  
Best Local Similarity 96.9%; Pred. No. 1.7e-119;  
Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDLRAGDSWGMCLACTVLMHLPAVPALNRITGDPGPGPSIQKTYDLTRYLHQLSLAGT 60  
DB 1 MDLRAGDSWGMCLACTVLMHLPAVPALNRITGDPGPGPSIQKTYDLTRYLHQLSLAGT 60

QY 61 YLNYLGPPNPBPDPFPPRLGAGTLPRAVTNLEVMRSLNDRLLTONYEAASHLCTYLRGL 120  
DB 61 YLNYLGPPNPBPDPFPPRLGAGTLPRAVTNLEVMRSLNDRLLTONYEAASHLCTYLRGL 120

QY 121 NRQAATAEIRSLAHFCTSLQGLGSIAGWATLGYLPQPLPGTEPMAAPGPAHSDFLQ 180  
DB 121 NRQAATAEIRSLAHFCTSLQGLGSIAGWATLGYLPQPLPGTEPMTWGPASDFLQ 180

QY 181 KMDDFWLKEIQTLWLRSAKDFNRLKKMKOPPAASVTLHLEAHGF 225  
DB 181 KMDDFWLKEIQTLWLRSAKDFNRLKKMKOPPAASVTLHLEAHGF 225

## RESULT 8

US-09-106-182-3  
; Sequence 3, Application US/09106182  
; Patent No. 6046035  
; GENERAL INFORMATION:  
; APPLICANT: Shi, Yangu  
; APPLICANT: Ruben, Steve  
; TITLE OF INVENTION: Cardiotrophin-like Cytokine  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc  
; STREET: 9410 Key West Ave  
; CITY: Rockville  
; STATE: MD  
; COUNTRY: US  
; ZIP: 20850  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/106,182  
; FILING DATE: Herewith  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/051,053  
; FILING DATE: 30-JUN-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brookes, A. Anders  
; REGISTRATION NUMBER: 36,373  
; REFERENCE/DOCKET NUMBER: PF385  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 301-309-8504  
; TELEFAX: 301-309-8439  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 203 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-106-182-3

Query Match 9.7%; Score 118.5; DB 3; Length 203;

Best Local Similarity 27.5%; Pred. No. 9.4e-05;  
Matches 49; Conservative 26; Mismatches 84; Indels 19; Gaps 6;

QY 40 IQKTYDLTRYLHQLSLAGTLYLNYLGPPNPBPDPFPPRLGAGTLPRAVTNLEVMRSLNDRLLTONYEAASHLCTYLRGL 120  
DB 27 IROTINILARLLTKYADQDLLEBYVOOGEPFGLPGFSPRLPLAGISGPAHAGIPV--- 83

QY 97 LNDRLRNLQVNEAASHLCTYLRGLNRQA-----TAELRSLAHFCTSLQGLGSIAGW 151  
DB 84 -SERLR--QDAALASALPALIDAVRRQAEINPRAVRLRLSLLEDAARQVRLGAAGVETVL 140

QY 152 ATLAGY---PLQPLPGTEPMAAPGPAHSDFLQKMDFWLKEIQTLWLRSAKDFNRL 205  
DB 141 AALGAAGPVPPEPV-ATSALFTSNAAGVSAKVLGLHVGGLGGEWVSRTREGDLGQL 197

## RESULT 9

US-08-233-609-3  
; Sequence 3, Application US/08233609

MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/792,019B  
FILING DATE: 03-FEB-1997  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: COOK, ROBERT R.  
REGISTRATION NUMBER: 31,602  
REFERENCE/DOCKET NUMBER: A-442  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 225 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-792-019B-2

Query Match  
Best Local Similarity 97.5%; Score 1193; DB 1; Length 225;  
Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDLRADSWGMGLACTCTVLMHLPVAVPALNRTGDPGPGPSIQKTYDLTRYLEHQLRSIAGT 60  
DB 1 MDLRADSWGMGLACTCTVLMHLPVAVPALNRTGDPGPGPSIQKTYDLTRYLEHQLRSIAGT 60  
QY 61 YNYLGGPPNEPDFFNPRLGAEITLPRATVNLVWMSLNDRLRLTONYEAVSHLLCYLRGL 120  
DB 61 YNYLGGPPNEPDFFNPRLGAEITLPRATVNLVWMSLNDRLRLTONYEAVSHLLCYLRGL 120  
QY 121 NQAAATAEIRSLAHFCTSLQGLISIGVMAALGYPLPQPLPGTEPTWTPGPAHSDFIQ 180  
DB 121 NQAAATAEIRSLAHFCTSLQGLISIGVMAALGYPLPQPLPGTEPTWTPGPAHSDFIQ 180  
QY 181 KMDDFWLKELQTLWMSAKDFNRLKKKQPPAAVTLHLGAHGF 225  
DB 181 KMDDFWLKELQTLWMSAKDFNRLKKKQPPAAVTLHLGAHGF 225

RESULT 5  
US-09-106-182-2  
Sequence 2, Application US/09106182  
Patent No. 6046035  
GENERAL INFORMATION:  
APPLICANT: Shi, Yangu  
APPLICANT: Ruben, Steve  
TITLE OF INVENTION: Cardiotrophin-Like Cytokine  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Human Genome Sciences, Inc  
STREET: 9410 Key West Ave  
CITY: Rockville  
STATE: MD  
COUNTRY: US  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/106,182  
FILING DATE: Herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/051,053  
FILING DATE: 30-JUN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Brookes, A. Anders  
REGISTRATION NUMBER: 36,173  
REFERENCE/DOCKET NUMBER: PF385

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-309-8504  
TELEFAX: 301-309-8439  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 225 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-106-182-2

Query Match  
Best Local Similarity 97.5%; Score 1193; DB 3; Length 225;  
Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDLRADSWGMGLACTCTVLMHLPVAVPALNRTGDPGPGPSIQKTYDLTRYLEHQLRSIAGT 60  
DB 1 MDLRADSWGMGLACTCTVLMHLPVAVPALNRTGDPGPGPSIQKTYDLTRYLEHQLRSIAGT 60  
QY 61 YNYLGGPPNEPDFFNPRLGAEITLPRATVNLVWMSLNDRLRLTONYEAVSHLLCYLRGL 120  
DB 61 YNYLGGPPNEPDFFNPRLGAEITLPRATVNLVWMSLNDRLRLTONYEAVSHLLCYLRGL 120  
QY 121 NQAAATAEIRSLAHFCTSLQGLISIGVMAALGYPLPQPLPGTEPTWTPGPAHSDFIQ 180  
DB 121 NQAAATAEIRSLAHFCTSLQGLISIGVMAALGYPLPQPLPGTEPTWTPGPAHSDFIQ 180  
QY 181 KMDDFWLKELQTLWMSAKDFNRLKKKQPPAAVTLHLGAHGF 225  
DB 181 KMDDFWLKELQTLWMSAKDFNRLKKKQPPAAVTLHLGAHGF 225

RESULT 6  
US-08-988-819-2  
Sequence 2, Application US/08988819  
Patent No. 6054294  
GENERAL INFORMATION:  
APPLICANT: CHANG, MING-SHI  
TITLE OF INVENTION: NEUROTROPHIC FACTOR NNT-1  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSER: AMGEN INC.  
STREET: ONE AMGEN CENTER DRIVE  
CITY: THOUSAND OAKS  
STATE: CA  
COUNTRY: USA  
ZIP: 91320  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/988,819  
FILING DATE: 12-DEC-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/792,019  
FILING DATE: 03-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: COOK, ROBERT R.  
REGISTRATION NUMBER: 31,602  
REFERENCE/DOCKET NUMBER: A-442A  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 225 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-988-819-2

Query Match  
Best Local Similarity 97.5%; Score 1193; DB 3; Length 225;  
Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Db 121 NROAATAEIRSLAHFCTSLQGLSIGVWATLGYPLPQPLGTEPAMAPGPAHSDFLQ 180  
Qy 161 KMDDFWLKELQTLWLRSAKDFNRLKKKQPPAASVTLLHLEAHGF 225  
Db 161 KMDDFWLKELQTLWLRSAKDFNRLKKKQPPAASVTLLHLEAHGF 225

## RESULT 2

US-08-988-819-5  
Sequence 5, Application US/08988819  
Patent No. 6054294

GENERAL INFORMATION:  
APPLICANT: CHANG, MING-SHI  
TITLE OF INVENTION: NEUROTROPHIC FACTOR NNT-1  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: AMGEN INC.  
STREET: ONE AMGEN CENTER DRIVE  
CITY: THOUSAND OAKS  
STATE: CA  
COUNTRY: USA  
ZIP: 91320  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/988,819  
FILING DATE: 12-DEC-1997  
CLASSIFICATION: 536  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/792,019  
FILING DATE: 03-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: COOK, ROBERT R.  
REGISTRATION NUMBER: 31,602  
REFERENCE/DOCKET NUMBER: A-442A  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 225 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-988-819-5

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Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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## RESULT 3

US-09-016-534-5  
Sequence 5, Application US/09016534  
Patent No. 6143874  
GENERAL INFORMATION:  
APPLICANT: CHANG, MING-SHI

APPLICANT: ELLIOTT, GARY S.  
APPLICANT: SARMIENTO, ULLA  
APPLICANT: SENALDI, GIORGIO  
TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: AMGEN INC.  
STREET: ONE AMGEN CENTER  
CITY: THOUSAND OAKS  
STATE: CA  
COUNTRY: USA  
ZIP: 91320  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/016,534  
FILING DATE:  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/792,019  
FILING DATE: 03-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: COOK, ROBERT R.  
REGISTRATION NUMBER: 31,602  
REFERENCE/DOCKET NUMBER: A-442B  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 225 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-016-534-5

Query Match 100.0%; Score 1224; DB 3; Length 225;  
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Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDLRAGDSWGMILACICTYLMHLPAVPALNRTGDPGPGPSIQTYDLTRYLEHQRLSLAGT 60  
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## RESULT 4

US-08-792-019B-2  
Sequence 2, Application US/08792019B  
Patent No. 5741772  
GENERAL INFORMATION:  
APPLICANT: CHANG, MING-SHI  
TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: AMGEN INC.  
STREET: 1840 DEHAVILLAND DRIVE  
CITY: THOUSAND OAKS  
STATE: CA  
COUNTRY: USA  
ZIP: 91320  
COMPUTER READABLE FORM:

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

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Run on: February 9, 2004, 06:15:41 ; Search time 15 Seconds  
(without alignments)  
634.663 Million cell updates/sec

Title: US-09-931-704-5

Perfect score: 1224  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
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Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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11	110.5	9.0	203	1	US-08-286-304-3
12	110.5	9.0	203	1	US-08-442-745-3
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#### ALIGNMENTS

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; Sequence 5, Application US/08792019B
; Patent No. 5741772
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; GENERAL INFORMATION:
; APPLICANT: CHANG, MING-SHI
; TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC.
; STREET: 1840 DEHAVILLAND DRIVE
; CITY: THOUSAND OAKS
; STATE: CA
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/792,019B
; FILING DATE: 03-FEB-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: COOK, ROBERT R.
; REGISTRATION NUMBER: 31,602
; REFERENCE/DOCKET NUMBER: A-442
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 225 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
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; Query Match
; Best local Similarity 100.0%; Score 1224; DB 1; Length 225;
; Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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AUTHORS	1 Senaldi, G.		
TITLE	Methods and compositions for treating ige-related disease using m		
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 Senaldi, G., Varnum, B.C., Sarmiento, U., Lile, J.,  
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 Freeman, D., Mann, F., Simonet, W.S., Boone, T., and Chang, M.S.  
 Novel neurotrophin-1/B cell-stimulating factor-3: a cytokine of the  
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 Proc. Natl. Acad. Sci. U.S.A. 96 (20), 11458-11463 (1999)  
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 MEDLINE 99432254  
 PUBMED 10500198  
 REFERENCE 2 (bases 1 to 797)

AUTHORS Senaldi, G., Varnum, B., Sarmiento, U., Lile, J., Starnes, C.,  
 Scully, S., Guo, J., Elliott, G., McNinch, J., Freeman, D., Shaltee, C.,  
 Mann, F., Simonet, W.S., Boone, T., and Chang, M.S.  
 TITLE Direct Submission  
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 Matches 717; Conservative 0; Mismatches 61; Indels 1; Gaps 1;  
 Qy 5 ATTTAAAGCTTGGCCGAGGCGGGGCTGGCCCTCCCACTCCGCGAGCTTCGGAGAGAG 64  
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Db	120 CAGGATGCTGTGGCAGCTCCCTGCGAGGCGAGCTTAAATGCGACAGGAGATCCAGGCC 179		
Qy	202 TGGCGCCCTCCATCCAGAAAACCTATGACTCAACCCGCTACCTGAGAGCATCACTCCAG 261		
Db	180 TGGCGCCCTCCATCCAGAAAACCTATGACTCAACCCGCTACCTGAGAGCATCACTCCAG 239		
Qy	262 CTTAGCTGGGACCTACTGTAATCTACTGGGGCCCCCTTTCAACGAGCTGATCTTCAATCC 321		
Db	240 CTTAGCTGGGACCTACTGTAATCTACTGGGGCCCCCTTTCAACGAGCTGATCTTCAATCC 299		
Qy	322 TCCCTCGACTGGGGGCGAGAACTCTGCCACAGGGCCACGGCTCAACTTGGAACTGGGCGAAG 381		
Db	300 TCCCGCGCTGGGGGCGAGAACTCTGCCACAGGGCCACCTTGTACTTGGAGGTGGCGAAG 359		
Qy	382 CCTCAATGACAGGCTGGCGCTGACCCAGAACTATAGAGGCTTACAGTCACTCTGTTGTTA 441		
Db	360 CTTCAATGACAACTGGGGCTGACCCAGAACTATAGAGGCTTACAGTCACTCTGTTGTTA 419		
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Qy	562 CCCACTGCCCCAGCCTCTGCGACAGGAGCTGAGCCAGCTGGAGCCCTGGCCGCCACAG 621		
Db	540 CCCACTGCCCCAGCCTGCTGGAGACTGAACCACTTGGACTCTGGCCCTGCCCCACAG 599		
Qy	622 TGACTTCTTCACAGAAATGAGTGACTTTGCTGCTGAAGAGAGCTGCGACTGATG 681		
Db	600 TGACTTCTTCACAGAAATGAGTGACTTTGCTGCTGAAGAGAGCTGCGACTGATG 659		
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Db	660 GCGTTCGCGCCAGAGACTTCAACCGGCTTAAAGAGAGATGCAAGCTTCAGACGTTCACT 719		
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DEFINITION Homo sapiens cardiotrophin-like cytokine CLC mRNA, complete cds.			
ACCESSION AF172854			
VERSION AF172854.1 GI:5852980			
KEYWORDS			
SOURCE Homo sapiens (human)			
ORGANISM Homo sapiens			
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
1 (bases 1 to 1689)			
Shi,Y., Wang,W., Yourey,P.A., Gohari,S., Zukauskas,D., Zhang,J.,			
Ruben,S. and Alderson,R.F.			
Computational EST database analysis identifies a novel member of			
the neurotrophic cytokine family			
Biochem. Biophys. Res. Commun. 262 (1), 132-138 (1999)			
JOURNAL			

[illegible]

Db	600	CTGGCTGCTGTAAGAGAGCTGCAGACCTTGGCTGTGGCGCTCGGACCAAGGACTTTCAACGGGCT	655
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Db	720	CTGACTTCTGACCTT 734	
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DEFINITION	Cardiotropin-like cytokine.		
ACCESSION	BD132824		
VERSION	BD132824.1 GI:23227769		
KEYWORDS	JP 2002507125-A/1.		
SOURCE	unidentified		
ORGANISM	unidentified		
REFERENCE	1 (bases 1 to 1710)		
AUTHORS	Shi, Y. and Ruben, S.M.		
TITLE	Cardiotropin-like cytokine		
JOURNAL	Patent: JP 2002507125-A 1 05-MAR-2002;		
COMMENT	HUMAN GENOME SCIENCES INC		
	PN JP 2002507125-A/1		
	PD 05-MAR-2002		
	PF 29-JUN-1998 JP 199505681		
	PI 30-JUN-1997 US 60/051311		
	PI YANGU SHI STEVEN M RUBEN		
	PC C07K14/435,C07K14/52,C07K16/24,C12N1/21,C12N15/19,C12N15/64 CC		
	Strandness: Single;		
FEATURES	CC Topology: Linear;		
source	PH Key	Location/Qualifiers	
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	FT sig peptide	46..126	
	FT mat peptide	127..720.	
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Best Local Similarity	91.7%; Pred. No. 2,5e-134;		
Matches 674; Conservative	0; Mismatches 60; Indels 1; Gaps 1;		
Qy	49	GCCCTTGGAGAGAGAGCCGCGCCCGGCGCCGCGCCCGGCGCCAGCCGATGAGACCTCGAGC	108
Db	1	GCTCCGGAGAGAGAGCCGCGCCCGGCGCCGCGCGG-CGCCAGCCATGAGACCTCGAGC	59
Qy	109	AGGGAGACTCGTGGGGAGATTACTTGGCTAATGACAGGTGCTGTGGCACTTCCCTGACT	168
Db	60	AGGGAGACTCGTGGGGAGATTACTTGGCTGATGACAGGTGCTGTGGCACTTCCCTGAGT	119
Qy	169	GCCAGCTCTAATTCGACAGAGATCCAGGACCTGGGCGCCCTCATCCAGAAAACCTATGA	228
Db	120	GCCAGCTCTAATTCGACAGAGAGCCAGGACCTGGGCGCCCTCATCCAGAAAACCTATGA	179
Qy	229	CTCACCCTCTAATTCGAGAGCATCACTCGACCTTACTGGAGCTACTCTGAATCACT	288
Db	180	CTCACCCTCTAATTCGAGAGCACTCGACCTTGGCTGGAGCTTCTGAATCACT	239
Qy	289	GGGGCCCCCTTTCAAGAGCTTCAATCTCTCTCGACTGGGGGAGAAAACCTGGCC	348
Db	240	GGGGCCCCCTTTCAAGAGCTTCAATCTCTCTCGAGCTGGGGGAGAAAACCTGGCC	299
Qy	349	CAGGGCCACGCTCACTTGAATGATGTGGGAACCTCAATGACAGGCTGGCTGACCA	408
Db	300	CAGGGCCACGCTTGAATGATGTGGGAACCTCAATGACAGGCTGGCTGACCA	359

OY	GAACATATAGAGCGTACAGTCACTCTCTGTGTTACTTGGGTGGCCCAACCGTACGGCTGC	409
Db	GAATCTAGAGGCTCTACACCACTTCTGTGTACTTGGTGGCTCAACCGTACGGCTGC	360
OY	CACAGCTGAATCTCCGACGTAGCTGTGGCCCACTTCTGTATCAAGCTCCAGGGCTGTCTGG	469
Db	CACGTCTAGCTGTGGCCGACGCTGTGGCCCACTTCTGTACACAGCTCCAGGGCTGTCTGG	420
OY	CAGCATTTGCAGGTGTCTATGGCGACGCTTGGCTAACCACTGCCCCAGCTCTTGGCAGGGAC	539
Db	CAGCATTTGCGGGCGTCAATGAGAGCTCTGGGGTCAACCACTGGCCCGCTGCTGGGAC	480
OY	TGAGCAGACCTGGGGCCCTGGGCGCTGGCCACAGTGACTTCTCCAGAAAGATGATGACTT	589
Db	TGAACCCACTTGAATCTCTGGGCGCTGGCCACAGTACTTCTCCAGAAAGATGACGACTT	540
OY	CTGGCTGTGAAGAGAGTGCAGACCTGTGCTATGTGGCTTCAACCAAGAGACTTCAACCGGCT	649
Db	CTGGCTGTGAAGAGAGTGCAGACCTGTGCTGTGGGGCTGTGGCCAAAGAGACTTCAACCGGCT	600
OY	TAAAGAGAAGATGCAGCTCTCAGCAGCTTCACTCAACCTTGACCTTGAAGGACATGTGTTT	709
Db	CAAGAGAAGATGCAGCTCTCAGCAGCTGACGTCACTCTGACACTGGGGGCTCATGTGCTT	660
OY	CTGACCTTGAACCTT 783	769
Db	CTGACTTCTGACCTT 734	720

RESULT 12  
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 DEFINITION Homo sapiens cardiotrophin-like cytokine (CLC) mRNA, complete cds.  
 ACCESSION AY049779  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 680)  
 Hu.X., Xu.Y., Zhang, B., Peng, X., Yuan, J. and Qiang, B.  
 Direct Submision  
 Submitted (30-JUN-2001) Department of Biochemistry, Institute of  
 Basic Medical Science, Chinese Academy of Medical Sciences, 5 Dong  
 Dan San Tiao, Beijing 100005, P.R. China  
 Location/Qualifiers  
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CDS	125 a	239 c	191 g	125 t
BASE COUNT				
ORIGIN				
Query Match	72.1%	Score 590.4	DB 9	Length 680
Best Local Similarity	91.8%	Fred. No. 7.9e-126		
Matches 624	Conservative	0	Mismatches 56	Indels 0
			Gaps	0

OY	93	CCATGGAACCTCCGAGACAGAGGGAACTCGTGGGGGATATTGAGCTTGGCTCATGACAGGGTCT	152
Db	1	CCATGGAACCTCCGAGACAGAGGGAACTCGTGGGGGATATTGAGCTTGGCTCATGACAGGGTCT	60
OY	153	GGCAACCTCCCTGCAAGTGGCAAGCTCTTAAATGCGACAGAGATTCAGAGCCCTGGCCCTCCA	212
Db	61	GGCAACCTCCCTGCAAGTGGCAAGCTCTTAAATGCGACAGAGATTCAGAGCCCTGGCCCTCCA	120
OY	213	TCGAGAAAACCTATGACTCTCAACCGGCTAAGCTGGAGCATCAACTCCGACAGCTTAAAGTGGGA	272
Db	121	TCGAGAAAACCTATGACTCTCAACCGGCTAAGCTGGAGCAACCACTCCGACAGCTTAAAGTGGGA	180
OY	273	CCTACCTGAACTACCTGGGGGCCCCCTTTCAGACGAGCTGACCTTCAATCTCTCGACATGG	332
Db	181	CCTACCTGAACTACCTGGGGGCCCCCTTTCAGACGAGCTGACCTTCAATCTCTCGACATGG	240
OY	333	GGGCGAAGAACTCTGACCCGAGGCGCAACGCTCACTTGGAAAGTGGCGAAGGCTCAATATGACA	392
Db	241	GGGCGAAGAACTCTGACCCGAGGCGCAACGCTCACTTGGAAAGTGGCGAAGGCTCAATATGACA	300
OY	393	GACTGCGGCTGACCCGAGAACTATGAGGCGTACAGTCACTCTCTGTATTACTTGCATGGCC	452
Db	301	AACTGCGGCTGACCCGAGAACTATGAGGCGCTACAGGCACTTCTGTATTACTTGCATGGCC	360
OY	453	TCAACCGTCAAGGCTGCGCACAGCTGAACTCCGACGTAAGCTTGGGCCCACTTCTGTACAGCC	512
Db	361	TCAACCGTCAAGGCTGCGCACAGCTGAACTCCGACGTAAGCTTGGGCCCACTTCTGTACAGCC	420
OY	513	TCCAGGGGCTGCTGGGCGACATTCGACAGGTGTCAATGGCCGACCGTTGGCTTAAACCACTGGCCCC	572
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OY	573	AGCCTTGGCCAGGAGACTGAGCGCAGACGCTGGGCCCCCTGGGCCCTGGCCACAGTGACTTCTGCC	632
Db	481	AGCCTTGGCCAGGAGACTGAGCGCAGACGCTGGGCCCCCTGGGCCCTGGCCACAGTGACTTCTGCC	540
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Db	541	AGAGATGATGATGACTTCTGCTGTGTGTGAAGAGCTGACAGACTCTGCTATGCGGCTTACAGCCA	600
OY	693	AGGACTTCAACCGGCTTAAAGAAAGATGCAAGCTTCCAGCAGCTTCAAGTCAACCTTGCACCT	752
Db	601	AGGACTTCAACCGGCTTAAAGAAAGATGCAAGCTTCCAGCAGCTTCAAGTCAACCTTGCACCC	660
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LOCUS	ACI09138	269155 bp	DNA	linear	ROD 20-MAY-2007
DEFINITION	Mus musculus, clone RP23-41B4, complete sequence.				
ACCESSION	ACI09138				
VERSION	ACI09138.10	GI:30911144			
KEYWORDS	HTG.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	1 (bases 1 to 269155)				
TITLE	Birren, B., Nusbaum, C. and Lander, E.				
JOURNAL	Mus. musculus, clone RP23-41B4				
REFERENCE	Unpublished				
AUTHORS	2 (bases 1 to 269155)				
	Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavsky, L., Bouckgalter, B., Brown, A., Camarata, J., Campolongo, A., Chang, J., Chazaro, B., Choquel, Y., Colangelo, M., Collins, S., Collimore, A., Cook, A., Cooke, P., DeRellano, K., Dewar, K., Diaz, J. S., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,				

**TITLE**  
**JOURNAL**  
**REFERENCE**  
**AUTHORS**

Kamauf, A., Karatas, A., Kells, C., Larocque, K., Macleazres, R.,  
 Landers, T., Lehoczy, J., Levine, R., Liu, G., Maclean, C.,  
 Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M.,  
 McEwan, P., McKernan, K., Meldrum, J., Meneus, L., Mihova, T.,  
 Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C.,  
 Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J.,  
 Peterson, K., Phunhthang, P., Pierre, N., Pollara, V., Raymond, C.,  
 Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J.,  
 Seery, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,  
 Strauss, N., Sudbramanian, A., Talamas, J., Testaye, S., Theodore, J.,  
 Topham, K., Travers, M., Travis, N., Triggillo, J., Vassiliev, H.,  
 Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.-J., Young, G.,  
 Zainoun, J., Zemlek, L., Zimmer, A. and Zody, M.  
 Direct Submission  
 Submitted (03-FEB-2002) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 3 (bases 1 to 269155)

**TITLE**  
**JOURNAL**  
**REFERENCE**  
**AUTHORS**

Birren, B., Nussbaum, C., Lander, E., Abouelleil, A., Allen, N.,  
 Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T.,  
 Boguslavsky, L., Boukhalter, B., Camarata, J., Chang, J., Choepel, Y.,  
 Collumore, A., Cook, A., Cooke, P., Corum, B., DeCellano, K.,  
 Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S.,  
 Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S.,  
 Graham, L., Grand-Pierre, N., Haez, N., Hagopian, D., Haos, B.,  
 Hall, J., Horton, L., Hulme, N., Iliev, I., Johnson, R., Jones, C.,  
 Kamauf, A., Karatas, A., Kells, C., Landers, T., Levine, R.,  
 Lindblad-Toh, K., Liu, G., Liu, A., Madditt, R., Mayne, R.,  
 Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M.,  
 Meldrum, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J.,  
 Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P.,  
 O'Neill, D., Oliver, J., Peterson, K., Phunhthang, P., Pierre, N.,  
 Rachupata, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P.,  
 Roman, J., Schauer, S., Schupbach, R., Seaman, S., Seery, P., Smith, C.,  
 Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M.,  
 Talamas, J., Testaye, S., Theodore, J., Topham, K., Travers, M.,  
 Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X.,  
 Wyman, D., Young, G., Zainoun, J., Zemlek, L., Zimmer, A. and Zody, M.  
 Direct Submission  
 Submitted (26-APR-2003) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 4 (bases 1 to 269155)

**TITLE**  
**JOURNAL**  
**REFERENCE**  
**AUTHORS**

Birren, B., Nussbaum, C., Lander, E., Abouelleil, A., Allen, N.,  
 Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T.,  
 Boguslavsky, L., Boukhalter, B., Camarata, J., Chang, J., Choepel, Y.,  
 Collumore, A., Cook, A., Cooke, P., Corum, B., DeCellano, K.,  
 Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S.,  
 Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S.,  
 Graham, L., Grand-Pierre, N., Haez, N., Hagopian, D., Haos, B.,  
 Hall, J., Horton, L., Hulme, N., Iliev, I., Johnson, R., Jones, C.,  
 Kamauf, A., Karatas, A., Kells, C., Landers, T., Levine, R.,  
 Lindblad-Toh, K., Liu, G., Liu, A., Madditt, R., Mayne, R.,  
 Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M.,  
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 Rachupata, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P.,  
 Roman, J., Schauer, S., Schupbach, R., Seaman, S., Seery, P., Smith, C.,  
 Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M.,  
 Talamas, J., Testaye, S., Theodore, J., Topham, K., Travers, M.,  
 Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X.,  
 Wyman, D., Young, G., Zainoun, J., Zemlek, L., Zimmer, A. and Zody, M.  
 Direct Submission  
 Submitted (20-MAY-2003) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 On May 20, 2003 this sequence version replaced gi:30141982.  
 All repeats were identified using RepeatMasker:  
 Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

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Contact: sequence submissions@genome.wi.mit.edu
----- Project Information
Center project name: L14003
Center clone name: 41_B_18
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repeat_region   /rpt_family="MT2B"
                 18770..18904

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OY	816	GCTT	819
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DEFINITION	AC140073	302961 bp	DNA linear HTG 23-FEB-2003
ACCESSION	AC140073		
VERSION	AC140073.2	GI:28475471	
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULUTOP.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	1 (bases 1 to 302961)		
TITLE	McPherson, J.D. and Waterston, R.H.		
JOURNAL	The sequence of Mus musculus clone		
REFERENCE	Unpublished		
AUTHORS	2 (bases 1 to 302961)		
TITLE	McPherson, J.D. and Waterston, R.H.		
JOURNAL	Direct Submission		
REFERENCE	Submitted (20-FEB-2003) Genome Sequencing Center, 4444 Forest Park		
AUTHORS	Parkway, St. Louis, MO 63108, USA		
TITLE	3 (bases 1 to 302961)		
JOURNAL	McPherson, J.D. and Waterston, R.H.		
REFERENCE	Direct Submission		
AUTHORS	Submitted (23-FEB-2003) Genome Sequencing Center, 4444 Forest Park		
TITLE	Parkway, St. Louis, MO 63108, USA		
JOURNAL	On Feb 23, 2003 this sequence version replaced gi:28436314.		
COMMENT			

Query Match	Similarity	66.0%	Score 540.8	DB 10	Length 269155
Best Local	Similarity	99.6%	Pred. No. 1,1e-114		
Matches	542	Conservative	0	Mismatches	2
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----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: M05SC
Web site: http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@wustl.wustl.edu
Project information
Center project name: M_BA0282N20
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----- Summary Statistics -----
Sequencing vector: M13, %
Sequencing vector: plasmid, %
Chemistry: Dye-Primer ET; % of reads
Chemistry: Dye-terminator Big Dye; % of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 291448 bases at least Q40
Consensus quality: 292863 bases at least Q30
Consensus quality: 294071 bases at least Q20
Insert size: 182000; agarose-fp
Insert size: 303053; sum-of-contigs
Quality coverage: 11.12 in Q20 bases; agarose-fp
Quality coverage: 8.09 in Q20 bases; sum-of-contigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 16 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
1 1459: contig of 1459 bp in length
1460 1559: gap of unknown length
1560 5475: contig of 3916 bp in length
5476 5575: gap of unknown length
5576 10311: contig of 4736 bp in length
10312 14114: gap of unknown length
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* 17750 24465: contig of 6716 bp in length
* 24466 24565: gap of unknown length
* 33177: contig of 8612 bp in length
* 33277: gap of unknown length
* 33278 40901: contig of 7624 bp in length
* 40902 41001: gap of unknown length
* 41002 48966: contig of 7965 bp in length
* 48967 62429: gap of unknown length
* 49067 62429: contig of 13363 bp in length
* 62430 62530: gap of unknown length
* 62530 77998: contig of 15469 bp in length
* 77999 78098: gap of unknown length
* 78099 103060: contig of 24962 bp in length
* 103061 127124: contig of 23964 bp in length
* 127125 127224: gap of unknown length
* 127225 185465: gap of unknown length
* 185465 185564: gap of unknown length
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* 231093 302961: contig of 71869 bp in length.
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Best Local Similarity 99.6%; Pred. No. 1.1e-114;
Matches 542; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 336 CAGAACTCTGCCAGGGGCCGCTCAACTTGAAGTGTGGCGAAGCCTCAATGACAGGC 395
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## RESULT 15

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LOCUS Sequence 19 from Patent WO0155219.
DEFINITION AX205060
ACCESSION AX205060
VERSION AX205060.1 GI:15394299
KEYWORDS
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SOURCE  
ORGANISM  
synthetic construct  
synthetic construct  
artificial sequences.

REFERENCE  
1 Elson, G. and Gauchat, J. F.  
Scentfr/nnt-1 fusion protein  
Patent: WO 0155219-A 19 02-AUG-2001;  
JOURNAL  
PIERRE FABRE MEDICAMENT (FR)

## FEATURES

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## BASE COUNT

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Query Match 62.2%; Score 509.2; DB 6; Length 1692;  
Best Local Similarity 91.1%; Pred. No. 4e-107;  
Matches 541; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

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Qy	236	CGCTACTGAGAGATCACTCCGACAGTGAAGTGGAGACTTGAACCTAAGTGGGCC	295
Db	1126	CGCTACTGAGAGATCACTCCGACAGTGAAGTGGAGACTTGAACCTAAGTGGGCC	1185
Qy	296	CGTTCAAGAGGCTGACTTCAATCTCCGACCTGGGGGCAAGAACTCGCCAGGGCC	355
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Qy	416	GAGGCTTACATGATCACTCTGTGTACTTGGCGTGCCTCAACGCTACGGCTGCACAGCT	475
Db	1306	GAGGCTTACATGATCACTCTGTGTACTTGGCGTGCCTCAACGCTACGGCTGCACAGCT	1365
Qy	476	GAATCGGAGCTAGCTGGGCCACTTCTGTACAGGCTCCAGGGGCTGGTGGGAGCATTT	535
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Qy	536	GCAGTGTATGCGGAGAGCTTGCTACCACTGCCCCAGGCTTGCACAGGAGCTGAGCCA	595
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Job time : 3292.64 secs

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GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: February 9, 2004, 06:14:57 ; Search time 35.5 Seconds  
(without alignments)  
1006.013 Million cell updates/sec

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Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

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Minimum DB seq length: 0
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## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1226	100.0	225	19	AAW29715	Human neurotrophilin-1
2	1226	100.0	225	19	AAW56141	Human neurotrophilin-1
3	1226	100.0	225	20	AAW94466	Human neurotrophilin-1
4	1226	100.0	225	21	AAW97813	Human NTR-1 protein
5	1226	100.0	225	22	AAW63543	Human neurotrophilin-1
6	1226	100.0	225	23	AAW78176	Human neurotrophilin-1
7	1226	100.0	225	22	AAW25831	Human neurotrophilin-1
8	1214	99.0	223	22	AAW0828	Human neurotrophilin-1
9	1204	98.2	321	22	ABW11696	Human neurotrophilin-1

[illegible]

## ALIGNMENTS

	RESULT	1
ID	AAM29715	
XX	AAM29715 standard; Protein; 225 AA.	
AC	AAM29715;	
XX	09-NOV-1998 (first entry)	
DJ		
DE	Human neurotrophic factor NNT-1.	
XX	NNT-1; neurotrophic factor; human;	
KW	Alzheimer's disease; Parkinson s dis	
KW	peripheral neuropathy; dys trophy; C	
KW	common variable immunodeficiency; G	
KM	hypogammaglobulinaemia; X-linked ag	
KX	therapy.	
OS	Homo sapiens.	
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FT	Protein	28..225
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PN	M09833922-A1.	
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PD	06-AUG-1998.	
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FF	02-FEB-1998; 98WO-US02363.	

PR 30-JAN-1998; 98US-0016534.  
PR 03-FEB-1997; 97US-0792019.  
XX  
XX (AMGE-) AMGEN INC.  
PA  
XX Chang M, Elliot GS, Sarmiento U, Senaldi G;  
PI WPI; 1998-437475/37.  
DR N-PSDB; AAV47510, AAV47511.  
XX

PT Newly isolated nucleic acid encoding human or murine neurotrophic  
factor NNT-1 - useful for treatment of neurological and  
immunological diseases or inflammation, also as vaccine adjuvant  
XX  
XX Claim 12; Fig 3; 120pp; English.

CC This is the amino acid sequence of a novel neurotrophic factor,  
CC designated NNT-1, that is a growth factor for neurons and for B or  
CC T cells. It was deduced from isolated cDNA (see AAV47510) and  
CC genomic DNA (see AAV47511) clones. Vectors containing the cDNA or  
CC genomic DNA and host cells are provided for use in the production  
CC of NNT-1 polypeptides. These are used to treat: (i) neurological  
CC or immunological diseases, specifically Alzheimer's, Parkinson's  
CC or Huntington's diseases, amyotrophic lateral sclerosis,  
CC Charcot-Marie-Tooth syndrome, peripheral neuropathy, dystrophy and  
CC degeneration of the neural retina, or conditions characterised by T  
CC or B cell defects, e.g. common variable immunodeficiency (CVID),  
CC selective IGA deficiency, hypogammaglobulinaemia and X-linked  
CC agammaglobulinaemia (claimed), but many others disclosed; and (ii)  
CC inflammation. NNT-1 is also able to boost immunoreactivity and  
CC antibody production following vaccination, and, since it inhibits  
CC tumour necrosis factor production, it may also be useful for  
CC treating sepsis. In addition, cells that have been engineered to  
CC express NNT-1 can be implanted, or nucleic acids are delivered in  
CC gene therapy vectors.

SQ Sequence 225 AA;

Query Match 100.0%; Score 1226; DB 19; Length 225;  
Best Local Similarity 100.0%; Pred. No. 1.6e-118;  
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 YLNTYIGPPNPEDFNPRLGAETLPRAIVDLEWRSINDKRLTQNYEAYSHLCTYRGL 120  
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DB 121 NRQATTAELRSLAHFCTSLQGLGSIAGVMAALGYPLPGTEPTWTPGPAHSDFLQ 180  
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DB 181 KMDDFWLKELQTMWLRSAKDFNRLKKMQPPAAVTLHLGAHGF 225

RESULT 2  
AAW56141  
ID AAW56141 standard; Protein; 225 AA.  
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XX AAW56141;

DT 13-JUL-1998 (first entry)

XX Amino acid sequence of human neurotrophic factor NNT-1.

DE Human; neurotrophic factor; NNT-1; growth; motor; sympathetic; neuron;  
XX treatment; neurological disease; degeneration; Parkinson's disease;  
KW amyotrophic lateral sclerosis; ALS; Alzheimer's disease; stroke.  
XX

OS Homo sapiens.  
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XX Key Location/Qualifiers  
FH Peptide 1..27  
FT Peptide /note= "signal peptide"  
FT Protein 28..225  
FT Protein /note= "mature protein"

PN US5741772-A.  
XX  
XX 21-APR-1998.

PF 03-FEB-1997; 97US-0792019.

PR 03-FEB-1997; 97US-0792019.

PA (AMGE-) AMGEN INC.

PI Chang M;

DR WPI; 1998-260526/23.

DR N-PSDB; AAV22652.

PT Neurotrophic factor NNT-1 polypeptide and related nucleic acids -  
PT useful for stimulating growth of motor and sympathetic neurons  
XX  
XX Claim 1; Fig 3; 41pp; English.

CC The present sequence represents a human neurotrophic factor, designated  
CC NNT-1, which is capable of stimulating growth of motor or sympathetic  
CC neurons. The NNT-1 protein is useful in the treatment of neurological  
CC diseases characterised by the degeneration and death of particular  
CC classes of neurons. These diseases specifically include Parkinson's  
CC disease, amyotrophic lateral sclerosis (ALS), Alzheimer's disease,  
CC stroke and various degenerative disorders affecting vision.

SQ Sequence 225 AA;

Query Match 100.0%; Score 1226; DB 19; Length 225;  
Best Local Similarity 100.0%; Pred. No. 1.6e-118;  
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DB 61 YLNTYIGPPNPEDFNPRLGAETLPRAIVDLEWRSINDKRLTQNYEAYSHLCTYRGL 120  
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DB 121 NRQATTAELRSLAHFCTSLQGLGSIAGVMAALGYPLPGTEPTWTPGPAHSDFLQ 180  
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RESULT 3  
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ID AAW94466 standard; Protein; 225 AA.  
XX  
XX AAW94466;

DT 22-APR-1999 (first entry)

XX Human cardiostrophin-like cytokine protein.

DE Human; cardiostrophin-like cytokine; interleukin 6 cytokine family;  
XX CLC; IL-6; diagnosis; detection; immune system-related disorder;  
KW cancer; cardiac disorder; heart failure; hypertension; cancer;  
KW autoimmune disorder; infection.  
XX

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XX Homo sapiens.
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XX
XX Key
XX Location/Qualifiers
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XX 28..225
XX /label= Cardiotrophin-like_cytokine
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XX /note= "conserved domain"
XX 150..156
XX /label= CD-11
XX /note= "conserved domain"
XX 194..198
XX /label= CD-111
XX /note= "conserved domain"
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XX 07-JAN-1999.
XX
XX 29-JUN-1998; 98MO-US13129.
XX
XX 30-JUN-1997; 97US-0051311.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM, Shi Y;
XX
XX WPI; 1999-095678/08.
XX
XX N-PSDB; AAX16161.
XX
XX New isolated cardiotrophin-like cytokine nucleic acid - used to
XX develop products for treating cardiac and immune system disorders,
XX e.g. heart failure, hypertension, cancers, autoimmune disorders and
XX infections
XX
XX Claim 1; Fig 1; 103pp; English.
XX
XX The present invention relates to a novel cardiotrophin-like cytokine
XX (CLC) protein which is a member of the interleukin 6 (IL-6) cytokine
XX family. The present sequence represents the human CLC protein. The
XX present invention also describes screening methods for identifying
XX agonists and antagonists of CLC activity, as well as methods for
XX detecting cardiac and immune system-related disorders and
XX therapeutic methods for treating cardiac and immune system-related
XX disorders, e.g. heart failure, hypertension, cancers, autoimmune
XX disorders and infections.
XX
XX Sequence 225 AA:
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XX Query Match 100.0%; Score 1226; DB 20; Length 225;
XX Best Local Similarity 100.0%; Pred. No. 1.6e-118;
XX Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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XX 61 YLNYLGPPFNEDPFPRLGAETLPRAATVDLEWVRSLNDKRLTQNYEAYSHLLCYLRGL 120
XX |
XX 121 NRQAAFAELRRSLAHFCTSLQGLSIAQVMAALGYPLRQPLRGTEPTWTPGPAHSDFLQ 180
XX |
XX 121 NRQAAFAELRRSLAHFCTSLQGLSIAQVMAALGYPLRQPLRGTEPTWTPGPAHSDFLQ 180
XX |
XX 181 KYDDPFLKELQTLWRSAKDFRRLKKKQOPPAATLILGANGF 225
XX |
XX 181 KYDDPFLKELQTLWRSAKDFRRLKKKQOPPAATLILGANGF 225
XX |
XX DB 181 KYDDPFLKELQTLWRSAKDFRRLKKKQOPPAATLILGANGF 225
XX |
```

```
RESULT 4
AA87813
ID AA87813 standard; Protein; 225 AA.
XX
XX AA87813;
XX
XX 24-AUG-2000 (first entry)
XX
XX Human NNT-1 protein.
XX
XX NNT-1; human; neurotrophic factor; neurotrophic; neuroprotective; treatment;
XX anticonvulsant; antiparkinsonian; antidiabetic; ophthalmological;
XX nervous system degeneration; Alzheimer's disease; Parkinson's disease;
XX amyotrophic lateral sclerosis; Charcot-Marie-Tooth syndrome;
XX Huntington's disease; peripheral neuropathy; neural retina degeneration;
XX retinopathy; immune disorder; hematopoietic disorder.
XX
XX Homo sapiens.
XX
XX US6054294-A.
XX
XX 25-APR-2000.
XX
XX 12-DEC-1997; 97US-0988819.
XX
XX 03-FEB-1997; 97US-0792019.
XX
XX (AMGE-) AMGEN INC.
XX
XX Chang M;
XX
XX WPI; 2000-338492/29.
XX
XX N-PSDB; AAA39481.
XX
XX New nucleic acids encoding neurotrophic factors useful for stimulating
XX growth of motor or sympathetic neurons for treating neuron cell damage
XX
XX Claim 1c; Fig 3; 42pp; English.
XX
XX This invention describes a novel nucleic acid molecule (I) encoding a
XX novel neurotrophic factor (NNT-1) (II) which has neurotrophic,
XX neuroprotective, anticonvulsant, antiparkinsonian, antidiabetic and
XX ophthalmological activity. (I) is useful for producing NNT-1
XX polypeptides which are useful for treating patients in whom various
XX cells of the central, autonomic, or peripheral nervous system have
XX degenerated and/or have been damaged by congenital disease, trauma,
XX mechanical damage, surgery, stroke, ischemia, infection, metabolic
XX disease, nutritional deficiency, malignancy and/or toxic agents. NNT-1
XX proteins are used to treat diseases like Alzheimer's, Parkinson's,
XX amyotrophic lateral sclerosis, Charcot-Marie-Tooth syndrome, Huntington's
XX disease, peripheral neuropathy induced by diabetes or other metabolic
XX disorders, and/or dystrophies or degeneration of the neural retina such
XX as retinitis pigmentosa, drug-induced retinopathies, stationary forms of
XX night blindness, progressive cone-rod degeneration, immune disorders and
XX hematopoietic disorders. (I) is effective in treating neurological
XX conditions and promotes neuron regeneration. Neural functions are
XX effectively restored in patients suffering from various neurological
XX disorders. This sequence represents the human NNT-1 protein described in
XX the method of the invention.
XX
XX Sequence 225 AA:
XX
XX Query Match 100.0%; Score 1226; DB 21; Length 225;
XX Best Local Similarity 100.0%; Pred. No. 1.6e-118;
XX Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 MDLRADDSWGMCLACTCTVLMHLPAPVAPALNRGTGDPGPGSIQKTYDLTRYLEHQLSLAGT 60
XX |
XX 1 MDLRADDSWGMCLACTCTVLMHLPAPVAPALNRGTGDPGPGSIQKTYDLTRYLEHQLSLAGT 60
XX |
XX 61 YLNYLGPPFNEDPFPRLGAETLPRAATVDLEWVRSLNDKRLTQNYEAYSHLLCYLRGL 120
XX |
XX 61 YLNYLGPPFNEDPFPRLGAETLPRAATVDLEWVRSLNDKRLTQNYEAYSHLLCYLRGL 120
XX |
```

Db 61 YLNTYLGPPNEDFNPRLGAEITLPRAVTDLEWMSLNDKRLTONYEAYSHLCTYRGL 120  
 Qy 121 NROAATAEIRRSIAHFTCTSLQGLSGIAGWMAALGYPLPOPLPGTEPTTPGPASDPLQ 180  
 Db 121 NROAATAEIRRSIAHFTCTSLQGLSGIAGWMAALGYPLPOPLPGTEPTTPGPASDPLQ 180  
 Qy 181 KMDDFWLKEIQTWLWRSKADFNRLKKKQPPAAAVTLHLGAHGF 225  
 Db 181 KMDDFWLKEIQTWLWRSKADFNRLKKKQPPAAAVTLHLGAHGF 225

RESULT 5  
 AAG63543  
 ID AAG63543 standard; Protein; 225 AA.  
 AC AAG63543;  
 XX 15-OCT-2001 (first entry)  
 DT 15-OCT-2001 (first entry)  
 DE Amino acid sequence of a human NNT-1 protein.  
 XX NNT-1; CLF-1; SCNTFRalpha; nervous system; neuron; nervous system;  
 KW neuro-muscular function; tumour; immune system; haematopoietic system;  
 KW reproductive system; liver; skeletal muscle; neurodegenerative disease;  
 KW amyotrophic lateral sclerosis; Parkinson's disease; Huntington's disease;  
 KW muscular mass; paralysis; cancer; obesity; fertility; endometriosis;  
 KW blastocyst implantation; thrombosis; retinal disease;  
 KW retinal pigmentosis.  
 XX Homo sapiens.  
 OS Homo sapiens.  
 PN WO200155172-A2.  
 XX 02-AUG-2001.  
 PD 02-AUG-2001.  
 PF 26-JAN-2001; 2001WO-FR00253.  
 XX 27-JAN-2000; 2000FR-0001035.  
 PR 12-OCT-2000; 2000FR-0013089.  
 XX (FABR ) FABRE MEDICAMENT SA PIERRE.  
 PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.  
 XX Elson G, Gauchat J, Plun-Favreau H, Chevalier S, Gascan H,  
 PI MPI: 2001-488773/53.  
 XX MPI: 2001-488773/53.  
 DR N-PSDB; AAH74484.  
 DR A complex comprising a NNT-1 protein and a CLF-1 and/or SCNTFRalpha  
 PT protein useful to treat neurodegenerative disease including Parkinson's  
 PT and Huntington's, obesity and cancer -  
 XX Claim 2; Page 58; 67pp; French.  
 PS The present sequence represents a human NNT-1 protein. The specification  
 CC describes a complex comprising a NNT-1 protein and a CLF-1 and/or  
 CC SCNTFRalpha protein. The NNT-1/CLF-1 complex is used to modulate  
 CC activity of the SCNTFRalpha/gp130/LiRbeta receptor complex, or to  
 CC induce phosphorylation of the tyrosine of gp130 and LiRbeta,  
 CC particularly where cells expressing the receptor complex are in the  
 CC central or peripheral nervous system, in neurons implicated in  
 CC neuro-muscular function or in skeletal muscle. The complex or  
 CC antibodies are also used to decrease the survival, growth or  
 CC proliferation of tumour cells or to facilitate the proliferation and/or  
 CC inhibit differentiation of cells stocks. The complex is also used to  
 CC modulate activity of the gp130/LiRbeta receptor or cells expressing  
 CC that receptor, particularly those cells implicated in the immune,  
 CC haematopoietic, nervous or reproductive system, the liver or skeletal  
 CC muscle. Molecules of the invention may be used to prevent or treat  
 CC neurodegenerative diseases including amyotrophic lateral sclerosis,  
 CC Parkinson's and Huntington's disease, to repair or regenerate nervous  
 CC or muscular tissue or to maintain muscular mass in paralysis patients.  
 CC They may also be used to treat cancer, obesity and associated diseases,

CC and to improve fertility, particularly to avoid endometriosis and/or  
 CC assist blastocyst implantation, thrombosis, or retinal disease,  
 CC particular retinal pigmentosis.  
 XX Sequence 225 AA;  
 SQ Query Match 100.0%; Score 1226; DB 22; Length 225;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-118;  
 Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDLRAGDSWGMALACTCTYLWHLPAVPALNRTGDPGPGSIOCTYDLTRYLHQLRSLAGT 60  
 Db 1 MDLRAGDSWGMALACTCTYLWHLPAVPALNRTGDPGPGSIOCTYDLTRYLHQLRSLAGT 60  
 Qy 61 YLNTYLGPPNEDFNPRLGAEITLPRAVTDLEWMSLNDKRLTONYEAYSHLCTYRGL 120  
 Db 61 YLNTYLGPPNEDFNPRLGAEITLPRAVTDLEWMSLNDKRLTONYEAYSHLCTYRGL 120  
 Qy 121 NROAATAEIRRSIAHFTCTSLQGLSGIAGWMAALGYPLPOPLPGTEPTTPGPASDPLQ 180  
 Db 121 NROAATAEIRRSIAHFTCTSLQGLSGIAGWMAALGYPLPOPLPGTEPTTPGPASDPLQ 180  
 Qy 181 KMDDFWLKEIQTWLWRSKADFNRLKKKQPPAAAVTLHLGAHGF 225  
 Db 181 KMDDFWLKEIQTWLWRSKADFNRLKKKQPPAAAVTLHLGAHGF 225

RESULT 6  
 AAU78176  
 ID AAU78176 standard; Protein; 225 AA.  
 AC AAU78176;  
 XX 05-JUN-2002 (first entry)  
 DT 05-JUN-2002 (first entry)  
 DE Human novel neurotrophic factor NNT1.  
 XX Human novel neurotrophic factor NNT1.  
 KW Human; NNT1; neurotrophic factor; IGF-related disease;  
 KW Type I allergic disease; allergic rhinitis; eczema; dermatitis;  
 KW pollinosis; asthma; immune disease; cancer; arteriosclerosis;  
 KW vascular restenosis; rheumatoid arthritis; psoriatic arthritis;  
 KW inflammatory arthritis; osteoarthritis; inflammatory joint disease;  
 KW autoimmune disease; multiple sclerosis; lupus; diabetes; endometriosis;  
 KW inflammatory bowel disease; transplant rejection; reproductive disorder;  
 KW graft versus host disease; infertility; miscarriage; preterm labour.  
 XX Homo sapiens.  
 OS Homo sapiens.  
 PN WO200215977-A2.  
 XX 28-FEB-2002.  
 PD 28-FEB-2002.  
 PF 17-AUG-2001; 2001WO-US25906.  
 XX 18-AUG-2000; 2000US-226436P.  
 PR 16-AUG-2001; 2001US-0931704.  
 XX (AMGE-) AMGEN INC.  
 PA Senaldi G;  
 XX MPI: 2002-280867/32.  
 DR MPI: 2002-280867/32.  
 DR N-PSDB; ABK11647.  
 DR Treating Immunoglobulin E-related disease, modulating IGE levels in a  
 PT patient, preventing IGF-related disease and treating allergic diseases,  
 PT involves administering NNT-1 inhibitor to a patient -  
 XX Claim 2; Fig 3; 63pp; English.  
 PS The invention relates to treating Immunoglobulin E (IGE)-related disease,  
 CC modulating IGE levels in a patient, preventing an IGF-related disease,  
 CC and treating allergic diseases, comprising administering a

CC therapeutically effective amount of novel neurotrophic factor (NNT)-1  
CC inhibitor to a patient. Also included are a method of diagnosing an  
CC IGF-related disease or susceptibility to an IGF-related disease, by  
CC determining the presence or susceptibility to an IGF-related disease, by  
CC encoding by a NNT1 nucleotide sequence, its fragment or naturally  
CC occurring variant, and diagnosing an IGF-related disease or  
CC susceptibility of an IGF-related disease based on the presence or amount  
CC of expression of the polypeptide and a pharmaceutical composition for use  
CC in treating IGF-related disease, comprising the NNT1 inhibitor.  
CC The NNT1 inhibitor is useful for preventing and treating IGF-related  
CC disease, modulating IGF levels, and treating allergic diseases e.g.  
CC Type I allergic disease, allergic rhinitis, eczema, dermatitis,  
CC pollinosis, asthma, immune diseases and disorders, diseases involving  
CC abnormal cell proliferation including cancer, arteriosclerosis and  
CC vascular restenosis, diseases and conditions relating to dysfunction of  
CC immune system including rheumatoid arthritis, psoriatic arthritis,  
CC inflammatory arthritis, osteoarthritis, inflammatory joint disease,  
CC autoimmune disease, multiple sclerosis, lupus, diabetes, inflammatory  
CC bowel disease, transplant rejection, and graft versus host disease, and  
CC reproductive diseases and disorders including infertility, miscarriage,  
CC preterm labour and delivery, and endometriosis. The present sequence  
CC represents human NNT1.

XX Sequence 225 AA;

Query Match 100.0%; Score 1226; DB 23; Length 225;

Best Local Similarity 100.0%; Pred. No. 1.6e-118; Indels 0; Gaps 0;

Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLRAGDSWGMGLACTCTVLMHLPVAVPALNRTGDPGPGPSIQKTYDTRYLEHQSLACT 60

Db 1 MDLRAGDSWGMGLACTCTVLMHLPVAVPALNRTGDPGPGPSIQKTYDTRYLEHQSLACT 60

QY 61 YNLYGPPNEDPFPNPRIGAEITLPRATYDLEWRSNDKRLTONYEYSHLCTLRGL 120

Db 61 YNLYGPPNEDPFPNPRIGAEITLPRATYDLEWRSNDKRLTONYEYSHLCTLRGL 120

QY 121 NNOAATFAELRRSLAHFCTSLQGLSIGVMAALGVPPLPGTEPTTPGPAHSDPQ 180

Db 121 NNOAATFAELRRSLAHFCTSLQGLSIGVMAALGVPPLPGTEPTTPGPAHSDPQ 180

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAVTLHLGAHGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAVTLHLGAHGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAVTLHLGAHGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAVTLHLGAHGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAVTLHLGAHGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAVTLHLGAHGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAVTLHLGAHGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAVTLHLGAHGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAVTLHLGAHGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAVTLHLGAHGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAVTLHLGAHGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAVTLHLGAHGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAVTLHLGAHGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAVTLHLGAHGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAVTLHLGAHGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAVTLHLGAHGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAVTLHLGAHGF 225

Db 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAVTLHLGAHGF 225

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAVTLHLGAHGF 225

XX PN W0200153455-A2.  
XX PD 26-JUL-2001.  
XX PF 22-DEC-2000; 2000WO-US35017.  
XX PR 23-DEC-1999; 99US-0471275.  
XX PR 21-JAN-2000; 2000US-0488725.  
XX PR 25-APR-2000; 2000US-0552317.  
XX PA (HYSE-) HYSEQ INC.  
XX PI Tang YT, Liu C, Dermanac RT;  
XX DR WPI; 2001-457603/49.  
XX DR N-PSDB; AAH9772.  
XX PT Isolated human polynucleotides encoding polypeptides, useful for the  
XX treatment and diagnosis of e.g. cancer, ulcers and HIV infection -  
XX Claim 20; Page 278; 1217bp; English.

XX AAH99166 to AAH99904 encode the human proteins given in AAM25225 to  
XX AAM25963. The proteins can have activities based on the tissues and  
XX cells they are expressed in, such as: antiinflammatory; antirheumatic;  
XX antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant;  
XX central nervous system; vitruide; anti-HIV; fungicide; antimutagen;  
XX cardiovascular; antianaemic; antiagregant; haemostatic; vulnery;  
XX anticulcer; osteopathic; dermatological; antiallergic; antiaesthetic;  
XX antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;  
XX antiparkinsonian; and immunostimulant. The proteins and polynucleotides  
XX encoding them can be used in gene therapy, antisense therapy and vaccine  
XX production. The proteins and polynucleotides are useful for screening for  
XX agonists or antagonists of a protein and for the treatment and diagnosis  
XX of disorders associated with the activity of a protein e.g. inflammation,  
XX rheumatoid arthritis, septic shock, pancreatic, cardiac dysfunction,  
XX neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal  
XX infections, autoimmunity, genetic diseases, haematopoietic disorders,  
XX anaemia, platelet disorders, thrombocytopenia, wounds, burns, ulcers,  
XX osteoporosis, severe combined immunodeficiency, eczema, allergic  
XX rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,  
XX Alzheimer's disease, Parkinson's disease, neurodegenerative and  
XX neurological disorders.

XX Sequence 253 AA;

Query Match 100.0%; Score 1226; DB 22; Length 253;

Best Local Similarity 100.0%; Pred. No. 1.9e-118; Indels 0; Gaps 0;

Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLRAGDSWGMGLACTCTVLMHLPVAVPALNRTGDPGPGPSIQKTYDTRYLEHQSLACT 60

Db 29 MDLRAGDSWGMGLACTCTVLMHLPVAVPALNRTGDPGPGPSIQKTYDTRYLEHQSLACT 88

QY 61 YNLYGPPNEDPFPNPRIGAEITLPRATYDLEWRSNDKRLTONYEYSHLCTLRGL 120

Db 89 YNLYGPPNEDPFPNPRIGAEITLPRATYDLEWRSNDKRLTONYEYSHLCTLRGL 148

QY 121 NNOAATFAELRRSLAHFCTSLQGLSIGVMAALGVPPLPGTEPTTPGPAHSDPQ 180

Db 149 NNOAATFAELRRSLAHFCTSLQGLSIGVMAALGVPPLPGTEPTTPGPAHSDPQ 208

QY 181 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAVTLHLGAHGF 225

Db 209 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAVTLHLGAHGF 253

QY 209 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAVTLHLGAHGF 253

Db 209 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAVTLHLGAHGF 253

QY 209 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAVTLHLGAHGF 253

Db 209 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAVTLHLGAHGF 253

QY 209 KMDDFWLKELQTLWMSAKDPNRLKKKQPPAAVTLHLGAHGF 253

XX 02-JUL-2001 (first entry)  
DT Human cardiotrophin-like cytokine (CLC) protein.  
XX  
DE Human cardiotrophin-like cytokine (CLC) protein.  
XX  
XX Human, biologically active complex; haemopoietin receptor; NR6;  
KW cardiotrophin-like cytokine; CLC; therapy; prophylaxis; proliferation;  
XX differentiation; cell survival; neurotrophic activity.  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..27  
FT /label= Signal\_peptide  
FT 28..223  
FT Protein /label= Human mature CLC protein  
FT /note= "Cardiotrophin-like cytokine"  
XX  
PN WO200127157-A1.  
XX  
PD 19-APR-2001.  
XX  
PF 06-OCT-2000; 2000MO-AU01216.  
XX  
PR 08-OCT-1999; 99AU-0003327.  
PR 12-MAY-2000; 2000AU-0007489.  
XX  
PA (AMRA-) AMRAD OPERATIONS PTY LTD.  
XX  
PI Nash A, Jachno KM, Fabri LJ, Reid K, Bartlett PF, Hilton DJ;  
PI Nakata Y, Hasegawa M;  
XX  
DR WPI; 2001-281978/29.  
DR N-PSDB; AAD04201.  
XX  
XX New biologically active complex comprising NR6 and  
PT cardiotrophin-like cytokine, for facilitating proliferation,  
PT differentiation and/or survival of a cell -  
XX  
XX Claim 32; Page 114-115; 123pp; English.  
XX  
XX The present invention relates to a biologically active complex comprising  
CC a haemopoietin receptor, NR6 and cardiotrophin-like cytokine (CLC).  
CC The complex is useful in the manufacture of a medicament for the  
CC treatment and/or prophylaxis of a subject, as it is involved in  
CC facilitating proliferation, differentiation and/or survival of a cell.  
CC The complex or its components have neurotrophic activity. The present  
CC sequence is human cardiotrophin-like cytokine (CLC) protein.  
XX  
SQ Sequence 223 AA;  
XX  
Query Match 99.0%; Score 1214; DB 22; Length 223;  
Best Local Similarity 100.0%; Pred. No. 2.8e-117;  
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 1 MDLRAGDSWGMALACTVLMHLPAVPALNRTGDPGPSPISOKTYDTRYLEHQLSLAGT 60  
DB 1 MDLRAGDSWGMALACTVLMHLPAVPALNRTGDPGPSPISOKTYDTRYLEHQLSLAGT 60  
QY 61 YANIYAGPPNEDPFPRIAGATLPRATVDLEWRSINDKRLTONYEAVSHLCTYLRGL 120  
DB 61 YANIYAGPPNEDPFPRIAGATLPRATVDLEWRSINDKRLTONYEAVSHLCTYLRGL 120  
QY 121 NROAATAEIRRSIAHCTSLIGLIGSIAGVMAALGPPLPGREPTTPGPAHSDFLQ 180  
DB 121 NROAATAEIRRSIAHCTSLIGLIGSIAGVMAALGPPLPGREPTTPGPAHSDFLQ 180  
QY 181 KMDDFMLLKEIQTWLMRSKADFNRLKKKQPPAAAVTTLHGLAH 223  
DB 181 KMDDFMLLKEIQTWLMRSKADFNRLKKKQPPAAAVTTLHGLAH 223

RESULT 9

ABBI1896  
ID ABBI1896 standard; peptide; 321 AA.  
XX  
AC ABBI1896;  
XX  
DT 11-JAN-2002 (first entry)  
XX  
DE Human cardiotrophin-like cytokine homologue, SEQ ID NO:2266.  
XX  
XX Human, cytokine; cell proliferation; cell differentiation; growth factor;  
KW haematopoiesis regulation; tissue growth; immunomodulatory; activin;  
KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;  
KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;  
KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;  
KW chronic inflammatory condition; proliferative retinopathy;  
KW atherosclerosis; coronary heart disease; arterial ischaemia;  
KW bone disorder; osteoporosis; vascular growth disorder;  
KW tissue regeneration; wound healing; infection; immune disorder;  
KW cell culture; drug screening; gene therapy; antiinflammatory;  
KW antiaesthetic; antiarthritic; haemostatic; antiarteriosclerotic;  
KW cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;  
KW antifungal; valnery; antituber.  
XX  
OS Homo sapiens.  
XX  
PN WO200157188-A2.  
XX  
PD 09-AUG-2001.  
XX  
PF 05-FEB-2001; 2001WO-US03800.  
XX  
PR 03-FEB-2000; 2000US-0496914.  
PR 27-APR-2000; 2000US-0560875.  
XX  
PA (HISE-) HISEQ INC.  
XX  
PI Tang YT, Liu C, Dzmanac RT;  
PI WPI; 2001-457740/49.  
XX  
DR N-PSDB; ABA09140.  
XX  
XX Human proteins and DNA encoding sequences useful for preventing,  
PT treating or ameliorating a medical condition in a mammalian subject  
PT e.g. arthritis and cancer -  
XX  
PS Claim 20; Page 273; 1963pp; English.  
XX  
XX Sequences ABBI0981-ABBI2330 represent 1350 novel human polypeptides, and  
CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The  
CC invention also relates to vectors and recombinant host cells comprising a  
CC nucleotide of the invention, methods of producing the novel polypeptides,  
CC antibodies against the polypeptides, methods of detecting the nucleotides,  
CC or polypeptides in a sample, and methods of identifying compounds which  
CC bind to polypeptides of the invention. Although novel, many of the  
CC polypeptides of the invention have homology to known proteins, and hence  
CC giving an insight into their probable biological activities, and hence  
CC potential therapeutic applications. The polypeptides of the invention may  
CC have various activities, including cytokine, cell proliferation or cell  
CC differentiation activities; stem cell growth factor activity;  
CC haematopoiesis regulatory activity; tissue growth activity;  
CC immunomodulatory activity; activin- or inhibin-related activities;  
CC chemotactic or chemokinetic activities; haemostatic, thrombotic or  
CC thrombolytic activities; receptor or ligand activities; or may be  
CC involved in oncogenesis, cancer cell proliferation or metastasis.  
CC Depending on their biological activities, polypeptides and nucleotides of  
CC the invention are useful for preventing, treating or ameliorating medical  
CC conditions, e.g., by protein or gene therapy. Such conditions include  
CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell  
CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),  
CC proliferative retinopathy, atherosclerosis, coronary heart disease,  
CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal  
CC vascular growth. Polypeptides involved with tissue regeneration and  
CC repair (or nucleic acids encoding them) may be used to promote wound



CC healing (e.g., of burns, incisions and ulcers), while those with  
CC immunomodulatory activities may be used in the treatment of viral,  
CC bacterial and fungal infections in addition to immune disorders.  
CC Polypeptides with growth factor activity may be used in cell cultures to  
CC promote cell growth. For example, such polypeptides may be used to  
CC manipulate stem cells in culture to give rise to neuroepithelial cells  
CC that can be used to augment or replace cells damaged by illness,  
CC autoimmune disease or accidental damage. The polypeptides and nucleotides  
CC may also be used in the diagnosis of the above conditions, and in drug  
CC screening techniques. The present sequence represents a novel human  
CC polypeptide of the invention.

XX Sequence 321 AA;

Query Match 98.2%; Score 1204; DB 22; Length 321;

Best Local Similarity 99.1%; Pred. No. 5e-116; 2; Indels 0; Gaps 0;

Matches 221; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 LRAGDSMGMLACTCTVLMHLPAPVAPALNRTGDPGSPSIOKTYDLTRYLEHQLRSLAGTYL 62  
DB 99 LPTGDSMGMLACTCTVLMHLPAPVAPALNRTGDPGSPSIOKTYDLTRYLEHQLRSLAGTYL 158  
QY 63 NYLGPPFNEPDPFNPRLGAETLPRAATVDLEWRSINDKRLTONYEAYSHLICYRGILNR 122  
DB 159 NYLGPPFNEPDPFNPRLGAETLPRAATVDLEWRSINDKRLTONYEAYSHLICYRGILNR 218  
QY 123 QATATLRSLAHFCTSLQGLSIGVMAALGYPLPQPLPCTEPTWTPGPAHSDFLQKM 182  
DB 219 QATATLRSLAHFCTSLQGLSIGVMAALGYPLPQPLPCTEPTWTPGPAHSDFLQKM 278  
QY 183 DDFWLKELQTLWLRSAKDFNRLKKMKOPPAAVTLHGANGF 225  
DB 279 DDFWLKELQTLWLRSAKDFNRLKKMKOPPAAVTLHGANGF 321

#### RESULT 10

AAAT79399 standard; Protein; 321 AA.

XX ID AAM79399;  
XX AC AAM79399;  
XX DT 06-NOV-2001 (first entry)  
XX DE Human protein SEQ ID NO 3045.  
XX KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;  
XX KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;  
XX KW tissue growth factor; immunomodulatory; cancer; leukaemia;  
XX KW nervous system disorder; arthritis; inflammation.

XX Homo sapiens.

XX WO200157190-A2.

XX PD 09-AUG-2001.

XX PF 05-FEB-2001; 2001MO-US04098.

XX PR 03-FEB-2000; 2000US-0496914.  
XX PR 27-APR-2000; 2000US-0560875.  
XX PR 20-JUN-2000; 2000US-0598075.  
XX PR 19-JUL-2000; 2000US-0620325.  
XX PR 01-SEP-2000; 2000US-0654936.  
XX PR 15-SEP-2000; 2000US-0663561.  
XX PR 20-OCT-2000; 2000US-0693325.  
XX PR 30-NOV-2000; 2000US-0728422.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;  
XX Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;  
XX Xue AJ, Yang Y, Wehrman T, Goodrich R;

DR WPI; 2001-476283/51.

DR N-PSDB; AAK52532.

XX Nucleic acids encoding polypeptides with cytokine-like activities,  
XX useful in diagnosis and gene therapy -

XX Claim 20; Page 237; 6221pp; English.

CC The invention relates to polynucleotides (AAK51456-AAK53435) and the  
CC encoded polypeptides (AAM78415-AAM80302) that exhibit activity relating to  
CC cytokine, cell proliferation or cell differentiation or which may induce  
CC production of other cytokines in other cell populations. The  
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or  
CC peptide therapy. The polypeptides have various cytokine-like activities,  
CC e.g. stem cell growth factor activity, haematopoiesis regulating  
CC activity, tissue growth factor activity, immunomodulatory activity and  
CC activin/inhibin activity and may be useful in the diagnosis and/or  
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and  
CC inflammation.  
CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666  
CC (AAM80020) are omitted as the relevant pages from the sequence listing  
CC were missing at the time of publication.

XX Sequence 321 AA;

Query Match 98.2%; Score 1204; DB 22; Length 321;

Best Local Similarity 99.1%; Pred. No. 5e-116; 2; Indels 0; Gaps 0;

Matches 221; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 LRAGDSMGMLACTCTVLMHLPAPVAPALNRTGDPGSPSIOKTYDLTRYLEHQLRSLAGTYL 62  
DB 99 LPTGDSMGMLACTCTVLMHLPAPVAPALNRTGDPGSPSIOKTYDLTRYLEHQLRSLAGTYL 158  
QY 63 NYLGPPFNEPDPFNPRLGAETLPRAATVDLEWRSINDKRLTONYEAYSHLICYRGILNR 122  
DB 159 NYLGPPFNEPDPFNPRLGAETLPRAATVDLEWRSINDKRLTONYEAYSHLICYRGILNR 218  
QY 123 QATATLRSLAHFCTSLQGLSIGVMAALGYPLPQPLPCTEPTWTPGPAHSDFLQKM 182  
DB 219 QATATLRSLAHFCTSLQGLSIGVMAALGYPLPQPLPCTEPTWTPGPAHSDFLQKM 278  
QY 183 DDFWLKELQTLWLRSAKDFNRLKKMKOPPAAVTLHGANGF 225  
DB 279 DDFWLKELQTLWLRSAKDFNRLKKMKOPPAAVTLHGANGF 321

#### RESULT 11

AAAT78415 standard; Protein; 260 AA.

XX ID AAM78415;  
XX AC AAM78415;  
XX DT 06-NOV-2001 (first entry)  
XX DE Human protein SEQ ID NO 1077.  
XX KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;  
XX KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;  
XX KW tissue growth factor; immunomodulatory; cancer; leukaemia;  
XX KW nervous system disorder; arthritis; inflammation.

XX Homo sapiens.

XX WO200157190-A2.

XX PD 09-AUG-2001.

XX PF 05-FEB-2001; 2001MO-US04098.

XX PR 03-FEB-2000; 2000US-0496914.  
XX PR 27-APR-2000; 2000US-0560875.  
XX PR 20-JUN-2000; 2000US-0598075.  
XX PR 19-JUL-2000; 2000US-0620325.

PR 01-SEP-2000; 2000US-0654936.  
 PR 15-SEP-2000; 2000US-0663561.  
 PR 20-OCT-2000; 2000US-0693325.  
 PR 30-NOV-2000; 2000US-0728422.  
 XX  
 XX (HYSR-) HYSRQ INC.  
 XX  
 XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;  
 PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;  
 PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;  
 XX  
 XX WPI: 2001-476283/51.  
 DR N-PSDB; AAKS1548.  
 XX  
 XX Nucleic acids encoding polypeptides with cytokine-like activities,  
 PT useful in diagnosis and gene therapy -  
 XX  
 XX Claim 20; Page 3306; 6221pp; English.  
 XX  
 XX The invention relates to polynucleotides (AAK51456-AAK53435) and the  
 CC encoded polypeptides (AAW78323-AAW80302) that exhibit activity elating to  
 CC cytokine, cell proliferation or cell differentiation or which may induce  
 CC production of other cytokines in other cell populations. The  
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or  
 CC peptide therapy. The polypeptides have various cytokine-like activities,  
 CC e.g. stem cell growth factor activity, haematopoiesis regulating  
 CC activity, tissue growth factor activity, immunomodulatory activity and  
 CC activating/inhibiting activity and may be useful in the diagnosis and/or  
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and  
 CC inflammation.  
 CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666  
 CC (AAW80020) are omitted as the relevant pages from the sequence listing  
 CC were missing at the time of publication.  
 CC  
 CC Sequence 260 AA;  
 SQ  
 Query Match 97.6%; Score 1197; DB 22; Length 260;  
 Best Local Similarity 98.7%; Pred. No. 2e-115;  
 Matches 220; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 3 LRAAGDSWGMACLCCTVLMHLPVAPALNRTGDPGPGSIQKTYDLTRYLHQLRSLAGT 62  
 DB 38 LRTGDSWGMACLCCTVLMHLPVAPALNRTGDPGPGSIQKTYDLTRYLHQLRSLAGT 97  
 QY 63 NYLGPPFNPDNPRLGAEITLPRAIVDLEWRSINDKRLTONYEAYSHLCTYRGLN 122  
 DB 98 NYLGPPFNPDNPRLGAEITLPRAIVDLEWRSINDKRLTONYEAYSHLCTYRGLN 157  
 QY 123 QAATAELRSLAHFCTSLQGLLSIAGVAAALGYPLPQPLPCTEPTWTGPAHSDP 182  
 DB 158 QAATAELRSLAHFCTSLQGLLSIAGVAAALGYPLPQPLPCTEPTWTGPAHSDP 217  
 QY 163 DDFWLLKELQVLMWSAKDFNRLKKMKOPPAAVTLHLGAHGF 225  
 DB 218 DDFWLLKELQVLMWSAKDFNRLKKMKOPPAAVTLHLGAHGF 260  
 RESULT 12  
 AAW29716  
 ID AAW29716 standard; Protein; 225 AA.  
 XX  
 XX AAW29716;  
 AC  
 XX  
 XX 09-NOV-1998 (first entry)  
 DT  
 XX  
 XX Mouse neurotrophic factor NNT-1.  
 DE  
 XX  
 XX NNT-1; neurotrophic factor; mouse; antiinflammatory; adjuvant;  
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease;  
 KW amyotrophic lateral sclerosis; Charcot-Marie-Tooth syndrome;  
 KW peripheral neuropathy; dystrophy; neural retina degeneration;  
 KW common variable immunodeficiency; CVID; selective IGA deficiency;  
 KW hypogammaglobulinaemia; X-linked agammaglobulinaemia; antiseptic;

KW therapy.  
 XX  
 XX Mus sp.  
 OS  
 XX  
 XX Key  
 FT Peptide 1..27 Location/Qualifiers  
 FT Protein /label= Sig\_peptide  
 FT 28..225 /label= Mat\_protein  
 XX  
 XX W09833922-A1.  
 PN  
 XX  
 XX 06-AUG-1998.  
 PD  
 XX  
 XX 02-FEB-1998; 98WO-US02363.  
 PF  
 XX  
 XX 30-JAN-1998; 98US-0016534.  
 PR 03-FEB-1997; 97US-0792019.  
 XX  
 XX (AMGE-) AMGEN INC.  
 PA  
 XX  
 XX Chang M, Elliot GS, Sarmiento U, Senaldi G;  
 PI WPI: 1998-437475/37.  
 DR N-PSDB; AAV47512.  
 DR  
 XX  
 XX Newly isolated nucleic acid encoding human or murine neurotrophic  
 PT factor NNT-1 - useful for treatment of neurological and  
 PT immunological diseases or inflammation, also as vaccine adjuvant  
 XX  
 XX Claim 13; Fig 5; 120pp; English.  
 PS  
 XX  
 XX This is the amino acid sequence of a murine neurotrophic factor,  
 CC designated NNT-1, that is a growth factor for neurons and for B or  
 CC T cells. It was deduced from isolated NNT-1 cDNA (see AAV47512).  
 CC Human NNT-1 (see AAW29715) is also provided. Vectors and host cells  
 CC for use in the production of human murine recombinant NNT-1  
 CC polypeptides. These are used to treat: (i) neurological or  
 CC immunological diseases, specifically Alzheimer's, Parkinson's  
 CC or Huntington's diseases, amyotrophic lateral sclerosis,  
 CC Charcot-Marie-Tooth syndrome, peripheral neuropathy, dystrophy and  
 CC degeneration of the neural retina, or conditions characterised by T  
 CC or B cell defects, e.g. common variable immunodeficiency (CVID),  
 CC selective IGA deficiency, hypogammaglobulinaemia and X-linked  
 CC agammaglobulinaemia (claimed), but many others disclosed; and (ii)  
 CC inflammation. NNT-1 is also able to boost immunoreactivity and  
 CC antibody production following vaccination, and, since it inhibits  
 CC tumor necrosis factor production, it may also be useful for  
 CC treating sepsis. In addition, cells that have been engineered to  
 CC express NNT-1 can be implanted, or nucleic acids are delivered in  
 CC gene therapy vectors.  
 XX  
 XX Sequence 225 AA;  
 SQ  
 Query Match 97.3%; Score 1193; DB 19; Length 225;  
 Best Local Similarity 96.9%; Pred. No. 4.3e-115;  
 Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 MDLRAAGDSWGMACLCCTVLMHLPVAPALNRTGDPGPGSIQKTYDLTRYLHQLRSLAGT 60  
 DB 1 MDLRAAGDSWGMACLCCTVLMHLPVAPALNRTGDPGPGSIQKTYDLTRYLHQLRSLAGT 60  
 QY 61 YINYVGPPFNPDNPRLGAEITLPRAIVDLEWRSINDKRLTONYEAYSHLCTYRGL 120  
 DB 61 YINYVGPPFNPDNPRLGAEITLPRAIVDLEWRSINDKRLTONYEAYSHLCTYRGL 120  
 QY 121 NROAATAELRSLAHFCTSLQGLLSIAGVAAALGYPLPQPLPCTEPTWTGPAHSDP 180  
 DB 121 NROAATAELRSLAHFCTSLQGLLSIAGVAAALGYPLPQPLPCTEPTWTGPAHSDP 180  
 QY 181 KMDDFWLLKELQVLMWSAKDFNRLKKMKOPPAAVTLHLGAHGF 225  
 DB 181 KMDDFWLLKELQVLMWSAKDFNRLKKMKOPPAAVTLHLGAHGF 225

## RESULT 13

AAW56142  
ID AAW56142 standard; Protein; 225 AA.

AC AAW56142;

DT 13-JUL-1998 (first entry)

DE Amino acid sequence of murine neurotrophic factor NNT-1.

KW Mouse; neurotrophic factor; NNT-1; growth; motor; sympathetic; neuron;  
KW treatment; neurological disease; degeneration; Parkinson's disease;  
KW amyotrophic lateral sclerosis; ALS; Alzheimer's disease; stroke.

OS Mus sp.

PH Key Location/Qualifiers

PT Peptide 1..27 /note= "signal peptide"

PT Protein 28..225 /note= "mature peptide"

PN US5741772-A.

PD 21-APR-1998.

PF 03-FEB-1997; 97US-0792019.

PR 03-FEB-1997; 97US-0792019.

PA (AMGE-) AMGEN INC.

PI Chang M;

DR WPI; 1998-260526/23.

DR N-PSDB; AAW22654.

PT Neurotrophic factor NNT-1 polypeptide and related nucleic acids -  
PT useful for stimulating growth of motor and sympathetic neurons

XX Claim 2; Fig 5; 41pp; English.

CC The present sequence represents a murine neurotrophic factor, designated  
CC NNT-1, which is capable of stimulating growth of motor or sympathetic  
CC neurons. The NNT-1 protein is useful in the treatment of neurological  
CC diseases characterized by the degeneration and death of particular  
CC classes of neurons. These diseases specifically include Parkinson's  
CC disease, amyotrophic lateral sclerosis (ALS), Alzheimer's disease,  
CC stroke and various degenerative disorders affecting vision.

XX Sequence 225 AA;

Query Match 97.3%; Score 1193; DB 19; Length 225;  
Best Local Similarity 96.9%; Pred. No. 4.3e-115;

Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDLRAGDSWGMIACTCTVLMHLPAVPALNRTGDPGPGPSIQKTYDLTRYLEHQLSLAGT 60  
DB 1 MDLRAGDSWGMIACTCTVLMHLPAVPALNRTGDPGPGPSIQKTYDLTRYLEHQLSLAGT 60

QY 61 YLNYLGPPEPDPNPPRLGAETLPATYDLEWYRSNDKRLTONYEAYSHLCTYRG 120  
DB 61 YLNYLGPPEPDPNPPRLGAETLPATYDLEWYRSNDKRLTONYEAYSHLCTYRG 120

QY 121 NROAATRAELRSLAHCTSLGSLGSIAGWMAALGVPOLPLPGTPTPGPASDFIQ 180  
DB 121 NROAATRAELRSLAHCTSLGSLGSIAGWMAALGVPOLPLPGTPTPGPASDFIQ 180

QY 181 KMDDFWLKELQTMWRSADFNRLKKKQPPAAATVTLHGAHF 225  
DB 181 KMDDFWLKELQTMWRSADFNRLKKKQPPAAATVTLHGAHF 225

## RESULT 14

AAW87814  
ID AAW87814 standard; Protein; 225 AA.

AC AAW87814;

DT 24-AUG-2000 (first entry)

DE Murine NNT-1 protein.

KW NNT-1; neurotrophic factor; neurotrophic; neuroprotective; treatment;  
KW anticonvulsant; antiparkinsonian; antidiabetic; ophthalmological;  
KW nervous system degeneration; Alzheimer's disease; Parkinson's disease;  
KW amyotrophic lateral sclerosis; Charcot-Marie-Tooth syndrome; murine;  
KW Huntington's disease; peripheral neuropathy; neural retina degeneration;  
KW retinopathy; immune disorder; hematopoietic disorder.

OS Mus sp.

PN US6054294-A.

PD 25-APR-2000.

PF 12-DEC-1997; 97US-0988819.

PR 03-FEB-1997; 97US-0792019.

PA (AMGE-) AMGEN INC.

PI Chang M;

DR WPI; 2000-338492/29.

DR N-PSDB; AAA39483.

PT New nucleic acids encoding neurotrophic factors useful for stimulating  
PT growth of motor or sympathetic neurons for treating neuron cell damage

XX Claim 2b; Fig 5; 42pp; English.

CC This invention describes a novel nucleic acid molecule (I) encoding a  
CC novel neurotrophic factor (NNT-1) (II) which has neurotrophic,  
CC neuroprotective, anticonvulsant, antiparkinsonian, antidiabetic and  
CC ophthalmological activity. (I) is useful for producing NNT-1  
CC polypeptides which are useful for treating patients in whom various  
CC cells of the central, autonomic, or peripheral nervous system have  
CC degenerated and/or have been damaged by congenital disease, trauma,  
CC mechanical damage, surgery, stroke, ischemia, infection, metabolic  
CC disease, nutritional deficiency, malignancy and/or toxic agents. NNT-1  
CC proteins are used to treat diseases like Alzheimer's, Parkinson's,  
CC amyotrophic lateral sclerosis, Charcot-Marie-Tooth syndrome, Huntington's  
CC disease, peripheral neuropathy induced by diabetes or other metabolic  
CC disorders, and/or dystrophies or degeneration of the neural retina such  
CC as retinitis pigmentosa, drug-induced retinopathies, stationary forms of  
CC night blindness, progressive cone-rod degeneration, immune disorders and  
CC hematopoietic disorders. (I) is effective in treating neurological  
CC conditions and promotes neuron regeneration. Neural functions are  
CC effectively restored in patients suffering from various neurological  
CC disorders. This sequence represents the murine NNT-1 protein described in  
CC the method of the invention.

XX Sequence 225 AA;

Query Match 97.3%; Score 1193; DB 21; Length 225;  
Best Local Similarity 96.9%; Pred. No. 4.3e-115;

Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDLRAGDSWGMIACTCTVLMHLPAVPALNRTGDPGPGPSIQKTYDLTRYLEHQLSLAGT 60  
DB 1 MDLRAGDSWGMIACTCTVLMHLPAVPALNRTGDPGPGPSIQKTYDLTRYLEHQLSLAGT 60



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OM protein - protein search, using ew model

Run on: February 9, 2004, 06:17:01 / Search time 33 Seconds  
(without alignments)  
1427.606 Million cell updates/sec

Title: US-09-931-704-2  
Perfect score: 1226  
Sequence: 1 MDLRAGDSWGMCLACTVLM.....KKKMGPPAAVTLHGANGF 225

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database :

1: Published Applications AA:  
2: /cgn2\_6/ptodata/1/pubppa/US07\_PUBCOMB.pep:\*  
3: /cgn2\_6/ptodata/1/pubppa/US09C\_PUBCOMB.pep:\*  
4: /cgn2\_6/ptodata/1/pubppa/US06\_NEW\_PUB.pep:\*  
5: /cgn2\_6/ptodata/1/pubppa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/1/pubppa/US08\_PUBCOMB.pep:\*  
7: /cgn2\_6/ptodata/1/pubppa/US08\_PUBCOMB.pep:\*  
8: /cgn2\_6/ptodata/1/pubppa/US09\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/1/pubppa/US09\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/1/pubppa/US09\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/1/pubppa/US09C\_PUBCOMB.pep:\*  
12: /cgn2\_6/ptodata/1/pubppa/US09C\_PUBCOMB.pep:\*  
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14: /cgn2\_6/ptodata/1/pubppa/US10B\_PUBCOMB.pep:\*  
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18: /cgn2\_6/ptodata/1/pubppa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1226	100.0	225	9 US-09-931-704-2	Sequence 2, Appl1
2	1226	100.0	225	15 US-10-212-793-2	Sequence 2, Appl1
3	1193	97.3	225	9 US-09-931-704-5	Sequence 5, Appl1
4	885	72.2	164	9 US-09-864-761-40014	Sequence 40014, A
5	124.5	10.2	203	15 US-10-212-793-3	Sequence 3, Appl1
6	118.5	9.7	203	10 US-09-896-856-3	Sequence 3, Appl1
7	118.5	9.7	203	12 US-10-407-303-3	Sequence 3, Appl1
8	118.5	9.7	203	15 US-10-107-931-3	Sequence 3, Appl1
9	96.5	7.9	243	9 US-09-810-052-5	Sequence 5, Appl1
10	96.5	7.9	243	11 US-09-791-497-8	Sequence 8, Appl1
11	96.5	7.9	243	14 US-10-000-776-6	Sequence 6, Appl1
12	92.5	7.5	860	15 US-10-156-761-11445	Sequence 11445, A
13	91.5	7.5	201	10 US-09-901-540-3	Sequence 3, Appl1
14	91.5	7.5	201	10 US-09-896-856-8	Sequence 8, Appl1
15	91.5	7.5	201	10 US-09-901-257-3	Sequence 3, Appl1

16	91.5	7.5	201	12 US-10-407-303-8	Sequence 8, Appl1
17	91.5	7.5	201	15 US-10-107-931-8	Sequence 8, Appl1
18	91.5	7.5	201	15 US-10-212-793-4	Sequence 4, Appl1
19	91.5	7.5	1182	15 US-10-024-368-6	Sequence 6, Appl1
20	91	7.4	195	10 US-09-770-361-5	Sequence 5, Appl1
21	91	7.4	195	12 US-10-281-643-5	Sequence 5, Appl1
22	91	7.4	195	12 US-10-383-916-5	Sequence 5, Appl1
23	91	7.4	195	15 US-10-226-759-5	Sequence 5, Appl1
24	91	7.4	242	11 US-09-791-497-2	Sequence 2, Appl1
25	91	7.4	242	14 US-10-000-776-2	Sequence 2, Appl1
26	90	7.3	232	9 US-09-810-052-2	Sequence 2, Appl1
27	88.5	7.2	1429	12 US-10-028-374-3	Sequence 3, Appl1
28	88.5	7.2	1429	12 US-10-183-770-3	Sequence 3, Appl1
29	87.5	7.1	1207	15 US-10-024-368-5	Sequence 5, Appl1
30	85	6.9	727	12 US-10-231-913-8	Sequence 9, Appl1
31	84.5	6.9	389	12 US-10-369-493-22941	Sequence 28941, A
32	84	6.9	411	12 US-10-369-493-562	Sequence 562, App
33	84	6.9	876	12 US-10-074-511-110	Sequence 110, App
34	83.5	6.8	275	15 US-10-156-761-12256	Sequence 12256, A
35	83	6.8	469	15 US-10-156-761-9695	Sequence 9695, App
36	83	6.8	625	10 US-09-771-161A-242	Sequence 242, App
37	83	6.8	625	10 US-09-771-161A-243	Sequence 243, App
38	82.5	6.7	984	15 US-10-024-368-2	Sequence 2, Appl1
39	82.5	6.7	1189	15 US-10-024-368-4	Sequence 4, Appl1
40	82.5	6.7	1189	15 US-10-122-013-17	Sequence 17, Appl1
41	82	6.7	200	10 US-09-770-361-8	Sequence 8, Appl1
42	82	6.7	200	12 US-10-281-643-8	Sequence 8, Appl1
43	82	6.7	200	12 US-10-383-916-8	Sequence 8, Appl1
44	82	6.7	200	15 US-10-226-759-8	Sequence 8, Appl1
45	81.5	6.6	218	10 US-09-893-737-28	Sequence 28, Appl1

## ALIGNMENTS

RESULT 1  
US-09-931-704-2  
Sequence 2, Application US/09931704  
Patent No. US20020041873A1  
GENERAL INFORMATION:  
APPLICANT: Senaldi, Giorgio  
TITLE OF INVENTION: Methods and Compositions for Treating IGE-Related Disease Using  
FILE REFERENCE: A-695  
CURRENT APPLICATION NUMBER: US/09/931,704  
CURRENT FILING DATE: 2001-08-16  
PRIOR APPLICATION NUMBER: US 60/226,436  
PRIOR FILING DATE: 2000-08-18  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 2  
LENGTH: 225  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-931-704-2

Query Match	100.0%	Score 1226	DB 9	Length 225
Best Local Similarity	100.0%	Pred. No. 5.9e-115	Mismatches 0	Indels 0
Matches 225	Conservative			Gaps 0
QY	1	MDLRAGDSWGMCLACTVLMHLPALNRRGDPGPGSIQKTYDLYLEHQRLSLAGT	60	
DB	1	MDLRAGDSWGMCLACTVLMHLPALNRRGDPGPGSIQKTYDLYLEHQRLSLAGT	60	
QY	61	YLVNIGPEPNEBDFNPRLGAEITLPRAIVDLEVMRLNDKRLRTQNYEAYSHLCTYRGL	120	
DB	61	YLVNIGPEPNEBDFNPRLGAEITLPRAIVDLEVMRLNDKRLRTQNYEAYSHLCTYRGL	120	
QY	121	NROATATLRSLAHFCTSLQGLGSLGVAALGYPLQPLPGTEPTWTEGPAHSDFLQ	180	
DB	121	NROATATLRSLAHFCTSLQGLGSLGVAALGYPLQPLPGTEPTWTEGPAHSDFLQ	180	
QY	181	KMDDEWLKELQYLMRSKQFNNLKKMGPPAAVTLHGANGF	225	

Db 181 KMDDFWLKELOTWLMRSKADFNRLKKKQPPAAAVTTLHGAHGF 225

RESULT 2  
US-10-212-793-2

Sequence 2, Application US/10212793  
Publication No. US20030087395A1  
GENERAL INFORMATION:  
APPLICANT: Shi et al.  
TITLE OF INVENTION: Cardiotrophin-Like Cytokine  
FILE REFERENCE: PF385D1C1  
CURRENT APPLICATION NUMBER: US/10/212,793  
CURRENT FILING DATE: 2002-08-07  
PRIOR APPLICATION NUMBER: US 09/438,299  
PRIOR FILING DATE: 1999-11-12  
PRIOR APPLICATION NUMBER: US 09/106,182  
PRIOR FILING DATE: 1998-06-29  
PRIOR APPLICATION NUMBER: US 60/051,311  
PRIOR FILING DATE: 1997-06-30  
NUMBER OF SEQ ID NOS: 24  
SEQ ID NO 2  
LENGTH: 225  
TYPE: PRT  
ORGANISM: homo sapiens  
FEATURE:  
NAME/KEY: signal  
LOCATION: (-27)..(-1)  
FEATURE:  
NAME/KEY: peptide  
LOCATION: (1)..(198)  
US-10-212-793-2

Query Match 100.0%; Score 1226; DB 15; Length 225;  
Best Local Similarity 100.0%; Pred. No. 5.9e-115;  
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLRAGDSWGMACLCCTVLMHLPAPVAPALNRGTDPGPGPSIOKTYDLTRYLEHQLRSLSLGT 60  
Db 1 MDLRAGDSWGMACLCCTVLMHLPAPVAPALNRGTDPGPGPSIOKTYDLTRYLEHQLRSLSLGT 60  
QY 61 YLNYGPPNEPDEFPRLGAETLPRAVYDLEWMSLNDKRLRNTONYEAYSHLCTYLRGL 120  
Db 61 YLNYGPPNEPDEFPRLGAETLPRAVYDLEWMSLNDKRLRNTONYEAYSHLCTYLRGL 120  
QY 121 NROATAEIRSLAHFCTSLQGLGSIAGVMAALGYPLPQPLGTEPTWTPGPAHSDFLQ 180  
Db 121 NROATAEIRSLAHFCTSLQGLGSIAGVMAALGYPLPQPLGTEPTWTPGPAHSDFLQ 180  
QY 181 KMDDFWLKELOTWLMRSKADFNRLKKKQPPAAAVTTLHGAHGF 225  
Db 181 KMDDFWLKELOTWLMRSKADFNRLKKKQPPAAAVTTLHGAHGF 225

RESULT 3  
US-09-931-704-5  
Sequence 5, Application US/09911704  
Patent No. US20020041873A1  
GENERAL INFORMATION:  
APPLICANT: Senaldi, Giorgio  
TITLE OF INVENTION: Methods and Compositions for Treating IGE-Related Disease Using N  
FILE REFERENCE: A-695  
CURRENT APPLICATION NUMBER: US/09/931,704  
CURRENT FILING DATE: 2001-08-16  
PRIOR APPLICATION NUMBER: US 60/226,436  
PRIOR FILING DATE: 2000-08-18  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 5  
LENGTH: 225  
TYPE: PRT  
ORGANISM: Murine

US-09-931-704-5

Query Match 97.3%; Score 1193; DB 9; Length 225;  
Best Local Similarity 96.9%; Pred. No. 1.2e-111;  
Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDLRAGDSWGMACLCCTVLMHLPAPVAPALNRGTDPGPGPSIOKTYDLTRYLEHQLRSLSLGT 60  
Db 1 MDLRAGDSWGMACLCCTVLMHLPAPVAPALNRGTDPGPGPSIOKTYDLTRYLEHQLRSLSLGT 60  
QY 61 YLNYGPPNEPDEFPRLGAETLPRAVYDLEWMSLNDKRLRNTONYEAYSHLCTYLRGL 120  
Db 61 YLNYGPPNEPDEFPRLGAETLPRAVYDLEWMSLNDKRLRNTONYEAYSHLCTYLRGL 120  
QY 121 NROATAEIRSLAHFCTSLQGLGSIAGVMAALGYPLPQPLGTEPTWTPGPAHSDFLQ 180  
Db 121 NROATAEIRSLAHFCTSLQGLGSIAGVMAALGYPLPQPLGTEPTWTPGPAHSDFLQ 180  
QY 181 KMDDFWLKELOTWLMRSKADFNRLKKKQPPAAAVTTLHGAHGF 225  
Db 181 KMDDFWLKELOTWLMRSKADFNRLKKKQPPAAAVTTLHGAHGF 225

RESULT 4  
US-09-864-761-40014  
Sequence 40014, Application US/09864761  
Patent No. US20020048763A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharon G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
APPLICANT: Chen, Wensheng  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
FILE REFERENCE: Aeomica-X-1  
CURRENT APPLICATION NUMBER: US/09/864,761  
CURRENT FILING DATE: 2001-05-23  
PRIOR APPLICATION NUMBER: US 60/180,312  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: US 09/632,366  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: GB 24263.6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00662  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00661  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00670  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: US 60/234,687  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: US 09/608,408  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 09/774,203  
PRIOR FILING DATE: 2001-01-29







[illegible]

```

RESULT 10
US-09-791-497-8
Sequence 8, Application US/09791497
Publication No. US20030008343A1
GENERAL INFORMATION:
APPLICANT: Timans, Jacqueline C.
APPLICANT: Kastelein, Robert A.
APPLICANT: Bazan, J. Fernando
APPLICANT: Pelanz, Stefan
TITLE OF INVENTION: Mammalian Cytokines; Related Reagents
FILE REFERENCE: DX0104042
CURRENT APPLICATION NUMBER: US/09/791,497
CURRENT FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: 09/627,697
PRIOR FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: 60/146,581
PRIOR FILING DATE: 1999-07-30
PRIOR APPLICATION NUMBER: 60/147,763
PRIOR FILING DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 243
TYPE: prt
ORGANISM: primate; surmised Homo sapiens
US-09-791-497-8

```

Query Match	7.9%	Score 96.5	DB 11	length 243
Best Local Similarity	23.7%	pred. NO. 0.21		
Matches	58	Conservative	104	Indels 57
				Gaps 9

```

1      RESULT 11
2      US-10-000-776-6
3      Sequence 6, Application US/10000776
4      Publication No. US20020164609A1
5      GENERAL INFORMATION:
6      APPLICANT: Timans, Jacqueline C.
7      APPLICANT: Pfanz, J. H.
8      APPLICANT: Kastelein, Robert A.
9      APPLICANT: Bazan, Jose F.
10     APPLICANT: Rennick, Donna
11     APPLICANT: de Waal Malefyt, Rene
12     APPLICANT: Cheung, Jeanne
13     TITLE OF INVENTION: MAMMALIAN CYTOKINES; RELATED REAGENTS
14     FILE REFERENCE: DX0104063
15     CURRENT APPLICATION NUMBER: US/10/000,776
16     CURRENT FILING DATE: 2001-11-30
17     PRIOR APPLICATION NUMBER: 09/791,497
18     PRIOR FILING DATE: 2001-02-22
19     PRIOR APPLICATION NUMBER: 09/627,897
20     PRIOR FILING DATE: 2000-07-27
21     PRIOR APPLICATION NUMBER: 60/146,581
22     PRIOR FILING DATE: 1999-07-30
23     PRIOR APPLICATION NUMBER: 60/147,763
24     PRIOR FILING DATE: 1999-08-06
25     NUMBER OF SEQ ID NOS: 13
26     SOFTWARE: PatentIn version 3.1
27     SEQ ID NO 6
28     LENGTH: 243
29     TYPE: PRT
30     ORGANISM: Homo sapiens
31     US-10-000-776-6

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Query Match	7.9%	Score 96.5	DB 14	Length 243
Best Local Similarity	23.7%	Pred. No. 0.21		
Matches 58	Conservative 26	Mismatches 104	Indels 57	Gaps 9

US-10-156-761-11445  
Sequence 11445, Application US/10156761  
Publication No. US20030119018A1  
GENERAL INFORMATION:  
APPLICANT: OMURA, SATOSHI  
APPLICANT: IKEDA, HARUO  
APPLICANT: ISHIKAWA, JUN  
APPLICANT: HORIKAWA, HIROSHI  
APPLICANT: SHIBA, TADAYOSHI  
APPLICANT: SAKAKI, YOSHIYUKI  
APPLICANT: HATTORI, MASAHIRA  
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDEST  
FILE REFERENCE: 249-262  
CURRENT APPLICATION NUMBER: US/10/156,761  
CURRENT FILING DATE: 2002-05-29

PRIOR APPLICATION NUMBER: JP 2001-204089  
PRIOR FILING DATE: 2001-05-30  
PRIOR APPLICATION NUMBER: JP 2001-272697  
PRIOR FILING DATE: 2001-08-02  
NUMBER OF SEQ ID NOS: 15109  
SEQ ID NO 11445  
LENGTH: 860  
TYPE: PRT  
ORGANISM: Streptomyces avermitilis  
US-10-156-761-11445

Query Match 7.5%; Score 92.5; DB 15; Length 860;  
Best Local Similarity 27.2%; Pred. No. 2.7;  
Matches 56; Conservative 22; Mismatches 101; Indels 27; Gaps 9;

QY 5 AGDSMGLACTCTVL--WLPVAPLNRITGDPG-----PGSICKTIDTRY 49  
DB 288 AQAATYALATVBEELLDWH--EGGPAVLKAGLSVRDLKRTAVADVPEPTAPWVELT-Y 345  
QY 50 LEHOLSLAGTYLNYLGPPFNEPDENPRLGAEITLPRATVDELVRSINDKRLTONYEA 109  
DB 346 AAGLASDGEABERYAATPAYDEWLEL--AAERMSRLAT---AWLAATRTAGIVGGRNA 400  
QY 110 YSHLCYL-RGLNRQATLRLSLAHFCTSLQGLSIGAWMALGYPLPPLPCTEPT 168  
DB 401 KERTLSALGPGLDRSAASEVRRRYVALLDLPDGASAPASVYARLW--ERPLRGTHPS 458  
QY 169 WTP--GPAHSDFLQKMDDFWLKELQ 192  
DB 459 PSPSSAPSSDDLKTRRLAEWTLSEAE 484

## RESULT 13

US-09-901-540-3  
Sequence 3, Application US/09901540  
Patent No. US20020102622A1  
GENERAL INFORMATION:  
APPLICANT: Botstein, David  
APPLICANT: Goddard, Audrey  
APPLICANT: Lawrence, David A.  
APPLICANT: Pennica, Diane  
APPLICANT: Roy, Margaret A.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Cardiotrophin-1 Compositions and Methods for the  
FILE REFERENCE: P253302  
CURRENT APPLICATION NUMBER: US/09/901,540  
CURRENT FILING DATE: 2001-07-09  
PRIOR APPLICATION NUMBER: 09/648,258  
PRIOR FILING DATE: 2000-08-25  
PRIOR APPLICATION NUMBER: US 09/033,114  
PRIOR FILING DATE: 1998-03-02  
PRIOR APPLICATION NUMBER: US 08/733,850  
PRIOR FILING DATE: 1996-10-18  
PRIOR APPLICATION NUMBER: US 08/443,129  
PRIOR FILING DATE: 1995-05-17  
PRIOR APPLICATION NUMBER: US 08/286,304  
PRIOR FILING DATE: 1994-08-05  
PRIOR APPLICATION NUMBER: US 08/233,609  
PRIOR FILING DATE: 1994-04-25  
PRIOR APPLICATION NUMBER: US 60/113,296  
PRIOR FILING DATE: 1998-12-22  
NUMBER OF SEQ ID NOS: 6  
SEQ ID NO 3  
LENGTH: 201  
TYPE: PRT  
ORGANISM: Human  
US-09-901-540-3

Query Match 7.5%; Score 91.5; DB 10; Length 201;  
Best Local Similarity 25.9%; Pred. No. 0.51;  
Matches 45; Conservative 24; Mismatches 92; Indels 13; Gaps 5;

QY 40 IQKTYDLTRYLEHQRLSLAGTYLNYLGPPFNEPDENPRLGAEITLPRATVDELVRSIND 99  
DB 27 IRTQTHSLHLTKVAEQLOQVQGPFGILPSPRLPYAGL-SAPAPSHAGLPHE 85  
QY 100 KRLTONTEANSHLCYLRGLNRQA-----TAEIRSLAHFCTSLQGLSIGAWMAL 154  
DB 86 RLRL--DAAALAAPEPLLDVACRQAEINPPARILRLRLDPAARQARALGAVAEALMAL 143  
QY 155 GPEPLPPLPCTEPT---TWTPGPAHSDFLQKMDDFWLKELQTWLMRSKDFNRL 205  
DB 144 G--AANRGPRAEPPPATASASATGVPPAKVGLRVCGLYREWLSRTGDLGQL 195

## RESULT 14

US-09-896-856-8  
Sequence 8, Application US/09896856  
Patent No. US20020137189A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Joffre  
Chien, Kenneth  
King, Kathleen  
Pennica, Diane  
Wood, William  
TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESS: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/896,856  
FILING DATE: 29-Jun-2001  
CLASSIFICATION: <unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/733,850  
FILING DATE: 18-OCT-1996  
APPLICATION NUMBER: US 08/471,112  
FILING DATE: 06-JUN-1995  
APPLICATION NUMBER: 08/233,609  
FILING DATE: 25-APR-1994  
APPLICATION NUMBER: 08/286304  
FILING DATE: 05-AUG-1994  
APPLICATION NUMBER: 08/443129  
FILING DATE: 17-MAY-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Conley, Delidre L.  
REGISTRATION NUMBER: 36,487  
REFERENCE/DOCKET NUMBER: P0894P1Dc1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-2066  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 201 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 8:  
US-09-896-856-8

Query Match 7.5%; Score 91.5; DB 10; Length 201;  
Best Local Similarity 25.9%; Pred. No. 0.51;  
Matches 45; Conservative 24; Mismatches 92; Indels 13; Gaps 5;  
QY 40 IQKTYDLTRYLEHQRLSLAGTYLNYLGPPFNEPDENPRLGAEITLPRATVDELVRSIND 99

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Db      27 IROTHSLAHLTRVYAEQLQEVYQLOGDFGLPSFSPRLPVAGL-SAPAPSHAGLPVHE 85
Qy      100 KRLTONYEAIVSHLCTYGLNROAA-----TALRSLAHFCTSLQGLIGSIAGVMAAL 154
Db      86 RLRL--DAAALALPPLDAVCRQAELNPRAPRLRLRLEDARQAARALGAAVEALLAAL 143
Qy      155 GYPLPQPLPCTEP---TWTPGPAHSDPLQMDPFMLKELOTWLRSAKDFNRL 205
Db      144 G--AANRGPAEPAPATASASATGVFPAKVGLGRVCGLYREWLSRTEGDLGQL 195
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## RESULT 15

```
US-09-901-257-3
/ Sequence 3, Application US/09901257
/ Patent No. US20020146707A1.
/ GENERAL INFORMATION:
/ APPLICANT: Botstein, David
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Lawrence, David A.
/ APPLICANT: Pennica, Diane
/ APPLICANT: Roy, Margaret A.
/ APPLICANT: Wood, William I.
/ TITLE OF INVENTION: Cardiotrophin-1 Compositions and Methods for the
/ FILE REFERENCE: P2533D3
/ CURRENT APPLICATION NUMBER: US/09/901,257
/ CURRENT FILING DATE: 2001-07-09
/ PRIOR APPLICATION NUMBER: 09/548,252
/ PRIOR FILING DATE: 2000-08-25
/ PRIOR APPLICATION NUMBER: US 09/033,114
/ PRIOR FILING DATE: 1998-03-02
/ PRIOR APPLICATION NUMBER: US 08/733,850
/ PRIOR FILING DATE: 1996-10-18
/ PRIOR APPLICATION NUMBER: US 08/443,129
/ PRIOR FILING DATE: 1995-05-17
/ PRIOR APPLICATION NUMBER: US 08/286,304
/ PRIOR FILING DATE: 1994-08-05
/ PRIOR APPLICATION NUMBER: US 08/233,609
/ PRIOR FILING DATE: 1994-04-25
/ PRIOR APPLICATION NUMBER: US 60/113,296
/ PRIOR FILING DATE: 1998-12-22
/ NUMBER OF SEQ ID NOS: 6
/ SEQ ID NO 3
/ LENGTH: 201
/ TYPE: PRT
/ ORGANISM: Human
US-09-901-257-3
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Query Match      7.5%; Score 91.5; DB 10; Length 201;
Best Local Similarity 25.9%; Pred. No. 0.51;
Matches 45; Conservative 24; Mismatches 92; Indels 13; Gaps 5;

Qy      40 IOKTYDLTRVLEHQLSLAGTYLVYLGPPNEBDPNPRLGAETLPRATVDLEVMRSIND 99
Db      27 IROTHSLAHLTRVYAEQLQEVYQLOGDFGLPSFSPRLPVAGL-SAPAPSHAGLPVHE 85
Qy      100 KRLTONYEAIVSHLCTYGLNROAA-----TALRSLAHFCTSLQGLIGSIAGVMAAL 154
Db      86 RLRL--DAAALALPPLDAVCRQAELNPRAPRLRLRLEDARQAARALGAAVEALLAAL 143
Qy      155 GYPLPQPLPCTEP---TWTPGPAHSDPLQMDPFMLKELOTWLRSAKDFNRL 205
Db      144 G--AANRGPAEPAPATASASATGVFPAKVGLGRVCGLYREWLSRTEGDLGQL 195
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Search completed: February 9, 2004, 06:26:16  
Job time : 34 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: February 9, 2004, 06:15:41; Search time 15 Seconds

(without alignments)  
634,663 Million cell updates/sec

Title: US-09-931-704-2

Perfect score: 1226  
Sequence: 1 MDLRAGDSWGMALCLCTVLM.....KKKMQPPAAAVTLHGAGHF 225

Scoring table:

BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

Issued Patents AA:\*  
1: /cgn2\_6/prodata/1/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/prodata/1/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/prodata/1/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/prodata/1/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/prodata/1/1aa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/prodata/1/1aa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1226	100.0	225	1	US-08-792-019B-2
2	1226	100.0	225	3	US-09-106-182-2
3	1226	100.0	225	3	US-08-988-819-2
4	1226	100.0	225	3	US-09-016-534-2
5	1193	97.3	225	1	US-08-792-019B-5
6	1193	97.3	225	3	US-08-988-819-5
7	1193	97.3	225	3	US-09-016-534-5
8	124.5	10.2	203	3	US-09-106-182-3
9	118.5	9.7	203	1	US-08-233-609-3
10	118.5	9.7	203	1	US-08-444-083-3
11	118.5	9.7	203	1	US-08-286-304-3
12	118.5	9.7	203	1	US-08-442-745-3
13	118.5	9.7	203	1	US-08-443-129-3
14	118.5	9.7	203	1	US-08-443-952-3
15	118.5	9.7	203	1	US-08-443-130-3
16	118.5	9.7	203	3	US-08-898-911-3
17	118.5	9.7	203	5	PCT-US95-04467-3
18	91.5	7.5	201	1	US-08-444-083-8
19	91.5	7.5	201	1	US-08-286-304-8
20	91.5	7.5	201	1	US-08-442-745-8
21	91.5	7.5	201	1	US-08-443-129-8
22	91.5	7.5	201	1	US-08-443-952-8
23	91.5	7.5	201	1	US-08-443-130-8
24	91.5	7.5	201	1	US-08-792-019B-11
25	91.5	7.5	201	3	US-09-106-182-4
26	91.5	7.5	201	3	US-08-988-819-11
27	91.5	7.5	201	3	US-08-898-911-8

28	91.5	7.5	201	3	US-09-016-534-11	Sequence 11, App1
29	91.5	7.5	201	4	US-09-648-183-3	Sequence 3, App1
30	91.5	7.5	201	5	PCT-US95-04467-8	Sequence 6, App1
31	91.5	7.5	1182	4	US-09-287-354-6	Sequence 5, App1
32	91	7.4	195	1	US-07-959-284-5	Sequence 5, App1
33	91	7.4	195	2	US-08-308-736A-5	Sequence 5, App1
34	91	7.4	195	4	US-08-645-107A-5	Sequence 5, App1
35	91	7.4	195	4	US-09-197-349-5	Sequence 5, App1
36	91	7.4	195	4	US-09-031-692-5	Sequence 5, App1
37	91	7.4	195	5	PCT-US92-08258-2	Sequence 2, App1
38	91	7.4	195	5	PCT-US93-09649A-5	Sequence 2, App1
39	91	7.4	195	5	PCT-US93-09649-5	Sequence 5, App1
40	89	7.3	737	4	US-09-252-991A-22539	Sequence 22539, A
41	87.5	7.1	1207	4	US-09-287-354-5	Sequence 5, App1
42	85.5	7.0	560	2	US-08-756-317-11	Sequence 11, App1
43	84.5	6.9	426	4	US-09-252-991A-29288	Sequence 29288, A
44	84	6.9	200	3	US-08-949-155-4	Sequence 4, App1
45	84	6.9	200	4	US-09-819-964-4	Sequence 4, App1

## ALIGNMENTS

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RESULT 1
US-08-792-019B-2
; Sequence 2, Application US/08792019B
; Patent No. 5741772
; GENERAL INFORMATION:
; APPLICANT: CHANG, MING-SHI
; TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC.
; STREET: 1840 DEHAVILLAND DRIVE
; CITY: THOUSAND OAKS
; STATE: CA
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/792,019B
; FILING DATE: 03-FEB-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: COOK, ROBERT R.
; REGISTRATION NUMBER: 31,602
; REFERENCE/DOCKET NUMBER: A-442
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 225 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-792-019B-2

Query Match      100.0%; Score 1226; DB 1; Length 225;
Best Local Similarity 100.0%; Pred. No. 2,2e-129;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MDLRAGDSWGMALCLCTVLMHLPALVLRNRTGDPGSPISIOKTYDLTRYLHQSLAGT 60
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DB      1 MDLRAGDSWGMALCLCTVLMHLPALVLRNRTGDPGSPISIOKTYDLTRYLHQSLAGT 60
      |||||||
QY      61 YNLYGPPNEDNPPRLGATLRLRAYTDLVWMSLNDKRLTLTONYEVSHLCTYKGL 120
      |||||||
DB      61 YNLYGPPNEDNPPRLGATLRLRAYTDLVWMSLNDKRLTLTONYEVSHLCTYKGL 120
      |||||||
QY      121 NQQAATVLRRLRSLAFTSLQGLSIGVMAALGYPLQPLRGTEPTWTPPAHSDFLO 180
      |||||||
```

Db 121 NROAATAEIRSRSLAHFCTSLQGLGSIAGVMAALGYPLPGTEPTWTPGPAHSDFLQ 180  
QY 181 KMDDFWLKELQTLWLRSAKDFNRLKKKQPPAAAVTLHLGAHGF 225  
Db 181 KMDDFWLKELQTLWLRSAKDFNRLKKKQPPAAAVTLHLGAHGF 225

## RESULT 2

US-09-106-182-2  
Sequence 2, Application US/09106182  
Patent No. 6046035  
GENERAL INFORMATION:  
APPLICANT: Shi, Yangu  
TITLE OF INVENTION: Cardiotrophin-Like Cytokine  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc  
STREET: 9410 Key West Ave  
CITY: Rockville  
STATE: MD  
COUNTRY: US  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/106,182  
FILING DATE: Herewith  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 60/051,053  
FILING DATE: 30-JUN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Brookes, A. Anders  
REGISTRATION NUMBER: 36,373  
REFERENCE/DOCKET NUMBER: PF385  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-309-8504  
TELEFAX: 301-309-8439  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 225 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-106-182-2

Query Match 100.0%; Score 1226; DB 3; Length 225;  
Best Local Similarity 100.0%; Pred. No. 2.2e-129; Indels 0; Gaps 0;  
Matches 225; Conservative 0; Mismatches 0;

QY 1 MDLRAGDSWGMACICTVLMHLPAVPALNRTGDPGPGPSIOKTYDLTRYLHQLSLAGT 60  
Db 1 MDLRAGDSWGMACICTVLMHLPAVPALNRTGDPGPGPSIOKTYDLTRYLHQLSLAGT 60  
QY 61 YLNYIGPPNEPDENPPRLGAETLPRATVDLEWRSINDKRLTONYEAYSHLLCYLRGL 120  
Db 61 YLNYIGPPNEPDENPPRLGAETLPRATVDLEWRSINDKRLTONYEAYSHLLCYLRGL 120  
QY 121 NROAATAEIRSRSLAHFCTSLQGLGSIAGVMAALGYPLPGTEPTWTPGPAHSDFLQ 180  
Db 121 NROAATAEIRSRSLAHFCTSLQGLGSIAGVMAALGYPLPGTEPTWTPGPAHSDFLQ 180  
QY 181 KMDDFWLKELQTLWLRSAKDFNRLKKKQPPAAAVTLHLGAHGF 225  
Db 181 KMDDFWLKELQTLWLRSAKDFNRLKKKQPPAAAVTLHLGAHGF 225

## RESULT 3

US-08-988-819-2

Sequence 2, Application US/08988819  
Patent No. 6054294  
GENERAL INFORMATION:  
APPLICANT: CHANG, MING-SHI  
TITLE OF INVENTION: NEUROTROPHIC FACTOR NNT-1  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: AMGEN INC.  
STREET: ONE AMGEN CENTER DRIVE  
CITY: THOUSAND OAKS  
STATE: CA  
COUNTRY: USA  
ZIP: 91320  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/988,819  
FILING DATE: 12-DEC-1997  
CLASSIFICATION: 536  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/792,019  
FILING DATE: 03-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: COOK, ROBERT R.  
REGISTRATION NUMBER: 31,602  
REFERENCE/DOCKET NUMBER: A-442A  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 225 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-988-819-2

Query Match 100.0%; Score 1226; DB 3; Length 225;  
Best Local Similarity 100.0%; Pred. No. 2.2e-129; Indels 0; Gaps 0;  
Matches 225; Conservative 0; Mismatches 0;

QY 1 MDLRAGDSWGMACICTVLMHLPAVPALNRTGDPGPGPSIOKTYDLTRYLHQLSLAGT 60  
Db 1 MDLRAGDSWGMACICTVLMHLPAVPALNRTGDPGPGPSIOKTYDLTRYLHQLSLAGT 60  
QY 61 YLNYIGPPNEPDENPPRLGAETLPRATVDLEWRSINDKRLTONYEAYSHLLCYLRGL 120  
Db 61 YLNYIGPPNEPDENPPRLGAETLPRATVDLEWRSINDKRLTONYEAYSHLLCYLRGL 120  
QY 121 NROAATAEIRSRSLAHFCTSLQGLGSIAGVMAALGYPLPGTEPTWTPGPAHSDFLQ 180  
Db 121 NROAATAEIRSRSLAHFCTSLQGLGSIAGVMAALGYPLPGTEPTWTPGPAHSDFLQ 180  
QY 181 KMDDFWLKELQTLWLRSAKDFNRLKKKQPPAAAVTLHLGAHGF 225  
Db 181 KMDDFWLKELQTLWLRSAKDFNRLKKKQPPAAAVTLHLGAHGF 225

## RESULT 4

US-09-016-534-2  
Sequence 2, Application US/09016534  
Patent No. 6143874  
GENERAL INFORMATION:  
APPLICANT: CHANG, MING-SHI  
APPLICANT: ELIOTT, GARY S.  
APPLICANT: SARMIENTO, ULLA  
APPLICANT: SENALDI, GIORGIO  
TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: AMGEN INC.  
STREET: ONE AMGEN CENTER  
CITY: THOUSAND OAKS

STATE: CA  
COUNTRY: USA  
ZIP: 91320  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/016,534  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/792,019  
FILING DATE: 03-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: COOK, ROBERT R.  
REGISTRATION NUMBER: 31,602  
REFERENCE/DOCKET NUMBER: A-442B  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 225 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-016-534-2

Query Match 100.0%; Score 1226; DB 3; Length 225;  
Best Local Similarity 100.0%; Pred. No. 2,2e-129;  
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLRAGDSWGMGLACTCTVLMHLPALNRTGDPGPGPSIQKTYDLTRYLEHQLRSAGT 60  
DB 1 MDLRAGDSWGMGLACTCTVLMHLPALNRTGDPGPGPSIQKTYDLTRYLEHQLRSAGT 60  
QY 61 YLNYLGPPNEPDPNPRIGAEITLPATVDLEWRSINDRLTONYEAVSHLLCYLRGL 120  
DB 61 YLNYLGPPNEPDPNPRIGAEITLPATVDLEWRSINDRLTONYEAVSHLLCYLRGL 120  
QY 121 NRQAATAEIRSLAHFCTSLQGLSGIAGVMALGYPLPQPLPGTEPTWPGPAHSDFLQ 180  
DB 121 NRQAATAEIRSLAHFCTSLQGLSGIAGVMALGYPLPQPLPGTEPTWPGPAHSDFLQ 180  
QY 181 KMDDFWLKELOTWLMRSKDPNRLKKKQPPAAAVTTLHGAGF 225  
DB 181 KMDDFWLKELOTWLMRSKDPNRLKKKQPPAAAVTTLHGAGF 225

RESULT 5  
US-08-792-019B-5  
Sequence 5, Application US/08792019B  
Patent No. 5741772  
GENERAL INFORMATION:  
APPLICANT: CHANG, MING-SHI  
TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: AMGEN INC.  
STREET: 1840 DEHAVILLAND DRIVE  
CITY: THOUSAND OAKS  
STATE: CA  
COUNTRY: USA  
ZIP: 91320  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/792,019B  
FILING DATE: 03-FEB-1997  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:

NAME: COOK, ROBERT R.  
REGISTRATION NUMBER: 31,602  
REFERENCE/DOCKET NUMBER: A-442  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 225 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-792-019B-5

Query Match 97.3%; Score 1193; DB 1; Length 225;  
Best Local Similarity 96.9%; Pred. No. 1.1e-125;  
Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDLRAGDSWGMGLACTCTVLMHLPALNRTGDPGPGPSIQKTYDLTRYLEHQLRSAGT 60  
DB 1 MDLRAGDSWGMGLACTCTVLMHLPALNRTGDPGPGPSIQKTYDLTRYLEHQLRSAGT 60  
QY 61 YLNYLGPPNEPDPNPRIGAEITLPATVDLEWRSINDRLTONYEAVSHLLCYLRGL 120  
DB 61 YLNYLGPPNEPDPNPRIGAEITLPATVDLEWRSINDRLTONYEAVSHLLCYLRGL 120  
QY 121 NRQAATAEIRSLAHFCTSLQGLSGIAGVMALGYPLPQPLPGTEPTWPGPAHSDFLQ 180  
DB 121 NRQAATAEIRSLAHFCTSLQGLSGIAGVMALGYPLPQPLPGTEPTWPGPAHSDFLQ 180  
QY 181 KMDDFWLKELOTWLMRSKDPNRLKKKQPPAAAVTTLHGAGF 225  
DB 181 KMDDFWLKELOTWLMRSKDPNRLKKKQPPAAAVTTLHGAGF 225

RESULT 6  
US-08-988-819-5  
Sequence 5, Application US/08988819  
Patent No. 6054294  
GENERAL INFORMATION:  
APPLICANT: CHANG, MING-SHI  
TITLE OF INVENTION: NEUROTROPHIC FACTOR NNT-1  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: AMGEN INC.  
STREET: ONE AMGEN CENTER DRIVE  
CITY: THOUSAND OAKS  
STATE: CA  
COUNTRY: USA  
ZIP: 91320  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/988,819  
FILING DATE: 12-DEC-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/792,019  
FILING DATE: 03-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: COOK, ROBERT R.  
REGISTRATION NUMBER: 31,602  
REFERENCE/DOCKET NUMBER: A-442A  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 225 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-988-819-5  
Query Match 97.3%; Score 1193; DB 3; Length 225;  
Best Local Similarity 96.9%; Pred. No. 1.1e-125;

Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDLRAGDSWGMCLACTVLMHLPAVPALNRGTDPGPGPSIQKTYDLTRYLHQLSLAGT 60  
DB 1 MDLRAGDSWGMCLACTVLMHLPAVPALNRGTDPGPGPSIQKTYDLTRYLHQLSLAGT 60

QY 61 YINYIGPPNEPDNPRLGAETLPRATVDLEWRSINDKRLTONYEAYSHLLCYLRGL 120  
DB 61 YINYIGPPNEPDNPRLGAETLPRATVDLEWRSINDKRLTONYEAYSHLLCYLRGL 120

QY 121 NQOATAEIRRSIAHFTCSLQGLSGIAGVMAALGYPLQPLPGTEPTWPGPAHSDFLQ 180  
DB 121 NQOATAEIRRSIAHFTCSLQGLSGIAGVMAALGYPLQPLPGTEPTWPGPAHSDFLQ 180

QY 181 KMDDFWLKELQTLWLRSAKDFNRLKKKQOPAAAVTTLHGAHGF 225  
DB 181 KMDDFWLKELQTLWLRSAKDFNRLKKKQOPAAAVTTLHGAHGF 225

## RESULT 7

US-09-016-534-5  
; Sequence 5, Application US/09016534  
; Patent No. 6143874  
; GENERAL INFORMATION:  
; APPLICANT: CHANG, MING-SHI  
; APPLICANT: ELLIOTT, GARY S.  
; APPLICANT: SARMIENTO, ULLA  
; APPLICANT: SENALDI, GIORGIO  
; TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: AMGEN INC.  
; STREET: ONE AMGEN CENTER  
; CITY: THOUSAND OAKS  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 91320  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/016,534  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/792,019  
; FILING DATE: 03-FEB-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: COOK, ROBERT R.  
; REGISTRATION NUMBER: 31,602  
; REFERENCE/DOCKET NUMBER: A-442B  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 225 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-016-534-5

Query Match 97.3%; Score 1193; DB 3; Length 225;  
Best Local Similarity 96.9%; Pred. No. 1.1e-125;  
Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDLRAGDSWGMCLACTVLMHLPAVPALNRGTDPGPGPSIQKTYDLTRYLHQLSLAGT 60  
DB 1 MDLRAGDSWGMCLACTVLMHLPAVPALNRGTDPGPGPSIQKTYDLTRYLHQLSLAGT 60

QY 61 YINYIGPPNEPDNPRLGAETLPRATVDLEWRSINDKRLTONYEAYSHLLCYLRGL 120  
DB 61 YINYIGPPNEPDNPRLGAETLPRATVDLEWRSINDKRLTONYEAYSHLLCYLRGL 120

QY 121 NQOATAEIRRSIAHFTCSLQGLSGIAGVMAALGYPLQPLPGTEPTWPGPAHSDFLQ 180  
DB 121 NQOATAEIRRSIAHFTCSLQGLSGIAGVMAALGYPLQPLPGTEPTWPGPAHSDFLQ 180

QY 181 KMDDFWLKELQTLWLRSAKDFNRLKKKQOPAAAVTTLHGAHGF 225  
DB 181 KMDDFWLKELQTLWLRSAKDFNRLKKKQOPAAAVTTLHGAHGF 225

## RESULT 8

US-09-106-182-3  
; Sequence 3, Application US/09106182  
; Patent No. 6046035  
; GENERAL INFORMATION:  
; APPLICANT: Shi, Yangu  
; APPLICANT: Ruben, Steve  
; TITLE OF INVENTION: Cardiotrophin-Like Cytokine  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc  
; STREET: 9410 Key West Ave  
; CITY: Rockville  
; STATE: MD  
; COUNTRY: US  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/106,182  
; FILING DATE: Herewith  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/051,053  
; FILING DATE: 30-JUN-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brookes, A. Anders  
; REGISTRATION NUMBER: 36,373  
; REFERENCE/DOCKET NUMBER: PF385  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 301-309-8439  
; TELEFAX: 301-309-8439  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 203 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-106-182-3

Query Match 10.2%; Score 124.5; DB 3; Length 203;  
Best Local Similarity 28.1%; Pred. No. 6.7e-06;  
Matches 50; Conservative 24; Mismatches 85; Indels 19; Gaps 5;

QY 40 IQKTYDLTRYLHQLSLAGTYLNYLNGPPNEPDNPRL---GAEITLPRATVDLEWRS 96  
DB 27 IROTINILARLTLTKYADQLLEBYVOOGGEPFGLPGSPPLRPLAGISGPAHAGLPV--- 83

QY 97 LNDKRLTONYEAYSHLLCYLRGINROA-----TAELRSLAHFTCSLQGLSGIAGV 151  
DB 84 ---SERLRQDAALASALPALIDAVRRQAEINPPARLRLSLDPAARQVRLGAIVETVL 140

QY 152 AALGY----PLQPLPGTEPTWPGPAHSDFLQKMDDFWLKELQTLWLRSAKDFNRL 205  
DB 141 AALGAAGVPPEPV-AISALFTGNSAAGVSAVYLGLHVGGLGGEWVSRTEGDLGL 197

RESULT 9  
US-08-233-609-3  
; Sequence 3, Application US/08233609



Patent No. 5534615  
GENERAL INFORMATION:  
APPLICANT: Baker, Joffre  
APPLICANT: Chien, Kenneth  
APPLICANT: King, Kathleen  
APPLICANT: Pennica, Diane  
APPLICANT: Wood, William  
TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/33,609  
FILING DATE: 25-APR-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Hasak, Janet E.  
REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: 894  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-1896  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 203 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

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Query Match Similarity      9.7%; Score 118.5; DB 1; Length 203;  
Best Local Similarity     28.8%; Pred.No. 3,1e-05;  
Matches    51; Conservative   21; Mismatches    88; Indels   17; Gaps    5
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Oy 40 IOKTYDRLRYVEHOLRSAGTLYANTLGGPFENPDNPPL---GAETLPRAVDELVWRS 96  
|::||::||::||::||::||::||::||::||  
Db 27 IRCHNHLARLTKTAEQLLEEVQOOGEPFGI PGSPFRLLPLAGSGPAFSAGLPV--- 83  
|::||::||::||::||::||::||::||  
Oy 97 LNDKLRITONYEAVSHLCYLGRNGROA-----TAELRSLAHCTSIQIGLSIAGYM 151  
|::||::||::||::||::||::||::||  
Db 84 ---SERLGQAALASVLPALDDAYARRQAEINPRAPRLIRSLIEDAAQRVALGAAVERTYTL 140  
|::||::||::||::||::||::||::||  
Oy 152 AALGYPL--POPPECTEPT-WTPGFASHDFLOXMDFWMLKEIQWLMSAADFNRL 205  
|::||::||::||::||::||::||::||  
Db 141 AALGAARGPGGEPIVTATLFTANSTAGIFSAAKVGI GFHYCGIGEMVERSTEEDCOL 197  
|::||::||::||::||::||::||::||

RESULT 10  
US-08-444-083-3  
Sequence 3, Application US/08444083  
Patent No. 5571675  
GENERAL INFORMATION:  
Applicant: Baker, Joffre  
Applicant: Chien, Kenneth  
Applicant: King, Kathleen  
Applicant: Pennica, Diane  
Applicant: Wood, William  
TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESSES:

ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/444,083  
FILING DATE: 17-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/233609  
FILING DATE: 25-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/286304  
FILING DATE: 05-AUG-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: 894PIDS  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-8674  
TELEFAX: 415/953-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 203 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-444-083-3

[illegible]





US-08-443-130-3

Query Match 9.7%; Score 118.5; DB 1; Length 203;  
 Best Local Similarity 28.8%; Pred. No. 3,1e-05;  
 Matches 51; Conservative 21; Mismatches 88; Indels 17; Gaps 5;

Qy	40	IQKTYDLTRYLEHQRLSLAGTYINYLQPPNEPDPNPRL--GAETLPRAIVLEWRS	96
Db	27	IRQTHNLARLLTKYAEQLLEEVYQOQGEPPGLPGFSPRLPLAGLSGPAPSHAGLPV---	83
Qy	97	LNDKRLTONYEAYSHLCTLRGLNROA-----TAELRSLAHFCTSLQGLGSIAGYM	151
Db	84	---SERLRQDAAALSVLPALLDVARRQAEINPRAPRLRSLEDAARQYVALGAAVETVL	140
Qy	152	AALGYPL--POLPGTEPT-WTPGPAHSDFLQMDDFMLIKEIQTWLWRSKDFNRL	205
Db	141	AALGAARGRGPEPVTATLFTANSTAGIFSAYVGFHVGGLYGEWVSRTGDLGQL	197

Search completed: February 9, 2004, 06:25:00  
 Job time : 17 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compen Ltd.

OM protein - protein search, using sw model

Run on: February 9, 2004, 06:14:57 / Search time 10.5 Seconds

(without alignment)  
1007.715 Million cell updates/sec

Title: US-09-931-704-2

Perfect score: 1226

Sequence: 1 MDLRAGDSWGLACTLVLM.....KKKQPPAAAVTLHGAGHF 225

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	124.5	10.2	203	CTP1_RAT	063086 rattus nov
2	118.5	9.7	203	CTP1_MOUSE	060753 mus musculi
3	94	7.7	423	CST_MOUSE	093he4 m galactosy
4	93	7.6	619	NXFL_HUMAN	09ub9 homo sapien
5	91.5	7.5	201	CTP1_HUMAN	01619 homo sapien
6	91.5	7.5	1182	HAIR_MOUSE	061445 mus musculi
7	91	7.4	195	CNTF_CHICK	002011 gallus gall
8	89.5	7.3	1313	MIP1_SCHPO	P87141 schizosacch
9	87.5	7.1	1181	HAIR_RAT	P97609 rattus nov
10	86	7.0	1009	M2B2_HUMAN	09245 homo sapien
11	85.5	7.0	560	PHAC_PSEOL	P26496 pseudomnas
12	84	6.9	200	CNTF_PIG	002732 sus scrofa
13	83	6.8	452	TLR_DROME	P18102 drosophila
14	82.5	6.7	1189	HAIR_HUMAN	043593 homo sapien
15	82	6.7	724	P85B_BOVIN	P23726 bos taurus
16	81	6.6	291	YM32_MYCTU	010515 mycobacteri
17	81	6.6	618	NXFL_RAT	088884 rattus nov
18	80.5	6.6	294	HUPK_RHOCA	P30797 rhodobacter
19	80.5	6.6	870	BCA1_HUMAN	P56645 homo sapien
20	80.5	6.6	1473	NAL1_HUMAN	P9C600 homo sapien
21	80	6.5	200	CNTF_RAT	P20294 rattus nov
22	80	6.5	422	Y140_HUMAN	014153 homo sapien
23	80	6.5	2261	RRP2_KUMPM	P30929 mumps virus
24	79	6.4	552	MPF2_MOUSE	09wv34 mus musculi
25	79	6.4	1621	ALK_MOUSE	P97793 mus musculi
26	78.5	6.4	390	YL28_STRCO	P40181 streptomyce
27	78.5	6.4	1102	CARB_STRCO	09kxre streptomyce
28	78	6.4	3680	DMD_CANPA	097592 canis famli
29	77	6.3	586	UL64_HCMVA	P14727 human cytom
30	77	6.3	587	UL64_HCMVT	P14727 human cytom
31	76.5	6.2	571	ATKA_MYCTU	P96371 mycobacteri
32	76.5	6.2	572	SYM_AERPE	09yvy3 aeropyrum p
33	76.5	6.2	995	M2B2_PIG	028949 sus scrofa

34	76	6.2	296	1	RECO_ANASP	Q8ypl9 anabaena sp
35	76	6.2	1001	1	PTPX_MOUSE	P80560 mus musculi
36	76	6.2	1132	1	BAT3_HUMAN	P46379 homo sapien
37	75.5	6.2	830	1	VBP3_HUMAN	Q13488 h vacuolar
38	75	6.1	199	1	CNTF_RABIT	P14188 oryctolagus
39	75	6.1	315	1	YNEF_ECOLI	P76147 escherichia
40	75	6.1	343	1	DEPA_SYNY3	P73212 synchocyst
41	75	6.1	450	1	TLR_DROVI	O16845 drosophila
42	75	6.1	917	1	SVI_STRAU	P41972 straphylococ
43	75	6.1	1620	1	ALK_HUMAN	Q9um73 homo sapien
44	74.5	6.1	346	1	Y52Q_YEAST	P53259 saccharomyc
45	74.5	6.1	409	1	NER1_MOUSE	O35657 mus musculi

## ALIGNMENTS

RESULT 1	CTP1_RAT	STANDARD	PRT	203 AA
AC	063086:			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	15-JUL-1998 (Rel. 36, Last annotation update)			
DE	Cardiotrophin-1 (CT-1).			
GN	CTP1.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
NC	NCBI_TaxId=10116;			
RP	[1]			
RC	SEQUENCE FROM N.A.			
RX	STRAIN=WiStar; TISSUE=Heart;			
RA	MEDLINE=96193659; PubMed=8604995;			
RA	Isnikawa M., Salto Y., Miyamoto Y., Kuwahara K., Ogawa E.,			
RA	Nakagawa O., Harada M., Masuda I., Nakao K.;			
RT	"CDNA cloning of rat cardiotrophin-1 (CT-1): augmented expression of			
RT	CT-1 gene in ventricle of genetically hypertensive rats.";			
RL	Biochem. Biophys. Res. Commun. 219:377-381(1996).			
CC	- FUNCTION: INDUCES CARDIAC MYOCYTE HYPERTROPHY IN VITRO. BINDS TO			
CC	AND ACTIVATES THE LEUKEMIA INHIBITORY FACTOR RECEPTOR (LIF			
CC	RECEPTOR)/GP 130 RECEPTOR COMPLEX.			
CC	- SUBCELLULAR LOCATION: Secreted (by similarity).			
CC	- TISSUE SPECIFICITY: EXPRESSED IN THE VENTRICLE AND ATRIUM OF ADULT			
CC	RATS. ALSO DETECTED IN THE LUNG, KIDNEY, LIVER, SKELETAL MUSCLE,			
CC	STOMACH AND URINARY BLADDER. NOT DETECTED IN BRAIN, COLON, TESTIS,			
CC	SPLEEN OR THYMUS. OVEREXPRESSED IN THE VENTRICLES IN THE CASE OF			
CC	HYPERTENSION AND HYPERTROPHY.			
CC	- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.			
CC	-----			
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CC	or send an email to <a href="mailto:license@sib-sib.ch">license@sib-sib.ch</a> ).			
CC	-----			
DR	EMBL; D78591; BAA11427.1; -			
DR	PIR; JC4645; JC4645.			
KW	Cytokine.			
SQ	SEQUENCE 203 AA; 21439 MW; DFB8921A2FALC832 CRC64;			
QY	Query Match	10.2%;	Score 124.5;	DB 1; Length 203;
DB	Best Local Similarity	28.1%;	Pred. No. 0.00018;	
QY	Matches 50; Conservative 24; Mismatches 85; Indels 19; Gaps 5;			
QY	40 IOKYTDLRYLYEHQRLAGTYLNTGPPNEBPNPRL---GAEFLPRAVTDLEWRS 96			
DB	27 IROTHNLRLRLTKRADQLLEBYVOQGEPFGSLGSPRLPLAGSGAPSPAGLPV--- 83			
QY	97 LNDKRLTQNTYEAWSHLLCYLRGLNRQAA-----TABRRSLAHFCTSLQGLGSIAGV 151			

DB 84 ---SERLQDAALALPALDLAVRRQAELNPRAPRLRLSLIEDAPARQVAFALGAATVTL 140  
 QY 152 AALGX-----PLRQPLRGTEPTWTPGPAHSDFLQKMDDFWLKELQTWLMSAKDNRL 205  
 DB 141 AALGAAGAAGPVEPV-ATISALFTSNSAGVAFKAVGLHVCGLYGBWVRTEGDLGQL 197

RESULT 2  
 CTF1\_MOUSE STANDARD; PRT; 203 AA.  
 AC Q60753;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE Cardiotrophin-1 (CT-1).  
 GN CTF1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95166785; PubMed=7862649;  
 RA Penica D., King K.L., Shaw K.J., Luis E., Rullamas J., Luoh S.-M.,  
 RA Darbonne W.C., Knutson D.S., Yen R., Chien K.R., Baker J.B.,  
 RA Wood W.I.;  
 RT "Expression cloning of cardiotrophin 1, a cytokine that induces  
 RT cardiac myocyte hypertrophy";  
 RL Proc. Natl. Acad. Sci. U.S.A. 92:1142-1146(1995).  
 CC -1- FUNCTION: INDUCES CARDIAC MYOCYTE HYPERTROPHY IN VITRO. BINDS TO  
 CC AND ACTIVATES THE LEUKEMIA INHIBITORY FACTOR RECEPTOR (LIF  
 CC RECEPTOR)/GP 130 RECEPTOR COMPLEX.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART, SKELETAL MUSCLE,  
 CC LIVER, LUNG AND KIDNEY. LOWER LEVELS IN TESTIS AND BRAIN. NO  
 CC EXPRESSION IN SPLEEN.  
 CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.  
 CC -----  
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 CC -----  
 DR EMBL, U18366; AAC52173.1; -.  
 DR PIR, I49153; I49153.  
 DR MGD, MGI:105115; Ctf1.  
 KW Cytokine.  
 SQ SEQUENCE 203 AA; 21509 MW; 8B3D414A0B3B232F CRC64;

Query Match 9.7%; Score 118.5; DB 1; Length 203;  
 Best Local Similarity 28.8%; Pred. No. 0.00065;  
 Matches 51; Conservative 21; Mismatches 88; Indels 17; Gaps 5;

QY 40 IOKTDLRLRYLEHQRSLAGTYLNTVIGPPENPDENPRL---GAEFLPRAVDLEWRS 96  
 DB 27 IROHNLRLALLTKVAEQLEBYVQOQGFGLPGSPPLPLIAGLSGPAHAGLPV--- 83  
 QY 97 LNDKRLRLTQNEAVSHLLCYLRLNROA-----TAELRSLAHCTSLQGLGSIAGVM 151  
 DB 84 ---SRRLQDAALALSVLPALDLAVRRQAELNPRAPRLRLSLIEDAPARQVAFALGAATVTL 140  
 QY 152 AALGXPL---POPLRGTEPTWTPGPAHSDFLQKMDDFWLKELQTWLMSAKDNRL 205  
 DB 141 AALGAAGAAGPVEPVATLFTANSTAGIFSAKVLGFHVCGLYGBWVRTEGDLGQL 197

RESULT 3  
 CST\_MOUSE STANDARD; PRT; 423 AA.  
 AC Q9JHE4; Q9D8V6;

DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DE 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Galactosylceramide sulfoltransferase (EC 2.8.2.11) (GalCer  
 DE sulfoltransferase) (Cerebroside sulfoltransferase) (3')-  
 DE phosphadenosine-5'-phosphosulfate:GalCer sulfoltransferase).  
 DE (3'-phosphadenosine-5'-phosphosulfate:GalCer sulfoltransferase).  
 GN CST OR GCST.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.  
 RC TISSUE=Kidney.  
 RX MEDLINE=20193614; PubMed=10727929;  
 RA Hirahara Y., Tsuda M., Wada Y., Honke K.;  
 RT "CDNA cloning, genomic cloning, and tissue-specific regulation of  
 RT mouse cerebroside sulfoltransferase";  
 RL Eur. J. Biochem. 267:1909-1917(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Pancreas;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanka I.,  
 RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matcuo Y., Nikaido I., Pesole G., Quackenbush J.,  
 RA Schiml L.M., Staudli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarali R., Bash G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Guestinch S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombert P.,  
 RA Norone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Saeki H., Sato K., Schoenbach C., Seya T., Shibata C., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,  
 RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kontsuki S.,  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection";  
 RL Nature 409:685-690(2001).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Colon;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Alechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stappleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshitsuki S., Carninci P., Prange C.,  
 RA Rana S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Boeck S.A., McEwan P.J., McKernan K.J., Malek J.A., Gnatratte P.H.,  
 RA Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huijck S.W.,  
 RA Villalón D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Heltan E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska V., Smalins D.E.,  
 RA Schnerich A., Schein J.F., Jones S.J.M., Matra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [4]  
 RP FUNCTION.  
 RX MEDLINE=21927584; PubMed=11917099;  
 RA Honke K., Hirahara Y., Dupree J., Suzuki K., Popko B., Fukushima K.,  
 RA Fukushima J., Nagasawa T., Yoshida N., Wada Y., Taniguchi N.;

```

RT "Paranodal junction formation and spermatogenesis require
RL sulfoglycolipids."
CC Proc. Natl. Acad. Sci. U.S.A. 99:4227-4232(2002).
CC -1 FUNCTION: Catalyzes the sulfation of membrane glycolipid. Seems
CC to prefer beta-1-glycosides at the nonreducing terminal of sugar
CC chains attached to a lipid moiety. Catalyzes the synthesis of
CC HSO3-3'-galactosylceramide (sulfolipide), a major lipid component of
CC the myelin sheath and of HSO3-3-monogalactosyalkylacylglycerol
CC (hemolipid), present in spermatozoa. Also acts on
CC lactosylceramide, galactosyl 1-alkyl-2-sn-glycerol and galactosyl
CC diacylglycerol (in vitro).
CC CC CATALYTIC ACTIVITY: 3'-phosphoadenylylsulfate + a
CC galactosylceramide = adenosine 3',5'-bisphosphate +
CC galactosylceramide sulfate.
CC -1 CATALYTIC ACTIVITY: 3'-phosphadenylylsulfate +
CC monogalactosyalkylacylglycerol = adenosine 3',5'-bisphosphate +
CC monogalactosyalkylacylglycerol sulfate.
CC -1 PATHWAY: Sphingolipid and glycerolipid biosynthesis.
CC -1 SUBCELLULAR LOCATION: Type II membrane protein. Golgi membrane (By
CC bimilarity).
CC -1 TISSUE SPECIFICITY: Expressed in brain, testis, kidney, stomach,
CC small intestine, liver, and lung. Not detected in heart, skeletal
CC muscle, and spleen.
CC -1 MISCELLANEOUS: Mice homozygous for a null mutation of the GGT gene
CC display hindlimb weakness from week 6 of age and subsequently show
CC a pronounced tremor and progressive ataxia. Myelin vacuolation is
CC observed in the cerebellar white matter, diencephalon, brainstem
CC and spinal anterior column. Male mice were infertile due to a
CC blocked spermatogenesis.
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DR EMBL; AB032940; BAA93009.1; -
DR EMBL; AB032939; BAA93008.1; -
DR EMBL; AK007645; BAB25160.1; -
DR EMBL; BC026806; AAB26806.1; -
DR MGI; MGI:1858277; Gcat.
DR GO; GO:0016021; C:Integral to membrane; IC.
DR GO; GO:0001733; F:galactosylceramide sulfotransferase activity; IDA.
DR GO; GO:0006682; P:galactosylceramide biosynthesis; IDA.
DR GO; GO:0042553; P:myelination; IMP.
DR GO; GO:0007283; P:spermatogenesis; IMP.
KW Transferase; Transmembrane; Glycoprotein.
KW DOMAIN
FT FT 1 12 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 13 35 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT (POTENTIAL).
FT DOMAIN 36 423 LUMENAL, CATALYTIC (POTENTIAL).
FT CARBOHYD 66 N-LINKED (GLYCANC. . .) (POTENTIAL).
FT CARBOHYD 312 312 N-LINKED (GLYCNC. . .) (POTENTIAL).
FT CONFLICT 18 18 L -> P (IN REF. 2).
FT CONFLICT 263 263 R -> Q (IN REF. 2).
FT CONFLICT 271 271 E -> K (IN REF. 2).
FT CONFLICT 358 358 Q -> R (IN REF. 1).
FT CONFLICT 392 392 R -> G (IN REF. 2).
FT CONFLICT 398 398 I -> T (IN REF. 1).
FO SEQUENCE 423 AA; 48968 MW; FD54A1A71F4AE46 CRC64;

Query Match 7.7%; Score 94; DB 1; Length 423;
Best Local Similarity 22.7%; Pred. No. 0.31;
Matches 55; Conservative 23; Mismatches 60; Indels 104; Gaps 12

44 YDLTRYLSHOLSLAGTYLVN---GAPP-----FNPP----- 72
|||:::||:|||||
Db YDPSPYNMAYIRNLFLPDLGVDSISLDPASPRQGEIILVEVERPHVLVLOEYVDSEGLVLR 263
-----DENPPLGAETLEPRAT-----VDLEWRSINDKRLRITONVEA 109
|||||::|::|

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Db      266  ELICWDLDEVLVFKLNARSDSVPRLSGBELVRARAWMLDLVRLYRHFN--ASPMRKRYEA 332
Qy      110  YSHLLCYLGNLRQA-ATLDELRS---LAHFCTSLQGLSSIA-----GWMAA 155
Db      322  F-----GREMRAEVLEALQANHEHRHICIDGGCAVGAIAODSAMQFMCPLGIKSI 372
Qy      154  LGVPLQPLRGTEPTMTGEPASDPLQKMDPFMLIKELQ-----TWLRSKADF 205
Db      374  LGYNLKKSII-----GPOHEQLCRRM---LTPEIQYLSLDIGANLWTKMKPLRDF 420
Qy      203  NR 204
Db      421  LR 422

RESULT 4
NXFL_HUMAN
ID      NXFL_HUMAN      STANDARD;      PRT;      619 AA.
AC      Q9UBI9; Q99799; Q9UQL2;
DT      28-FEB-2003 (Rel. 41, Created)
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DT      15-SEP-2003 (Rel. 42, Last annotation update)
DE      Nuclear RNA export factor 1 (Tap associating protein) (Tip-associated
       protein) (mRNA export factor TAP).
GN      NXFL OR TAP.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
[1]
RP      SEQUENCE FROM N.A., AND MOTRAGENESIS.
RC      TISSUE=Cervical carcinoma;
RX      BRAUN I.C., Rohrbach E., Schmitz C., Izaurrealde E.;
RT      "TAP binds to the constitutive transport element (CTE) through a novel
RT      RNA-binding motif that is sufficient to promote CTE-dependent RNA
RT      export from the nucleus.";
RL      EMBO J. 18:1953-1965(1999).
[2]
RP      SEQUENCE FROM N.A.
RC      MEDLINE=99257272; PubMed=10323864;
RX      Kang Y., Cullen B.R.;
RT      "The human Tap protein is a nuclear mRNA export factor that contains
RT      novel RNA-binding and nucleocytoplasmic transport sequences.";
RL      Genes Dev. 13:1126-1139(1999).
[3]
RP      SEQUENCE FROM N.A.
RC      MEDLINE=99384238; PubMed=10454577;
RX      Beer U., Tan W., Zolotukhin A.S., Tabernero C., Hudson E.A.,
RT      Felber B.K.;
RT      "Identification of novel import and export signals of human TAP, the
RT      protein that binds to the constitutive transport element of the type
RT      II retrovirus mRNAs.";
RL      Mol. Cell. Biol. 19:6306-6317(1999).
[4]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Placenta;
RX      MEDLINE=22388257; PubMed=12477932;
RA      Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA      Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Schuler G.D.,
RA      Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.M., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA      Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA      Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA      Brownstein M.J., Uebli T.B., Toshiyuki S., Carrinci P., Prange C.,
RA      Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhany S.J.,
RA      Bosak S.A., Mcwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA      Villalon D.K., Murthy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Fehey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA      Whitting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,
RA      Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA      Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

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RA Butterfield Y.S.N., Krzywinecki M.I., Skalska U., Smalins D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marx M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 [5]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lung;  
 RA Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K.,  
 RA Nakajima Y., Mizuno T., Morinaga M., Tanigami A., Fujiwara T., Ono T.,  
 RA Yamada K., Fujii Y., Ozaki K., Hiro M., Ohmori Y., Ota T., Suzuki Y.,  
 RA Ohsagai T., Nishi T., Shibahara T., Tanaka T., Nakamura Y.,  
 RA "NEO human cDNA sequencing project";  
 RT Submitted (FEB-2000) to the EMBL/Genbank/DBD databases.  
 [6]  
 RP SEQUENCE OF 61-619 FROM N.A.  
 RC TISSUE=Lymphocytes;  
 RA MEDLINE=97318898; PubMed=9175835;  
 RA Yoon D.-W., Lee H., Seol W., Demaria M., Rosenzweig M., Jung J.U.;  
 RT "Tap: a novel cellular protein that interacts with tip of herpesvirus  
 RT salivari and induces lymphocyte aggregation.";  
 RL Immunity 6:571-582(1997).  
 [7]  
 RP FUNCTION.  
 RA MEDLINE=98325379; PubMed=9660949;  
 RA Grueter P., Taberner C., von Kobbe C., Schmitt C., Saavedra C.,  
 RA Bachl A., Wilm M., Felder B.K., Izaurralde E.;  
 RT "TAP, the human homolog of Mex67p, mediates CTE-dependent RNA export  
 RT from the nucleus.";  
 RL Mol. Cell 1:649-659(1998).  
 [8]  
 RP CHARACTERIZATION.  
 RA MEDLINE=21282872; PubMed=11259411;  
 RA Braun I.C., Herold A., Rode W., Conti E., Izaurralde E.;  
 RT "Overexpression of TAP/p15 heterodimers bypasses nuclear retention and  
 RT stimulates nuclear mRNA export.";  
 RL J. Biol. Chem. 276:20536-20543(2001).  
 [9]  
 RP CHARACTERIZATION.  
 RA MEDLINE=20132240; PubMed=1066806;  
 RA von Kobbe C., Kutay U., Wilm M., Gorlich D., Carmo-Fonseca M.,  
 RA Izaurralde E.;  
 RT "The C-terminal domain of TAP interacts with the nuclear pore complex  
 RT and promotes export of specific CTE-bearing RNA substrates.";  
 RL RNA 6:136-158(2000).  
 [10]  
 RP MUTAGENESIS.  
 RA MEDLINE=21151125; PubMed=11256625;  
 RA Suyama M., Doerks T., Braun I.C., Sattler M., Izaurralde E., Bork P.;  
 RT "Prediction of structural domains of TAP reveals details of its  
 RT interaction with p15 and nucleoporins.";  
 RL EMBO Rep. 1:53-58(2000).  
 [11]  
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 102-372.  
 RA MEDLINE=20514125; PubMed=11060011;  
 RA Liker E., Fernandez E., Izaurralde E., Conti E.;  
 RT "The structure of the mRNA export factor TAP reveals a cis arrangement  
 RT of a non-canonical RNP domain and an LRR domain.";  
 RL EMBO J. 19:5587-5598(2000).  
 [12]  
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF COMPLEX WITH NXT1, AND X-RAY  
 RP CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF COMPLEX WITH NXT1-FG-REPEAT.  
 RA MEDLINE=21468398; PubMed=11583626;  
 RA Fribourg S., Braun I.C., Izaurralde E., Conti E.;  
 RT "Structural basis for the recognition of a nucleoporin FG repeat by  
 RT the NTF2-like domain of the TAP/p15 mRNA nuclear export factor.";  
 RL Mol. Cell 8:645-656(2001).  
 [13]  
 RP STRUCTURE BY NMR OF 551-619, AND MUTAGENESIS OF PHE-617.  
 RA MEDLINE=21912422; PubMed=11875519;  
 RA Grant R.P., Hurt E., Neuhäus D., Stewart M.;

RT "Structure of the C-terminal FG-nucleoporin binding domain of  
 RT Tap/NXF1.";  
 RL Nat. Struct. Biol. 9:247-251(2002).  
 CC -1- FUNCTION: Involved in the nuclear export of mRNA species bearing  
 CC retroviral constitutive transport elements (CTE) and in the export  
 CC of mRNA from the nucleus to the cytoplasm.  
 CC -1- SUBUNIT: Interacts with NXT1, NXF2, E1B-AP5, RAE1, the REF  
 CC proteins and with several nucleoporins.  
 CC -1- SUBCELLULAR LOCATION: Nuclear; localized predominantly in the  
 CC nucleoplasm and at both the nucleoplasmic and cytoplasmic foci of  
 CC the nuclear pore complex. Shuttles between the nucleus and the  
 CC cytoplasm.  
 CC -1- TISSUE SPECIFICITY: Expressed ubiquitously.  
 CC -1- DOMAIN: The minimal CTE binding domain consists of an RNP-  
 CC type RNA binding domain (RBD) and leucine-rich repeats.  
 CC -1- DOMAIN: The nucleoporin binding domain consists of a NTF2-like  
 CC domain and a UBA-like domain. The NTF2 domain heterodimerizes with  
 CC NXT1 AND NXF2. The formation of NXF1/NXF1 heterodimers is required  
 CC for NXF1-mediated nuclear mRNA export. The UBA-like domain  
 CC mediates direct interactions with nucleoporin-FG-repeats and is  
 CC necessary and sufficient for localization of NXF1 to the nuclear  
 CC rim. The conserved loop 594-NMD-596 of the UBA domain has a  
 CC critical role in the interaction with nucleoporins.  
 CC -1- DOMAIN: The leucine-rich repeats and the NTF2-domain are  
 CC essential for the export of mRNA from the nucleus.  
 CC -1- MISCELLANEOUS: The RNA-binding domain is a non-canonical RNP-type  
 CC domain.  
 CC -1- SIMILARITY: BELONGS TO THE NXF FAMILY.  
 CC -1- SIMILARITY: Contains 4 leucine-rich (LRR) repeats.  
 CC -1- SIMILARITY: Contains 1 NTF2 domain.  
 CC -1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.  
 CC -1- SIMILARITY: Contains 1 UBA-like domain.  
 CC  
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 CC  
 CC EMBL; AJ132712; CAA10753.1; -  
 CC EMBL; AF112880; AAD39102.1; -  
 CC EMBL; AF126246; AAD20016.1; -  
 CC EMBL; BC004904; AAH04904.1; -  
 CC EMBL; AK027192; -, NOT\_ANNOTATED\_CDS.  
 CC EMBL; U80073; AAB81111.1; -  
 CC PDB; 1F01; 03-NOV-00.  
 CC PDB; 1FT8; 11-DEC-00.  
 CC PDB; 1KOH; 27-FEB-02.  
 CC PDB; 1KOO; 27-FEB-02.  
 CC PDB; 1OAT; 20-FEB-03.  
 CC GeneW; HGNC:8071; NXF1.  
 CC GK; Q9UBU9; -  
 CC MIM; 602647; -  
 CC InterPro; IPR001611; LRR.  
 CC InterPro; IPR003603; LRRcap.  
 CC InterPro; IPR002075; NTF2.  
 CC InterPro; IPR005637; TAP\_C.  
 CC PDB; 1G05; 28-MAR-02.  
 CC PDB; 1JUG; 18-DEC-02.  
 CC PDB; 1JN5; 23-JUL-01.  
 CC Pfam; PF00560; LRR; 1.  
 CC Pfam; PF02136; NTF2; 1.  
 CC Pfam; PF03943; TAP\_C; 1.  
 CC PRINTS; PR00019; LEURICHRP.  
 CC SMART; SM00446; LRRcap; 1.  
 CC PROSITE; PS0177; NTF2\_DOMAIN; 1.  
 CC Transport; mRNA transport; Nuclear protein; RNA-binding; Repeat;  
 CC Leucine-rich repeat; Multigene family; 3D-structure.  
 CC DOMAIN 119 RNA-BINDING (RRM).  
 FT

Query Match

7.6%; Score 93; DB 1; Length 619;



Best Local Similarity 24.7%; Pred. No. 0.63;  
Matches 60; Conservative 32; Mismatches 93; Indels 58; Gaps 13;

QY 5 AGDSWML-----ALCTVYMLPVPALNRTGDP-GGSPISQKTYDLT---RYLEHOL 54  
DB 400 SGGROGLDVAHDACCSTIPETPNPAPSSIAEYFKOSRNKKDKDPLRRLKHKR 459  
QY 55 RSLACTVLYLVGPPFNPFPNP--PRLGATLPRATVDL-----EYWRSLNDKLR-LTON 106  
DB 460 LNVV-AFLNEL--PKQHDVNSFVVDISAQSTLLCPNSVNGVKEKDGSRDRLAFRT 516  
QY 107 Y---EAYSHLLCYLRG-LNRQATALRLRSIAHFCSTLQGLGSIAGVMAALGYPLPOP 161  
DB 517 FIAPVAPNSGLCTVNDLFLVRNASSEIQRAFA-----MPAP 553

QY 162 LPCTETPTTPGPAHSDFLOK-----MDPFWLKEIQTWLM---RSKDPNRLKKKKMP 212  
DB 554 TPSSSVFPTLSPQOEWLQAFSTQSGWNLWESQKCLQDNNWDYTRSAQAFTHLKAGELP 613

QY 213 AAA 215  
DB 614 EVA 616

RESULT 5  
CTFL\_HUMAN STANDARD; PRT; 201 AA.  
AC Q16619;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Cardiotoxin-1 (CT-1).  
GN CTFL\_HUMAN  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Heart;  
RX MEDLINE=96429882; PubMed=8833032;  
RA Pennica D., Swanson T.A., Shaw K.J., Kuang W.-J., Gray C.T.,  
RA Beatty B.G., Wood W.I.;  
RT "Human cardiotoxin-1: protein and gene structure, biological and  
RT binding activities, and chromosomal localization.";  
RL Cytokine 8:183-189(1996).  
CC -1- FUNCTION: INDUCES CARDIAC MYOCYTE HYPERTROPHY IN VITRO. BINDS TO  
CC AND ACTIVATES THE LEUKEMIA INHIBITORY FACTOR RECEPTOR (LIF  
CC RECEPTOR)/gp 130 RECEPTOR COMPLEX.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART, SKELETAL MUSCLE,  
CC PROSTATE AND OVARY. LOWER LEVELS IN LUNG, KIDNEY, PANCREAS,  
CC THYMUS, TESTIS AND SMALL INTESTINE. LITTLE OR NO EXPRESSION IN  
CC BRAIN, PLACENTA, LIVER, SPLEEN, COLON OR PERIPHERAL BLOOD  
CC LEUKOCYTES.  
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.  
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CC -----  
CC EMBL, U43033; AAD12173.1; .  
CC EMBL, U43033; AAD12173.1; JOINED.  
CC EMBL, U43033; AAD12173.1; JOINED.  
CC EMBL, U43033; AAS85223.1; .  
CC PIR, G02312; G02312.  
CC Genew, HGNC:2499; CTFL.  
CC MIM, 600435; .  
CC GO, GO:0005576; C:extracellular; TAS.

DR GO; GO:0005146; F:leukemia inhibitory factor receptor ligand . . .; TAS.  
DR GO; GO:0008283; P:cell proliferation; TAS.  
DR GO; GO:0007267; P:cell-cell signaling; TAS.  
DR GO; GO:0007517; P:muscle development; TAS.  
DR GO; GO:0007399; P:neurogenesis; TAS.  
DR GO; GO:0008284; P:positive regulation of cell proliferation; TAS.  
KW Cytokine; Polymorphism.  
FT VARIANT 92 92 A -> T (IN dbSNP:2234933).  
FT FTID=VAR 014938.  
SQ SEQUENCE 201 AA, 21227 MW, 0235A7B5745F875F CRC64;

Query Match 7.5%; Score 91.5; DB 1; Length 201;  
Best Local Similarity 25.9%; Pred. No. 0.21;  
Matches 45; Conservative 24; Mismatches 92; Indels 13; Gaps 5;

QY 40 IOKTDLRYLEHOLRSLAGTYLANTLGPFPNPFPNPRLGATLPRATVDLEWRSLND 99  
DB 27 IROTSLHLLTKVAEQQLQEVYQIQGDPFGILPSPSPRLPVAGL-SAPAPSHAGLPVHE 85

QY 100 KRLTONYEAYSHLLCYLRGLNRQAA-----TAEFRSLAHFCSTLQGLGSIAGVMAAL 154  
DB 86 RLRL--DAALALAPPLDVAICRQASLNPPAPRLRLRLLEDARARALGAAYVALLAL 143

QY 155 GYPLPQPLPGTEP---TWTPGPAHSDFLOKDDFWLKEIQTWLWSAKDFNRL 205  
DB 144 G--AANRGPRAEPAPATASASATGVPAKVLGLRVCGLYRWMRLRTSGDLQGL 195

RESULT 6  
HAIR\_MOUSE STANDARD; PRT; 1182 AA.  
AC Q61645;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Hairless protein.  
GN HR.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BA1B/C; TISSUE=Skin;  
RX MEDLINE=94329587; PubMed=8052649;  
RA Cachon-Gonzalez M.B., Fenner S., Coffin J.M., Moran C., Best S.,  
RA Stoye J.P.;  
RT "Structure and expression of the hairless gene of mice.";  
RT Proc. Natl. Acad. Sci. U.S.A. 91:7717-7721(1994).  
RL -1- FUNCTION: MAY ACT AS A TRANSCRIPTION FACTOR THAT COULD ACT ON TO  
CC REGULATE ONE OF THE PHASES OF HAIR GROWTH.  
CC -1- SUBCELLULAR LOCATION: Nuclear.  
CC -1- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN BRAIN, HAIR  
CC FOLLICLES AND INTERFOLLICULAR EPIDERMIS. NO EXPRESSION IN  
CC DERMIS.  
CC -1- DISEAS: HR MUTATION PRODUCES A NUMBER OF PLEIOTROPIC EFFECTS  
CC INCLUDING STRUCTURAL ABNORMALITIES OF EPITHELIAL CELLS IN THE HAIR  
CC FOLLICLES, HAIR LOSS TOWARDS THE END OF THE FIRST HAIR GROWTH  
CC CYCLE, AND THE FAILURE OF SUBSEQUENT HAIR GROWTH CYCLES. OLDER  
CC MICE CARRYING AN HR MUTATION HAVE BEEN REPORTED TO POSSESS ALTERED  
CC RATIOS OF T-CELL-DEPENDENT B-CELL RESPONSES. MICE HOMOZYGOUS FOR  
CC HR MUTATION ARE UNIQUELY SENSITIVE TO UV AND CHEMICALLY INDUCED  
CC SKIN TUMORS.  
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CC EMBL, Z32675; CAA83587.1; .

DR PIR; 148378; 148378.  
 DR MGD; MGI:96223; hr.  
 DR InterPro; IPR003347; TF\_Jm1C.  
 DR Pfam; PF02373; Jm1C; 1.  
 DR SMART; SM00558; Jm1C; 1.  
 DR Zinc-finger; DNA-binding; Nuclear protein; Transcription regulation;  
 KW Metal-binding.  
 FT ZN FING 595 620 C6-TYPE.  
 FT ZN FING 535 540 POLY-GLY.  
 FT DOMAIN 1182 AA; 127182 MW; EFBDBE62ABE1B40 CRC64;  
 SQ SEQUENCE

Query Match 7.5%; Score 91.5; DB 1; Length 1182;  
 Best Local Similarity 23.7%; Pred. No. 2;  
 Matches 70; Conservative 25; Mismatches 99; Indels 101; Gaps 17;

3 LRAGSGWGLACTCTVLMPLPAVPALNRGDPG-----PPG----- 38  
 DB 813 LRAGS--GIRKGL-----SLPSPVTRTLPSPGALLMIOEPKRGFHLFOEHWGQGPV 865  
 QY 39 ---SIQKTYDLTRYLEHQRLSLAGTY--LNYLGGP-----FNEBDFNPPRLG 80  
 DB 866 LVSGIQTRLRLSLMGHEALGTGGVQVLTALGPPPTMLDSTAFWEGSHETRP----- 921  
 QY 81 AETLPRAVYDLEWWSLNDK-LRLTON-----YEAVSHLLCYL-RGLNRQAT 126  
 DB 922 --KLDEGSV-LIHRTLGDKDASRVQNLASSLPPEYCAHQGKMLASYLPGLTLHPL 978  
 QY 127 AEL-----RSLAHFCTSLQGLGSIAGWAAALGYLPPLPTEPTETTPGPAH 175  
 DB 979 POLMAAYGVNSHRHGLTKNLCLVEVSDLSILVHAEOI-----PPWY--RAQ 1024  
 QY 176 SDFLOKMD--DFWLKELOTWLMR--SAKDFNLKKKQP--PAAAVTLHLGAG 224  
 DB 1025 KDFLSGLDGEGLMSGSGSTYVHWFRADQRIIRFLQWCPAGATLEPARG 1079

RESULT 7  
 ID CNTF\_CHICK STANDARD; PRT; 195 AA.  
 AC 002011;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE Ciliary neurotrophic factor (CNTF) (Growth promoting activity) (GPA).  
 GN CNF OR GPA.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92304573; PubMed=1610564;  
 RA Leung D.W., Parent A.S., Cachianes G., Lee A.L., Nikolic K.,  
 RA Esch F., Coulombe J.N., Blacher R.W., Eckenstein F.P., Nishi R.;  
 RA "Cloning, expression during development, and evidence for release of  
 RA a trophic factor for ciliary ganglion neurons.",  
 RL Neuron 8:1045-1053(1992).  
 CC - FUNCTION: CNTF IS A SURVIVAL FACTOR FOR VARIOUS NEURONAL CELL  
 CC TYPES. SEEMS TO PREVENT THE DEGENERATION OF MOTOR AXONS AFTER  
 CC AXOTOMY.  
 CC - SUBCELLULAR LOCATION: Cytoplasmic.  
 CC - TISSUE SPECIFICITY: NERVOUS SYSTEM.  
 CC - SIMILARITY: BELONGS TO THE CNTF FAMILY.  
 CC -----  
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 CC -----

DR EMBL; M80827; AAA8784.1; --  
 DR PIR; J0680; J0680.  
 DR HSSP; P26441; ICNT.  
 DR InterPro; IPR000151; C11\_neuro\_factor.  
 DR Pfam; PF01110; CNTF; 1.  
 DR ProDom; PD011041; C11\_neuro\_factor; 1.  
 KW Growth factor; Neuron.  
 SQ SEQUENCE 195 AA; 21330 MW; FEA076949DB34ACS CRC64;  
 Query Match 7.4%; Score 91; DB 1; Length 195;  
 Best Local Similarity 27.3%; Pred. No. 0.22;  
 Matches 51; Conservative 21; Mismatches 83; Indels 32; Gaps 9;

46 LTRYEHQRLSLAGTYLNYLNGPPFNEPDPNPRGLAETLPRAVYDLEWWSLNDKLRQTQ 105  
 DB 23 LARKRSVTDLLDIYVRQG-----LDASISVAAYDGVPTAAV--EKMAEGTQRLD 75  
 QY 106 N---YEAVSHLLCYLRLNQA--ATAELRRSLA-----HFCTSLQGLGSIAGWAA 152  
 DB 76 NLAAVRAVRTLLAQMLEQRELLGDTDAELGPALAAMLQVSAPVYHLBEIL-----EL 130  
 QY 133 ALGYLPPLPTEPTETTPGPAH--SDFLOKMDDFWLKELOTWLMRSKADENRLKKKQP 211  
 DB 131 SRGAPAEH---GSEP---PAPPRSLTFQOKLGRVIRELAQMAVRSYVDLRQLSKGPG 184  
 QY 212 PAAAVTL 218  
 DB 185 SGALGL 191

RESULT 8  
 ID MIP1\_SCHPO STANDARD; PRT; 1313 AA.  
 AC P87141;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE WD-repeat protein m1p1 facilitates function of the meiotic  
 GN MIP1 OR SPAC57A7.11.  
 OS Schizosaccharomyces pombe (Fission yeast).  
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
 OC Schizosaccharomyces.  
 OX NCBI\_TaxID=4896;  
 RN [1]  
 RP SEQUENCE FROM N.A., FUNCTION, AND SUBCELLULAR LOCATION.  
 RX MEDLINE=20115869; PubMed=10648609;  
 RA Shinozaki-Yabana S., Watanabe Y., Yamamoto M.;  
 RA "Novel WD-repeat protein Mip1 facilitates function of the meiotic  
 RA regulator Mei2p in fission yeast.",  
 RL Mol. Cell. Biol. 20:1234-1242(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=972;  
 RX MEDLINE=21848401; PubMed=11859360;  
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,  
 RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,  
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,  
 RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,  
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,  
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.D., Hunt S., Jagsis K.,  
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,  
 RA Mooney P., Moule S., Mungall K., Murphy J., Niblett D., Odell C.,  
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,  
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,  
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,  
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,  
 RA Woodward J., Voicakert G., Aert R., Robben J., Gymnopoulos B.,  
 RA Weltjens I., Vancstreels E., Rieger M., Schaefer M., Mueller-Auer S.,  
 RA Gabell K., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,  
 RA Bozzym K., Langer I., Beck A., Leirich H., Reinhardt R., Pohl T.M.,  
 RA Eger P., Zimmermann W., Weiler H., Wambolt R., Punnett B.,  
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,

[illegible]

ID	NAME	STANDARD	PRT	1009 AA
DB	1078 G 1078			
QY	224 G 224			
DB	1020 Y-RAQKDFSLGDLGEGWISPGSGSTVMVHFRAQDQRIIRPLQMVCPAGAGTLPEGAR			107
QY	170 TPQPAHSDFLOKMD-DFWILKELQTLWLR-SAKDFNLKKKQOP-PAAAVTLHLGAGH			223
DB	1020 Y-RAQKDFSLGDLGEGWISPGSGSTVMVHFRAQDQRIIRPLQMVCPAGAGTLPEGAR			107
QY	224 G 224			
DB	1078 G 1078			
QY	75 NRPPLAGETLPRAVVDLEWRSLNKK-----LRNQ-----NYEAVSHLLC			115
DB	919 RP-----KIDEGSV-LTLNRPDLDDKQESRVENLASSLPREYCAHQGKLNASTLPPLGL			971
QY	116 YLRGLNQAQATPAELRRS-----LAHFCTSLQGLGSIAGWAAIGYPLPQLPETERPTW			169
DB	972 TLNHLPEQLMAAYGVNHRHGLTKNLCVEKVSDDLISILVHAEOU-----PPW			1011
QY	170 TPQPAHSDFLOKMD-DFWILKELQTLWLR-SAKDFNLKKKQOP-PAAAVTLHLGAGH			223
DB	1020 Y-RAQKDFSLGDLGEGWISPGSGSTVMVHFRAQDQRIIRPLQMVCPAGAGTLPEGAR			107
QY	224 G 224			
DB	1078 G 1078			
QY	30 RTGDPGPGPSIQKTYDILTRYEHQRLSLAGTY-LNVLGPP-----ENEPDF			74
DB	859 RQGQPVLVSGIQKTLRLSLWMEALGTLGGQVQTLTALGPPQPTSLDSTAFWKGPSHDEA			918
QY	75 NRPPLAGETLPRAVVDLEWRSLNKK-----LRNQ-----NYEAVSHLLC			115
DB	919 RP-----KIDEGSV-LTLNRPDLDDKQESRVENLASSLPREYCAHQGKLNASTLPPLGL			971
QY	116 YLRGLNQAQATPAELRRS-----LAHFCTSLQGLGSIAGWAAIGYPLPQLPETERPTW			169
DB	972 TLNHLPEQLMAAYGVNHRHGLTKNLCVEKVSDDLISILVHAEOU-----PPW			1011
QY	170 TPQPAHSDFLOKMD-DFWILKELQTLWLR-SAKDFNLKKKQOP-PAAAVTLHLGAGH			223
DB	1020 Y-RAQKDFSLGDLGEGWISPGSGSTVMVHFRAQDQRIIRPLQMVCPAGAGTLPEGAR			107
QY	224 G 224			
DB	1078 G 1078			

```

Db          983 PSRPPGRIIVH 995

RESULT 11
ID PHAC_PSEOL STANDARD; PRT; 560 AA.
AC P26456;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Poly(3-hydroxyalkanoate) polymerase 2 (EC 2.3.1.-) (PHA polymerase 2)
DE (PHA synthase 2) (Polyhydroxyalkanoic acid synthase 2).
GN PHAC.
OS Pseudomonas oleovorans.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID:301;
RN [1]
RP SEQUENCE FROM N.A.
RC SPRAIN-GBOL;
RX MEDLINE=91115830; Pubmed=1989978;
RA Huisman G.W., Wontink E., Meima R., Kazemier B., Terpstra P.,
RA Wiltholt B.;
RT "Metabolism of poly(3-hydroxyalkanoates) (PHAs) by Pseudomonas
RT oleovorans. Identification and sequences of genes and function of the
RT encoded proteins in the synthesis and degradation of PHA.";
RL J. Biol. Chem. 266:2191-2198(1991).
CC -1- FUNCTION: P. OLEOVORANS ACCUMULATES POLY(3-HYDROXYALKANOATES) AFTER
CC GROWTH ON MEDIUM CHAIN LENGTH HYDROCARBONS. LARGE AMOUNTS OF THIS
CC POLYESTER ARE SYNTHESIZED WHEN CELLS ARE GROWN UNDER NITROGEN-
CC LIMITING CONDITIONS. WHEN NITROGEN IS RESUPPLIED IN THE MEDIUM,
CC THE ACCUMULATED PHA IS DEGRADED.
CC -1- SIMILARITY: BELONGS TO THE PHA/PHB SYNTHASE FAMILY.
CC -----
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CC -----
DR EMBL; M58445; AAA25934.1; -.
DR PIR; C38604; C38604.
DR InterPro; IPR000073; A/b_hydrolase.
DR Pfam; PF00561; abhydrolase_1.
KW PHA biosynthesis; transferase; Acyltransferase.
FT ACT SITE 296 296 POTENTIAL.
SQ SEQUENCE 560 AA; 62631 MW; E2CD844FC1616B83 CRC64;

Query Match 7.0%; Score 85.5; DB 1; Length 560;
Best Local Similarity 30.2%; Pctd. No. 2.8;
Matches 38; Conservative 17; Mismatches 42; Indels 29; Gaps 7;

```

DB	QY	DB	QY
5 PAKGFTPLPAISMNQ	135 HECTSLOGLSIAGWMALGYPLPOPLG	102 KQTRLM	191 LOTWLM
-----NATIGLGR-----	-----TEPTWTEGPAHSDPLQKMDFWLKE	107	196
DLSTLRNVSROS	-----		
-----LHPLHTA	51 HHHLALGGQLGRV-----		
50	ILGDTPLQPNRDRPRSDPTMSQNPYRRGLQA		
	-----YLAWQ		
	101		

RESULT 12

CNTE_PIG	ID	CNTE_PIG	STANDARD;	PRT;	200 AA.
AC	002732;				
AT	15-JUL-1998 (Rel. 36, Created)				

DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Ciliary neurotrophic factor (CNTF).  
GN CNTF.  
OS *Sus scrofa* (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98030048; PubMed=9363597;  
RA Weaks R.L., Ramsondar J.J., Gallagher D.S. Jr., Noguees C.,  
RA Piedrahita J.A.;  
RT "Isolation, characterization and chromosomal localization of the  
RT porcine ciliary neurotrophic factor (CNTF) gene.";  
RL *Anim. Genet.* 28:354-357(1997).  
CC -1- FUNCTION: CNTF IS A SURVIVAL FACTOR FOR VARIOUS NEURONAL CELL  
CC TYPES. SEEMS TO PREVENT THE DEGENERATION OF MOTOR AXONS AFTER  
CC AXOTOMY (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -1- TISSUE SPECIFICITY: NERVOUS SYSTEM (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE CNTF FAMILY.  
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CC -----  
DR EMBL: U57644; AAC27342.1; -  
DR HSP: P26441; 1CNT.  
DR Interpro: IPR000151; C11\_neuro\_factor.  
DR Pfam: PF01110; CNTF; 1.  
DR ProDom: PD011041; C11\_neuro\_factor; 1.  
DR Growth factor; Neurone.  
SQ SEQUENCE 200 AA; 22718 MW; 40507C4457ED6531 CRC64;  
  
Query Match 6.9%; Score 84; DB 1; Length 200;  
Best Local Similarity 24.7%; Pred. No. 1;  
Matches 47; Conservative 23; Mismatches 88; Indels 32; Gaps 9;  
  
QY 46 LRRYLEHQRSLAGTILANTLGPFPNPPRLGAEITPRATVDLEVRSLNDKRLQ 105  
DB 23 LARKRSDDLALMEAVYKIQG--LNF---NIMDSVDGVPMASTDR--WSELTAEERLQ 75  
QY 106 NTEAVSHLLCYLRGLNRQATAELRSLAHFCTS---LQGLSGINGVMAALGYPLPQ-- 160  
DB 76 NLRATYTRHVMRLARL-----LEQRREHFTPAEDDFHOAHITTVLQVAAFRYQLEELM 127  
QY 161 -----PLPTEPTPTGPAHSD--FLQKMDFFWLKELQTWLRSKDNRLKKKKQPPA 213  
DB 128 VLEHKKVPPSEADGTSLVGGGGLFKKLMGLKLVGLDSQWTVRSIRDLRVISSHQ----- 183  
QY 214 AAVTLHLGHN 223  
DB 184 AGVPAH-GSH 192  
  
RESULT 13  
TTL\_DROME  
ID TTL\_DROME STANDARD; PRT; 452 AA.  
AC P18102; O9VA33;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Tailless protein.  
GN TTL OR NR2E2 OR CG1378.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Archtopoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Oregon-R;  
RX MEDLINE=90304905; PubMed=2364433;  
RA Pignoni F., Balderelli R.M., Steingrimsson E., Diaz R.J.,  
RA Patapoutian A., Merlam J.R., Lengyel J.A.;  
RT "The Drosophila gene tailless is expressed at the embryonic terminl  
RT and is a member of the steroid receptor superfamily.";  
RL *Cell* 62:151-163(1990).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93157371; PubMed=8430097;  
RA Liao G.-J., Steingrimsson E., Pignoni F., Couray A.J., Lengyel J.A.;  
RT "Characterization of downstream elements in a Raf-1 pathway.";  
RL *Proc. Natl. Acad. Sci. U.S.A.* 90:858-862(1993).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Berkley;  
RX MEDLINE=20196006; PubMed=10731132;  
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutcliffe G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Chapple M., Pfeiffer B.D.,  
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA Abrell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beaslev E.M.,  
RA Beeson K.Y., Benos P.V., Bertan B.P., Bhandari D., Bolshakov S.,  
RA Borovda D., Botchan M.R., Bouck B., Brockstein P., Broctier P.,  
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Fabios B., DeJocher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doug L.E., Downes M., Dugan-Hoch S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Fertiera S., Fleischmann W.,  
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.U., Mei M.-H., Ibegwam C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kethum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merulov G., Milhina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pauley J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kimnos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spredling A.C., Stapleton M., Strong R., Sun E.,  
RA Svitek R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of Drosophila melanogaster.";  
RL *Science* 287:2185-2195(2000).  
RN [4]  
RP FUNCTION.  
RX MEDLINE=99287803; PubMed=10357938;  
RA Daniel A., Dummett K., Lengyel J.A., Hartenstein V.;  
RT "The control of cell fate in the embryonic visual system by atonal,  
RT tailless and Egfr signaling.";  
RL Development 126:2945-2954(1999).  
CC -1- FUNCTION: ORPHAN RECEPTOR THAT BINDS DNA AS A MONOMER TO HORMONE  
CC SITE SEQUENCE 5'-AATCA-3' IN WHICH THE 5' FLANKING NUCLEOTIDES  
CC PARTICIPATE IN DETERMINING RECEPTOR SPECIFICITY. THIS RECEPTOR  
CC BINDS TO THE CONSENSUS SEQUENCE (AG) (AG)AATCA. PLAYS A KEY ROLE  
CC IN THE ESTABLISHMENT OF NONMERAMERIC DOMAINS AT THE ANTERIOR AND  
CC POSTERIOR POLES OF THE EMBRYO. IT MAY ALSO PLAY A ROLE IN THE  
CC NERVOUS SYSTEM. THE MATERNAL TERMINAL PATHWAY ACTIVATES THE TTL

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CC GENE IN THE TERMINI; TELL ACTIVITY THEN REPERSES SEGMENTATION AND
CC ACTIVATES TERMINAL-SPECIFIC GENES IN THESE DOMAINS. INVOLVED IN
CC THE REGULATION OF EARLY EYE DEVELOPMENT. IN THE EMERSONIC VISUAL
CC SYSTEM ANTAGLE DRIVES CELLS TO OPTIC LOBE AS OPPOSED TO BOLWIG'S
CC ORCAN FATE.
CC -1 SUBUNIT: Monomer (By similarity).
CC -1 SUBCELLULAR LOCATION: Nuclear (Potential).
CC -1 TISSUE SPECIFICITY: BRAIN AND PERIPHERAL NERVOUS SYSTEM.
CC -1 DEVELOPMENTAL STAGE: DURING STAGE 10 FOUND IN THE ANTERIOR PART OF
CC THE VISUAL SYSTEM THAT LATER GIVES RISE TO THE ANTERIOR LIP OF THE
CC OPTIC LOBE. AT STAGE 12 ALSO FOUND IN THE POSTERIOR LIP OF THE
CC OPTIC LOBE. IN THIRD LARVAL INSTAR EXPRESSED IN THE OPTIC LOBE OF
CC THE LARVAL BRAIN AND IN THE EYE ANTENNAL DISK, BOTH IN ANTENNAL
CC AND EYE PORTION.
CC -1 SIMILARITY: Belongs to the nuclear hormone receptor family. NR2
CC subfamily.
CC -----
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CC CC
DR EMBL; M34639; AAA28936.1; -.
DR EMBL; AF019362; AAB7137.1; -.
DR EMBL; AE003775; AAF5709.1; -.
DR PIR; A35602; A35602.
DR HSSP; P10826; IHRA;.
DR TRANSFAC; T00789; -.
DR FLYBase; FBgn0003720; t11.
DR GO; GO:0007369; P:gastrulation; NAS.
DR GO; GO:0007362; P:terminal region determination; IGI.
DR GO; GO:0008293; P:torso receptor signaling pathway; IGI.
DR InterPro; IPRO00536; Hormone rec lig.
DR InterPro; IPRO01623; Strchnm_receptor.
DR InterPro; IPRO01628; Znf_Casteroid.
DR Pfam; PF00104; hormone_rec; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PRO0398; STRDHOMONER.
DR PRINTS; PR00047; STROIDINGER.
DR PRODOM; PD000035; Znf_Casteroid; 1.
DR SMART; SMO0430; HOL1; 1.
DR SMART; SMO0399; Znf_C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR_1.
KW Receptor; Transcription regulation; DNA-binding; Nuclear protein; Zinc-finger; Activator; Repressor; Developmental protein..
FT DN BIND 34 101 NUCLEAR RECEPTOR-TYPE.
FT ZN_FING 34 54 C4-type.
FT ZN_FING 70 96 C4-type.
FT DOMAIN 244 389 LIGAND-BINDING (BY SIMILARITY).
FT FT 262 265 POLY-LIU.
SQ SEQUENCE 452 AA; 50549 MW; A4BBFFDEB93A37C CRC64;
Query Match 6.8%; Score 83; DB 1; Length 452;
Best Local Similarity 23.8%; Pred. NO. 3.6;
Matches 34; Conservative 11; Mismatches 32; Indels 66; Gaps 6;
QY 115 CYLGSLNRQAATAE-----LRRLAFCSTLSGLDIASGV-----ALG 155
Db 96 CFEEVGNNDAVAQHENGPRNSTLRIMAYAKAMMG---AGEMQIDPAEILMNTALTG 150
QY 156 YP-LPOPLTEPTTPGPASDFLOKDMDFWLKELQTWLRSAXDNFRLLKKMQPPAA 214
Db 151 FRGYRMRPGRLQRAGAHHRIAMAFAQ-----PPPSA 181
QY 215 AVTL-----HIGANGF 225
Db 182 AAVLDLVSRVVRPHHPVHQGNHG 204

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HAIR_HUMAN	STANDARD;	PRT;	1189 AA.
ID	043593; Q9NP61;		
DT	15-JUL-1999 (Rel. 38, Created)		
DT	28-FEB-2003 (Rel. 41, Last sequence update)		
DT	28-FEB-2003 (Rel. 41, Last annotation update)		
DE	Hairless protein.		
GN	HR.		
OS	Homo sapiens (human).		
OC	Eumycota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.		
OX	NCBI_TaxId=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A. (ISOFORM LONG), AND VARIANT ALONC ALA-1022.		
RX	MEDLINE=9811143; PubMed=9445480;		
RA	Almad W., Ul Haque M.F., Brincolini V., Tsou H.C., Ul Haque S.,		
RA	Lam H., Alta V.M., Owen J., Delaquerie M., Frank J.,		
RA	Cesarihlmi-Friedman P.B., Leask A., McGrath J.A., Peacocke M.,		
RA	Almad M., Ott J., Christiano A.M.,		
RT	"Alpecia Universalis associated with a mutation in the human hairless		
RT	gene.";		
RL	Science 279:720-724(1998).		
RN	[2]		
RP	SEQUENCE FROM N.A. (ISOFORM LONG), REVISIONS TO 572 AND 774, AND		
RP	TISSUE SPECIFICITY.		
RC	TISSUE=Peripheral blood leukocytes, and Skin fibroblast;		
RX	MEDLINE=99162400; PubMed=10051399;		
RA	Almad W., Zlotogorski A., Panteleyev A.A., Lam H., Almad M.,		
RA	Ul Haque M., Abdallah H.M., Dregan L., Christiano A.M.;		
RT	"Genomic organization of the human hairless gene (HR) and		
RT	identification of a mutation underlying congenital atrichia in an Arab		
RT	paestinian family.";		
RL	Genomics 56:141-148(1999).		
RN	[3]		
RP	SEQUENCE FROM N.A., VARIANT ALONC ASP-1136, TISSUE SPECIFICITY, AND		
RP	ALTERNATIVE SPLICING.		
RC	TISSUE=Brain, Retal brain, and Peripheral blood leukocytes;		
RX	MEDLINE=98409456; PubMed=9736769;		
RA	Cichon S., Anker M., Vogt I.R., Rohleder H., Putzstuck M., Hillmer A.,		
RA	Panteleyev A.A., Almad M., McGrath J.A., Christiano A.M.;		
RT	"A missense mutation in the zinc-finger domain of the human hairless		
RT	gene underlies congenital atrichia in a family of Irish travellers.";		
RL	Am. J. Hum. Genet. 63:984-991(1998).		
CC	-1- FUNCTION: MAY ACT AS A TRANSCRIPTION FACTOR THAT COULD ACT ON TO		
CC	REGULATE ONE OF THE PHASES OF HAIR GROWTH.		
CC	-1- SUBCELLULAR LOCATION: Nuclear.		
CC	-1- ALTERNATIVE PRODUCTS:		
CC	Event-Alternative splicing; Named isoforms=2;		
CC	Comment=Additional isoforms seem to exist;		
CC	Name=Long;		
CC	IsoId=O43593-1; Sequence=Displayed;		
CC	Name=Short;		
CC	IsoId=O43593-2; Sequence=VSP 004276;		
CC	-1- TISSUE SPECIFICITY: Strongest expression of both isoforms is seen		
CC	in the small intestine, weaker expression in brain and colon, and		
CC	trace expression is found in liver, pancreas, spleen, thymus,		
CC	stomach, salivary gland, appendix and trachea. Long isoform is		
CC	always the most abundant. Long isoform is exclusively expressed at		
CC	low levels in kidney and testis and short isoform exclusively at		
CC	high levels in the skin.		
CC	-1- DISEASE: DEFECTS IN HR ARE THE CAUSE OF ALOPECIA UNIVERSALIS		
CC	(ALONC); A RARE AUTOSOMAL RECESSIVE FORM OF HAIR LOSS. IT IS		
CC	CHARACTERIZED BY HAIR FOLLICLES WITHOUT HAIR.		

CC -1- DISEASE: DEFECTS IN HR ARE THE CAUSE OF ATRICHTIA WITH PAPULAR  
 CC LESIONS (APL) (ALSO KNOWN AS CONGENITAL ATRICHTIA). THIS AUTOSOMAL  
 CC RECESSIVE DISEASE IS CHARACTERIZED BY PAPILLARY LESIONS OVER MOST  
 CC OF THE BODY AND ALMOST COMPLETE ABSENCE OF HAIR.  
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 CC -----  
 DR EMBL; AF039196; AAC32258.2; -;  
 DR EMBL; AJ277249; CAB87577.2; -;  
 DR EMBL; AJ277250; CAB87577.2; JOINED.  
 DR EMBL; AJ277251; CAB87577.2; JOINED.  
 DR EMBL; AJ277252; CAB87577.2; JOINED.  
 DR EMBL; AJ277253; CAB87577.2; JOINED.  
 DR EMBL; AJ400825; CAB87577.2; JOINED.  
 DR EMBL; AJ400826; CAB87577.2; JOINED.  
 DR EMBL; AJ400827; CAB87577.2; JOINED.  
 DR EMBL; AJ400828; CAB87577.2; JOINED.  
 DR EMBL; AJ400829; CAB87577.2; JOINED.  
 DR EMBL; AJ400830; CAB87577.2; JOINED.  
 DR EMBL; AJ400831; CAB87577.2; JOINED.  
 DR EMBL; AJ400832; CAB87577.2; JOINED.  
 DR EMBL; AJ400833; CAB87577.2; JOINED.  
 DR EMBL; AJ400834; CAB87577.2; JOINED.  
 DR EMBL; AJ400835; CAB87577.2; JOINED.  
 DR EMBL; AJ400836; CAB87577.2; JOINED.  
 DR EMBL; AJ400837; CAB87577.2; JOINED.  
 DR EMBL; AJ277165; CAB86602.1; -;  
 DR Gene; HGNC:5172; HR.  
 DR MIM; 603302; -;  
 DR MIM; 209550; -;  
 DR MIM; 209500; -;  
 DR GO; GO:0005634; C:nucleus; NAS.  
 DR GO; GO:0003700; P:transcription factor activity; NAS.  
 DR GO; GO:0003551; P:regulation of transcription; DNA-dependant; NAS.  
 DR InterPro; IPR003347; TF\_jmjc.  
 DR Pfam; PF02373; jmjc; 1.  
 DR SMART; SM00558; Jmjc; 1.  
 KW Zinc-finger; DNA-binding; Nuclear protein; Transcription regulation;  
 KW Metal-binding; Alternative splicing; Disease mutation.  
 FT ZN-FING 600 625  
 FT VARSPIC 1072 1126  
 FT VARIANT 620 620  
 FT FT 1022 1022  
 FT VARIANT 1136 1136  
 FT FT 337 337  
 FT FT 446 446  
 FT FT 584 584  
 FT SEQUENCE 1189 AA; 127509 MW; 582448587168B5DF CRC64;  
 Query Match 6.7%; Score 82.5; DB 1; Length 1189;  
 Best Local Similarity 23.3%; Pred. No. 14;  
 Matches 71; Conservative 23; Mismatches 92; Indels 119; Gaps 15;  
 QY 3 LRAGDSW-GMLACTVLMHLPAVPAALNRTPGPGP-----S1 40  
 DB 818 LRAGDRLRGLGLPLRPVPRRLPPGALLMLQEPQCPRRGFLPQEHNRQGPVLVSGI 877  
 QY 41 OKTYDRLRYLHQLRSLAGTY--LNTLGRP-----FNPPDNRPP----- 77  
 DB 878 QRTLOGNLWGTALGALGGVQVALSPGPPQPSLCSITFWGSGWPELRPKSDEGSVLL 937  
 QY 78 ---RLGAEFLP-----ATVDEVMRSLNDKRLT-----QNEYAY----- 110

DB 938 LHRALGDEDTSRVEMTAAASLPPEYCALHGKLNILASLYLPPGIALNPLRLEPQMLAAVGSBH 997  
 QY 111 -SHL-----LCYLRGNRQAATAELRLSLAHFCTSLQGLGSLAGMALGLYPLPLPPT 165  
 DB 998 RGHLETKNLG-----VEVADLVSLVHADTLP----- 1024  
 QY 166 EPTWTPGPAHSDFLQKMD--DFWLKEIQTWLMR--SAKDFRLKKKQP--PAAAVTLH 219  
 DB 1025 -PAW--HRAQDFLSGLDGEGLMRSQSVSTYWHFRADQNRIRPLQWCPAGAGLE 1081  
 QY 220 LGAHG 224  
 DB 1082 PGAPG 1086  
 RESULT 15  
 ID P85B\_BOVIN STANDARD; PRT; 724 AA.  
 AC P23726;  
 DT 01-NOV-1991 (Rel. 20, Created)  
 DT 01-NOV-1991 (Rel. 20, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Phosphatidylinositol 3-kinase regulatory beta subunit (PI3-kinase  
 DE p85-beta subunit) (Pcdins-3-kinase p85-beta).  
 GN PIK3R2.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91191567; PubMed=1707345;  
 RA Otsu M., Hiles I.D., Goot I., Fry M.J., Ruiz-Larrea F., Panayotou G.,  
 RA Thompson A., Dhand R., Hsuan J., Totty N., Smith A.D., Morgan S.J.,  
 RA Courtneidge S.A., Parker P.J., Waterfield M.D.;  
 RT "Characterization of two 85 kd proteins that associate with receptor  
 RT tyrosine kinases, middle-T/pp60c-src complexes, and p13-kinase.";  
 RL Cell 65:91-104(1991).  
 RN [2]  
 RP CIRCULAR DICHOISM AND FLUORESCENCE SPECTROSCOPY.  
 RX MEDLINE=93049176; PubMed=1330535;  
 RA Panayotou G., Bax B., Gout I., Federwisch M., Wroblewski B., Dhand R.,  
 RA Fry M.J., Blundell T.L., Wollmer A., Waterfield M.D.;  
 RT "Interaction of the p85 subunit of PI 3-kinase and its N-terminal SH2  
 RT domain with a PDGF receptor phosphorylation site: structural features  
 RT and analysis of conformational changes.";  
 RL EMBO J. 11:4261-4272(1992).  
 CC -1- FUNCTION: BINDS TO ACTIVATED (PHOSPHORYLATED) PROTEIN-TYROSINE  
 CC KINASES, THROUGH ITS SH2 DOMAIN, AND ACTS AS AN ADAPTER, MEDIATING  
 CC THE ASSOCIATION OF THE P110 CATALYTIC UNIT TO THE PLASMA MEMBRANE.  
 CC -1- SUBUNIT: HETERODIMER OF A P110 (CATALYTIC) AND A P85 (REGULATORY)  
 CC SUBUNITS.  
 CC -1- SIMILARITY: BELONGS TO THE PI3K P85 SUBUNIT FAMILY.  
 CC -1- SIMILARITY: Contains 1 Rho-GAP domain.  
 CC -1- SIMILARITY: Contains 2 SH2 domains.  
 CC -1- SIMILARITY: Contains 1 SH3 domain.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC the European Bioinformatics Institute. There are no restrictions on its  
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 CC -----  
 DR EMBL; M61746; AAA79510.1; -;  
 DR HSSP; P23727; 2PNB.  
 DR InterPro; IPR001720; PI3kinase\_P85.  
 DR InterPro; IPR000198; RhoGAP.  
 DR InterPro; IPR000980; SH2.  
 DR InterPro; IPR001452; SH3.  
 DR Pfam; PF00620; RhoGAP; 1.

DR Pfam; PF00017; SH2; 2.  
DR Pfam; PF00018; SH3; 1.  
DR PRINTS; PR00678; PI3KINASEP85.  
DR PRINTS; PR00401; SH2DOMAIN.  
DR Prodom; PD000093; SH2; 2.  
DR SMART; SM00324; RhogAP; 1.  
DR SMART; SM00352; SH2; 2.  
DR SMART; SM00326; SH3; 1.  
DR PROSITE; PS50238; RhogAP; 1.  
DR PROSITE; PS50001; SH2; 2.  
DR PROSITE; PS50002; SH3; 1.  
KW SH3 domain; SH2 domain; Repeat.  
FT DOMAIN 4 80 SH3.  
FT DOMAIN 109 291 RHO-GAP.  
FT DOMAIN 326 421 SH2 1.  
FT DOMAIN 618 712 SH2 2.  
SQ SEQUENCE 724 AA; 81059 MW; 9D2BA8B6DB087098 CRC64;

Query Match 6.7%; Score 82; DB 1; Length 724;  
Best Local Similarity 21.9%; Pred. No. 8.1;  
Matches 66; Conservative 25; Mismatches 71; Indels 140; Gaps 16;

QY 6 GDSWGLAQLCTVLMHLPAVPALN-RTGDPGEGPSIQKTYDLTRYLHQRLSLAGTYLNY 64  
DB 42 GVAEGNERCPQSVGW---MGLNERTKRGDFP-----GTYVEF 77  
QY 65 LGP-----PNEPDPNPP-----R 78  
DB 78 LGPVALARPPRRPGRPPLPARPRDGPPEPGLTLPDLPQGFSPDVAPPILVKLVETIER 137  
QY 79 LGAETL---PRAT-----VDLEWRSINDKRLTONYEAVSHLLCYLRGLNRQAATAEL 129  
DB 138 TGLDSYRPPPPAVRTDWSLSDVEGW---DAAALSDGVKGF--LIALPAPLVTPESAABA 191  
QY 130 RSSL-----AHFCTSIQGL---LGSING-----VMAALGY----- 156  
DB 192 HRALREAGPVPAPALEPPTLPPLHHAULTLRFLLQHLGKRVAGRAPAPGPAVRALGATFGPLL 251  
QY 157 ----PLPQPLPGTEPTWT-PCPAHSDPLQKMDFWLLKELQTLWRSADFNRLKKKQOP 211  
DB 252 LRAPPSPSPPGAPDGTETPT---DFPALIVEKLIQEHLE-----EQEVAP 295  
QY 212 PA 213  
DB 296 PA 297

Search completed: February 9, 2004, 06:15:33  
Job time : 13.5 secs









A:Residues: 1-955 <MAT>  
 A:Cross-references: EMBL:AB012266; NID:d1227741; PIDN:BAA32791.1; PID:d1033757  
 A:Experimental source: brain  
 C:Genetics:  
 A:Gene: w1z

Query Match  
 Best Local Similarity 27.8%; Pred. No. 9.1;  
 Matches 35; Conservative 19; Mismatches 48; Indels 24; Gaps 7;

QY 22 LPVPAALNRTGDPGPGPSIQKTYDILTRYLEHQLSLAG--TYLNTYLP-----PNEPD 73  
 DB 615 LPLSLPASRPGRKPGAGPT-----QVPR--ELSLSPITGSKPSAASYLGPVATKRPLQEDR 667  
 QY 74 FNPRLGAEPLPRATVDLEWRSINDKRLTQNYEAVSHLLCYLRGL--NRQAATAELR 130  
 DB 668 FLPAEYKATYIQTLELPPKA-KTLHKK-----TSHSTACECELGYENRKALASHAR 721  
 QY 131 RSLAHF 136  
 DB 722 AHLRQF 727

## RESULT 10

T00248  
 zinc finger protein w1zL - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 22-Jan-1999 #sequence\_revision 22-Jan-1999 #text\_change 05-Nov-1999  
 R:Accession: T00248  
 R:Matsumoto, K.; Ishii, N.; Yoshida, S.; Shiosaka, S.; Wanaka, A.; Tohyama, M.  
 A:Submitted to the EMBL Data Library, March 1998  
 A:Description: Molecular cloning and distinct developmental expression pattern of splice  
 A:Reference number: Z14130  
 A:Accession: T00248  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-1561 <MAT>  
 A:Cross-references: EMBL:AB012265; NID:d1227740; PIDN:BAA32790.1; PID:d1033756  
 A:Experimental source: brain  
 C:Genetics:  
 A:Gene: w1z

Query Match  
 Best Local Similarity 27.8%; Pred. No. 17;  
 Matches 35; Conservative 19; Mismatches 48; Indels 24; Gaps 7;

QY 22 LPVPAALNRTGDPGPGPSIQKTYDILTRYLEHQLSLAG--TYLNTYLP-----PNEPD 73  
 DB 1221 LPLSLPASRPGRKPGAGPT-----QVPR--ELSLSPITGSKPSAASYLGPVATKRPLQEDR 1273  
 QY 74 FNPRLGAEPLPRATVDLEWRSINDKRLTQNYEAVSHLLCYLRGL--NRQAATAELR 130  
 DB 1274 FLPAEYKATYIQTLELPPKA-KTLHKK-----TSHSTACECELGYENRKALASHAR 1327  
 QY 131 RSLAHF 136  
 DB 1328 AHLRQF 1333

## RESULT 11

T34916  
 transferase - Streptomyces coelicolor  
 C:Species: Streptomyces coelicolor  
 C:Date: 05-Nov-1999 #sequence\_revision 05-Nov-1999 #text\_change 02-Sep-2000  
 C:Accession: T34916  
 R:Oliver, K.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
 A:Submitted to the EMBL Data Library, January 1998  
 A:Reference number: Z21558  
 A:Accession: T34916  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-640 <OL1>  
 A:Cross-references: EMBL:AL021409; PIDN:CAA16181.1; GSPDB:GN00070; SCOEDB:SC3F7.10

A:Experimental source: strain A3(2)

C:Genetics:  
 A:Gene: SCORDB:SC3F7.10  
 C:Superfamily: glycine C-acetyltransferase homology  
 F:287-624/Domain: glycine C-acetyltransferase homology <GCA>

Query Match  
 Best Local Similarity 27.1%; Score 86.5; DB 2; Length 640;  
 Matches 50; Conservative 13; Mismatches 64; Indels 57; Gaps 9;

QY 22 LPVPAALNRTGDPGPGPSIQKTYDILTRYLEHQL--RSLAGTYLNTYLP-----PNEPD 78  
 DB 100 LPVAPVA-EGTGDPVTEAVVAAMRQYQRIHQIGADLEG-----E 140  
 QY 79 LGAETLPRAATVDLEWRSINDKRLTQNYEAVSHLLCYLRGINRQAATAELRSLAHPT 138  
 DB 141 LGVDSVVLTSVAEE--TRSLGLT-----GAAPDAAGATTIRALA--D 179  
 QY 139 SLQGLAGSAGVMAALGYPLPQPLGTEPTWPGFASDFLOKMDFFWLKELQTMWRS 198  
 DB 180 ALRGL-----VAAAPGTAIVPEAAPATGAA-APAGRGGNP-----APGADGMDHRS 225  
 QY 199 AKDF 202  
 DB 226 MKDF 229

## RESULT 12

C38604  
 poly(3-hydroxyalkanoate) polymerase (EC 2.7.7.-) 3 - Pseudomonas oleovorans  
 C:Species: Pseudomonas oleovorans  
 C:Date: 23-Aug-1991 #sequence\_revision 23-Aug-1991 #text\_change 08-Sep-2000  
 C:Accession: C38604  
 R:Huisman, G.W.; Winkler, B.; Meima, R.; Kazemier, B.; Terpstra, P.; Witholt, B.  
 J. Biol. Chem. 266, 2191-2196, 1991  
 A:Title: Metabolism of poly(3-hydroxyalkanoates) (PHAs) by Pseudomonas oleovorans. Ident  
 A:Reference number: A38604; MUID:91115830; PMID:1989978  
 A:Accession: C38604  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-560 <HU1>  
 A:Cross-references: GB:M58445; NID:G151441; PIDN:AAA25934.1; PID:G151444  
 C:Superfamily: poly(3-hydroxyalkanoic acid) synthase phbC  
 C:Keywords: nucleic acid; transferase

Query Match  
 Best Local Similarity 30.2%; Pred. No. 6.4;  
 Matches 38; Conservative 17; Mismatches 42; Indels 29; Gaps 7;

QY 77 PRLGAEPLPRATVDLEWRSINDKRLTQNYEAVSHLLCYLRGINRQAATAELRSL--A 134  
 DB 5 PAKGPTLPATSNVQ-----NALIGLRG-----DLISLKNVSRK-----LRHPLHTA 50  
 QY 135 HECTSLQGLAGSAGVMAALGYPLPQPLG--TEPTWPGFASDFLOKMDFFWLKE 190  
 DB 51 HHLALGGQLGRV-----ILGDTPLQPNRPDRSDPLWSONPFYRRLGLQ--YLAWQ 101  
 QY 191 LQTMW 196  
 DB 102 KQTRLM 107

## RESULT 13

F72511  
 probable cystathionine gamma-synthase APE2068 - Aeropyrum pernix (strain K1)  
 C:Species: Aeropyrum pernix  
 C:Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 20-Jun-2000  
 C:Accession: F72511  
 R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Hatakeyama, Y.; Jin-no, K.; Takat  
 awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, U.; K  
 DNA Res. 6, 83-101, 1999  
 A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr  
 A:Reference number: AF2450; MUID:99310339; PMID:10382966

A:Accession: F72511  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-389 <KAW>  
 A:Cross-References: DDBJ:AP000063; NID:95105654; PIDN:BAA81078.1; PID:95105766  
 A:Experimental source: strain K1  
 C:Genetics:  
 A:Gene: ABE2068  
 C:Superfamily: O-succinylhomoserine (thiol)-lyase

Query Match 6.9%; Score 84.5; DB 2; Length 389;  
 Best Local Similarity 22.9%; Pred. No. 5;  
 Matches 47; Conservative 19; Mismatches 78; Indels 61; Gaps 8;

QY 43 TYDLRYLEHQLSLAGTTLANTLGPFPNPPRLGAEPLPRATVDLEVRSL----- 97  
 DB 107 TGGSTRSLLEMLSSITGIEVRLAGPWE-----LLDLCVADLIVES 150  
 QY 98 --NDKRLTONYEAYSHLLCYLGLNRQATAELR-----RSL--AHFCTS 139  
 DB 151 MANPTLRVPP-----LSGIYREAGSCGVVVNTPATPIAYPLRGAAHY--S 197  
 QY 140 LQGLGSIAGVMAALGYPLPQPL-PGTEPTWTPGPAHSDFLQMDFFLLKELQTWLWS 198  
 DB 198 LBSLTGYIAGHNDVVGSLGRVEEDLEPLMMRKILGTIMQPIDAY-----LAWRG 249  
 QY 199 AKDFNRLLKKKQPPAAAVTLHLGAH 223  
 DB 250 MKTLKARFEAGRAAVEVAEMWESH 274

## RESULT 14

AD3633  
 Hypothetical protein BMEI10989 [imported] - Brucella melitensis (strain 16M)  
 C:Species: Brucella melitensis  
 C:Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 01-Feb-2002  
 C:Accession: AD3633  
 R:DelVecchio, V.G.; Kaparatel, V.; Redkar, R.J.; Patra, G.; Muir, C.; Los, T.; Ivanova, P.; Mazur, M.; Goldsman, E.; Selkov, E.; Elser, P.H.; Haglue, S.; O'Callaghan, D.; Letesee Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002  
 A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis  
 A:Reference number: AD3252; PMID:11756688  
 A:Accession: AD3633  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-200 <KUR>  
 A:Cross-References: GB:AE008918; PIDN:AAL54231.1; PID:917985203; GSPDB:GN00191  
 A:Experimental source: strain 16M  
 C:Genetics:  
 A:Gene: BMEI10989  
 A:Map position: 11

Query Match 6.9%; Score 84; DB 2; Length 200;  
 Best Local Similarity 24.3%; Pred. No. 2.4;  
 Matches 56; Conservative 22; Mismatches 84; Indels 68; Gaps 13;

QY 10 GMLACCTVLMHLPAYPALNRGDPGPGSIQKTYDLTRYLEHQLSLAGTTLANTLGYGPP 69  
 DB 2 GLLAGALV--LPSLPAEAKTQQAAMPNATSPHQADVYL--LRGFADISTGTI---- 51  
 QY 70 NEPDFNPRLGAEPLPRATVDLEVR-----WRSINDKRLTONYEAYSHLLCYLRG--LNR 122  
 DB 52 -----DEIGAE-LQAAGVNAHVQGAAMRLVYN--RIVADQKXGHLPLVILIGSLGA 101  
 QY 123 QAA--TAELRSLAHFCTSLQGLGSIAGVMAALGYPLPQPLPGT-----EPTW 169  
 DB 102 NAAIYIAEBELR-----RGIAVDYATFAATG--PDPLFGVVRVNVFYPKQHG 149  
 QY 170 ----TGPCPAHSDFLQMDFFLLKELQTWLMSAKDFNRLLKKKQPPAAAVTLHLGA 215  
 DB 150 GLPLVGPFPFHGLENR-----FSNAKOVGHFNIEKQRPLOA 187

## RESULT 15

F75439  
 Probable cell wall synthesis protein - Deinococcus radiodurans (strain R1)  
 C:Species: Deinococcus radiodurans  
 C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 31-Mar-2000  
 C:Accession: F75439  
 R:White, O.; Elesen, J.A.; Heideberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Uterback, T.; Zalewski, C.; Me S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.  
 Science 286, 1571-1577, 1999  
 A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.  
 A:Reference number: A75250; MUID:20036896; PMID:10567266  
 A:Accession: F75439  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-411 <WHI>  
 A:Cross-References: GB:AE001958; GB:AE000513; NID:96458805; PIDN:AAF10649.1; PID:9645880  
 A:Experimental source: strain R1  
 C:Genetics:  
 A:Gene: DR1076  
 A:Map position: 1

Query Match 6.9%; Score 84; DB 2; Length 411;  
 Best Local Similarity 24.6%; Pred. No. 6;  
 Matches 56; Conservative 25; Mismatches 77; Indels 70; Gaps 11;

QY 2 DLKADDSKGMACCTVLMHLPAYPALNRGDPGPGSIQKTYDLTRYLEHQLSLAGT 61  
 DB 212 EYLAADRVALRAELPSEMSLRGPVLLLSGG-GRGHVAAAADVLT-----ELGNL-GR 264  
 QY 62 LNYLGPFPNPPRLGAEPLPRATVDLEVRSLNDKRLTONYEAYSHLLCYLRGIN 121  
 DB 265 VQVLVPASRGQ-----GTETIGATV-----HHLGFRRLDLP 296  
 QY 122 RQAAVLAELRSLAHFCTSLQGLGSIAGV---MAALGYPLP--QPLPGTEPTWTPGPAH 175  
 DB 297 RLAAASDL-----VVGKAGGLTVAEATALGVPLIYVAPIPGQ-----EHN 337  
 QY 176 SPFLQMDFFLLKELQTWLMSAKDFNRLLKKKQPPAAAVTLHLGA 222  
 DB 338 ADFLERHG-----AGLWARRAHDDVRPVLRLDPAEHARLSAGA 376

Search completed: February 9, 2004, 06:17:41  
 Job time : 21 secs

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OM nucleic - nucleic search, using bw model

Run on: February 9, 2004, 06:10:24 ; Search time 349.674 Seconds  
(without alignments)  
8395.991 Million cell updates/sec

Title: US-09-931-704-1

Perfect score: 797  
Sequence: 1 attaaagcttcgacgagcc.....tctccttcgtccccc 797

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 2449703 seqs, 1841816367 residues

Total number of hits satisfying chosen parameters: 4899406

Minimum DB seq length: 0  
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Post-processing: Maximum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database :
- 1: Published Applications NA.\*
  - 2: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*
  - 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*
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  - 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq.\*
  - 13: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq.\*
  - 14: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq.\*
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  - 16: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq.\*
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  - 18: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	797	100.0	797	US-09-931-704-1	Sequence 1, Appl1
2	749.4	94.0	1710	US-10-212-793-1	Sequence 1, Appl1
3	669.4	84.0	819	US-09-931-704-4	Sequence 4, Appl1
4	523.4	65.7	5087	US-09-931-704-3	Sequence 3, Appl1
5	493.4	61.9	495	US-09-864-761-23175	Sequence 23175, A
6	369	46.3	492	US-09-864-761-6462	Sequence 6462, Ap
7	269.4	33.8	283	US-09-765-231A-75	Sequence 75, Appl1
8	175.8	22.1	809	US-10-027-632-134702	Sequence 134702,
9	175.8	22.1	396	US-10-212-793-7	Sequence 7, Appl1
10	80.2	10.1	65	US-09-908-975-29446	Sequence 29446, A
11	58.6	5.9	2320	US-10-102-806-266	Sequence 266, App
12	46.8	5.6	68750	US-10-014-717-1	Sequence 1, Appl1
13	44.8	5.5	3195	US-10-295-027-1127	Sequence 1127, Ap
14	43.6	5.5	3195	US-10-285-976-54	Sequence 54, Appl1
15	43.6	5.5	3195	US-10-285-976-54	Sequence 54, Appl1

16	43.6	5.5	3195	US-10-205-823-143	Sequence 143, App
17	41.8	5.2	594	US-10-140-472-10	Sequence 10, Appl1
18	41.8	5.2	594	US-10-141-761-10	Sequence 10, Appl1
19	41.8	5.2	594	US-10-142-885-10	Sequence 10, Appl1
20	41.8	5.2	594	US-10-142-885-10	Sequence 10, Appl1
21	41.8	5.2	594	US-10-137-871-10	Sequence 10, Appl1
22	41.8	5.2	594	US-10-140-805-10	Sequence 10, Appl1
23	41.8	5.2	594	US-10-140-864-10	Sequence 10, Appl1
24	41.8	5.2	594	US-10-140-923-10	Sequence 10, Appl1
25	41.8	5.2	594	US-10-141-756-10	Sequence 10, Appl1
26	41.8	5.2	594	US-10-141-759-10	Sequence 10, Appl1
27	41.8	5.2	594	US-10-123-155-10	Sequence 10, Appl1
28	41.8	5.2	594	US-10-146-731-10	Sequence 10, Appl1
29	41.8	5.2	1581	US-10-369-493-13081	Sequence 43081, A
30	40.8	5.1	980	US-10-175-523-176	Sequence 176, App
31	40.4	5.1	1083	US-10-156-761-2132	Sequence 3132, App
32	40.4	5.1	9025608	US-10-156-761-1	Sequence 1, Appl1
33	40.2	5.0	586	US-10-008-063-1	Sequence 1, Appl1
34	40.2	5.0	586	US-10-152-363A-59	Sequence 59, Appl1
35	39.8	5.0	653	US-10-184-644-402	Sequence 402, App
36	39.8	5.0	653	US-10-184-634-402	Sequence 402, App
37	39.8	5.0	2247	US-10-156-761-7471	Sequence 7471, App
38	39.8	5.0	4641	US-10-369-493-24230	Sequence 24230, A
39	39.2	4.9	786	US-10-259-165-705	Sequence 705, App
40	39.2	4.9	5452	US-10-292-798-1189	Sequence 1189, App
41	39.2	4.9	5452	US-10-017-161-1481	Sequence 1481, App
42	39.2	4.9	9025608	US-10-156-761-1	Sequence 1, Appl1
43	39	4.9	440	US-10-063-665-52	Sequence 52, Appl1
44	39	4.9	440	US-10-184-644-202	Sequence 202, App
45	39	4.9	440	US-10-184-634-202	Sequence 202, App

ALIGNMENTS

RESULT 1  
US-09-931-704-1  
Sequence 1, Application US/09931704  
Patent No. US20020041873A1  
GENERAL INFORMATION:  
APPLICANT: Senaldi, Giorgio  
TITLE OF INVENTION: Methods and Compositions for Treating IGE-Related Disease Using N  
FILE REFERENCE: A-695  
CURRENT APPLICATION NUMBER: US/09/931,704  
CURRENT FILING DATE: 2001-08-16  
PRIOR APPLICATION NUMBER: US 60/226,436  
PRIOR FILING DATE: 2000-08-18  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1  
LENGTH: 797  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (90)..(764)  
OTHER INFORMATION:  
NAME/KEY: mat\_peptide  
LOCATION: (171)..()  
OTHER INFORMATION: Met at -27  
US-09-931-704-1  
Query Match 100.0%; Score 797; DB 9; Length 797;  
Best Local Similarity 100.0%; Pred. No. 4.2e-204;  
Matches 797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATTAAGCTTCGCGGAGCCGCGCTCCCTCCACCTCCGCGAGGAGGAGGAGG 60  
DB 1 ATTAAGCTTCGCGGAGCCGCGGCTCCCTCCACCTCCGCGAGGAGGAGG 60  
QY 61 CCGACCCGCGCGGAGCCGCGAGCCGCGAGGAGGAGGAGGAGGAGGAGGAGG 120

Db 61 CCGCACCAGGCGGCGCCAGCCCGCCAGCTCCAGCAGGAGGACTCGTGGGGGA 120  
QY 121 TGTAGCGTGGCTGTGACGAGTGTCTGGGACCTCCCTGAGTGGCAGCTCAATCGCA 180  
Db 121 TGTAGCGTGGCTGTGACGAGTGTCTGGGACCTCCCTGAGTGGCAGCTCAATCGCA 180  
QY 181 CAGGGAGCCAGGAGCTGGGCGGCTCCATCCAGAAAACCTATGACCTCACCGGTA 240  
Db 181 CAGGGAGCCAGGAGCTGGGCGGCTCCATCCAGAAAACCTATGACCTCACCGGTA 240  
QY 241 AGCAGCACTCCGAGCTGGTGGGAGCTATGTGAACCTAGGAGGAGGAGCTGTTGACT 300  
Db 241 AGCAGCACTCCGAGCTGGTGGGAGCTATGTGAACCTAGGAGGAGGAGCTGTTGACT 300  
QY 301 AGCAGCACTCCGAGCTGGTGGGAGCTATGTGAACCTAGGAGGAGGAGCTGTTGACT 360  
Db 301 AGCAGCACTCCGAGCTGGTGGGAGCTATGTGAACCTAGGAGGAGGAGCTGTTGACT 360  
QY 361 TGGAGGTGTGGGAGGAGCTCAATGACAACTGGGAGTGAACGAACTACAGGAGCTTACA 420  
Db 361 TGGAGGTGTGGGAGGAGCTCAATGACAACTGGGAGTGAACGAACTACAGGAGCTTACA 420  
QY 421 GGCACCTTGTGTGTACTTGGCTGGCTCAACCTGAGGCTGCACTGCTGAGCTGCGCC 480  
Db 421 GGCACCTTGTGTGTACTTGGCTGGCTCAACCTGAGGCTGCACTGCTGAGCTGCGCC 480  
QY 481 GGCAGCTGGGAGGAGCTTGTGACAGGAGCTGAGGAGGAGCTGAGGAGGAGCTGAGGAG 540  
Db 481 GGCAGCTGGGAGGAGCTTGTGACAGGAGCTGAGGAGGAGCTGAGGAGGAGCTGAGGAG 540  
QY 541 TGGAGGCTTGGGAGTACCCAGCTGCGGAGCGCTGGCTGGGAGTGAACCTGTTGAGCTC 600  
Db 541 TGGAGGCTTGGGAGTACCCAGCTGCGGAGCGCTGGCTGGGAGTGAACCTGTTGAGCTC 600  
QY 601 CTGGGCTGGGAGTACCCAGCTGCGGAGCGCTGGCTGGGAGTGAACCTGTTGAGCTC 660  
Db 601 CTGGGCTGGGAGTACCCAGCTGCGGAGCGCTGGCTGGGAGTGAACCTGTTGAGCTC 660  
QY 661 TGCAGAGCTGGGAGTGGGAGCTGGGAGGAGCTTCAACCGGCTCAAGAAAGATGAGCAGC 720  
Db 661 TGCAGAGCTGGGAGTGGGAGCTGGGAGGAGCTTCAACCGGCTCAAGAAAGATGAGCAGC 720  
QY 721 CTGCAGAGCTGAGTCAACCTGAGCCTGGGAGCTTCAACCTGAGCTTCAACCTTCT 780  
Db 721 CTGCAGAGCTGAGTCAACCTGAGCCTGGGAGCTTCAACCTGAGCTTCAACCTTCT 780  
QY 781 CCTCTTGGCTGCGGCGCC 797  
Db 781 CCTCTTGGCTGCGGCGCC 797

## RESULT 2

US-10-212-793-1  
; Sequence 1, Application US/10212793  
; Publication No. US20030087395A1  
; GENERAL INFORMATION:  
; APPLICANT: Shi et al.  
; TITLE OF INVENTION: Cardiotrophin-Like Cytokine  
; FILE REFERENCE: PF865D1C1  
; CURRENT APPLICATION NUMBER: US/10/212,793  
; PRIOR FILING DATE: 2002-08-07  
; PRIOR APPLICATION NUMBER: US 09/438,299  
; PRIOR FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: US 09/106,182  
; PRIOR FILING DATE: 1998-06-29  
; PRIOR APPLICATION NUMBER: US 60/051,311  
; NUMBER OF SEQ ID NOS: 24  
; SEQ ID NO 1  
; LENGTH: 1710  
; TYPE: DNA  
; ORGANISM: homo sapiens  
; FEATURE:

; LOCATION: CDS  
; OTHER INFORMATION: (46)..(720)  
; FEATURE:  
; NAME/KEY: sig\_peptide  
; LOCATION: (46)..(126)  
; FEATURE:  
; NAME/KEY: mat\_peptide  
; LOCATION: (127)..(720)  
US-10-212-793-1

Query Match 94.0%; Score 749.4; DB 15; Length 1710;  
Best Local Similarity 99.9%; Pred. No. 2.6e-191;  
Matches 750; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 45 GCTTCGGGAGAGGAGCGGAGCCGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 104  
Db 1 GCTTCGGGAGAGGAGCGGAGCCGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 60  
QY 105 GGGGAGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 164  
Db 61 GGGGAGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120  
QY 165 CGAGCTTCAATCGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 224  
Db 121 CGAGCTTCAATCGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180  
QY 225 CTACCGGCTTCAATCGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 284  
Db 181 CTACCGGCTTCAATCGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240  
QY 285 GGGGCGGCTTCAATCGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 344  
Db 241 GGGGCGGCTTCAATCGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300  
QY 345 AGGAGCACTGTGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 404  
Db 301 AGGAGCACTGTGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360  
QY 405 AACTAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 464  
Db 361 AACTAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420  
QY 465 ACTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 524  
Db 421 ACTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480  
QY 525 AGCATTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 584  
Db 481 AGCATTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540  
QY 585 GAACCACTTGGAGCTCCGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 644  
Db 541 GAACCACTTGGAGCTCCGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600  
QY 645 TGGCTGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 704  
Db 601 TGGCTGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660  
QY 705 AAGAAAGAGATGAGAGCTTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 764  
Db 661 AAGAAAGAGATGAGAGCTTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720  
QY 765 TGACTTGTGAGCTTCT 795  
Db 721 TGACTTGTGAGCTTCT 751

## RESULT 3

US-09-931-704-4  
; Sequence 4, Application US/09931704  
; Patent No. US20020041873A1  
; GENERAL INFORMATION:  
; APPLICANT: Senaldi, Giorgio



TITLE OF INVENTION: Methode and Compositions for Treating Ige-Related Disease Using N  
FILE OF INVENTION: Inhibitors  
FILE REFERENCE: A-695  
CURRENT APPLICATION NUMBER: US/09/931,704  
CURRENT FILING DATE: 2001-08-16  
PRIOR APPLICATION NUMBER: US 60/226,436  
PRIOR FILING DATE: 2000-08-18  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 4  
LENGTH: 819  
TYPE: DNA  
ORGANISM: Murine  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (95)..(769)  
OTHER INFORMATION:  
NAME/KEY: mat.peptide  
LOCATION: (176)..()  
OTHER INFORMATION:  
NAME/KEY: mat.peptide  
LOCATION: (176)..(769)  
OTHER INFORMATION:  
NAME/KEY: s19.peptide  
LOCATION: (95)..(175)  
OTHER INFORMATION:  
US-09-931-704-4

Query Match 84.0%; Score 669.4; DB 9; Length 819;  
Best Local Similarity 92.0%; Pred. No. 7.1e-170;  
Matches 717; Conservative 0; Mismatches 61; Indels 1; Gaps 1;

1 ATTAAGCTTCCCGGAGGCGGCGGCTGCGCTCCCTCCCTCCGACGCTCCGGAAGAGG 60  
5 ATTAAGCTTCCCGGAGGCGGCGGCTGCGCTCCCTCCCTCCGACGCTCCGGAAGAGG 64  
61 CCGACCCGCGGCGGCGGCGGCGGCTGCGCTCCCTCCCTCCGACGCTCCGGAAGAGG 119  
65 CCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 124  
120 ATGTTAGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 179  
125 ATGTTAGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 184  
180 ACAGGAGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 239  
185 ACAGGAGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 244  
240 GAGCAGCAGCTCCGAGCTTGGCTGGAGCTTGAACCTGAGGCGGCGGCGGCGGCGGCGGCGG 299  
245 GAGCAGCAGCTCCGAGCTTGGCTGGAGCTTGAACCTGAGGCGGCGGCGGCGGCGGCGGCGG 304  
300 GAGCAGCAGCTCCGAGCTTGGCTGGAGCTTGAACCTGAGGCGGCGGCGGCGGCGGCGGCGG 359  
305 GAGCAGCAGCTCCGAGCTTGGCTGGAGCTTGAACCTGAGGCGGCGGCGGCGGCGGCGGCGG 364  
360 TTGAGAGTGGGAGGAGCTTGAACCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 419  
365 TTGAGAGTGGGAGGAGCTTGAACCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 424  
420 AGCAGCAGCTTCTGTTACTTGGTGGGCTCAACCGTCAAGGCTGAGGCGGCGGCGGCGGCGG 479  
425 AGTCACTCTCTGTTACTTGGTGGGCTCAACCGTCAAGGCTGAGGCGGCGGCGGCGGCGGCGG 484  
480 CGCAGCTTGGGCGGAGCTTGAACCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 539  
485 CGTACCTTGGGCGGAGCTTGAACCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 544  
540 ATGAGAGCTTGGGCGGAGCTTGAACCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 599  
545 ATGAGAGCTTGGGCGGAGCTTGAACCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 604  
600 CTTGAGCTTGGGCGGAGCTTGAACCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 659

DB 605 CTTGAGCTTGGGCGGAGCTTGAACCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 664  
QY 660 CTTGAGCTTGGGCGGAGCTTGAACCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 719  
DB 665 CTTGAGCTTGGGCGGAGCTTGAACCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 724  
QY 720 CTTGAGCTTGGGCGGAGCTTGAACCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 778  
DB 725 CTTGAGCTTGGGCGGAGCTTGAACCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 783

RESULT 4  
US-09-931-704-3  
Sequence 3, Application US/09931704  
Patent No. US20020041873A1

GENERAL INFORMATION:  
APPLICANT: Senaldi, Giorgio

TITLE OF INVENTION: Methode and Compositions for Treating Ige-Related Disease Using N

FILE REFERENCE: A-695  
CURRENT APPLICATION NUMBER: US/09/931,704

CURRENT FILING DATE: 2001-08-16  
PRIOR APPLICATION NUMBER: US 60/226,436  
PRIOR FILING DATE: 2000-08-18  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 3

LENGTH: 5087  
TYPE: DNA  
ORGANISM: Homo sapiens

FEATURE:  
NAME/KEY: misc.feature  
LOCATION: (137)..(138)

OTHER INFORMATION: product = "INTERVENING UNSEQUENCED REGION OF >1KB"  
US-09-931-704-3

Query Match 65.7%; Score 523.4; DB 9; Length 5087;  
Best Local Similarity 99.8%; Pred. No. 1.1e-130;  
Matches 524; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

271 ATCTGAATCTAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 330  
3363 AGCTGAATCTAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3422  
331 CAGAGACTTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 390  
3423 CAGAGACTTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3482  
391 TGGGCTGAGCCAGAGCTTGAACCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 450  
3483 TGGGCTGAGCCAGAGCTTGAACCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3542  
451 ACCGTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 510  
3543 ACCGTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3602  
511 AGGCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 570  
3603 AGGCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3662  
571 CGCTGCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 630  
3663 CGCTGCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3722  
631 AGATGAGAGCTTGGGCGGAGCTTGAACCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 690  
3723 AGATGAGAGCTTGGGCGGAGCTTGAACCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3782  
691 ACTTGAACCGGCTCAAGAGAGATGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 750  
3783 ACTTGAACCGGCTCAAGAGAGATGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3842

QY 751 GGGCTCATGGCTTGTGACTTGTGACCTTCTCTTGGCTCCCC 795  
DB 3843 GGGCTCATGGCTTGTGACTTGTGACCTTCTCTTGGCTCCCC 3887

RESULT 5  
US-09-864-761-23175/c  
; Sequence 23175, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharon G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY  
; FILE REFERENCE: Aecmca-X-1  
; CURRENT FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 09/608,408  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 09/774,203  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 49117  
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 23175  
; LENGTH: 495  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO AC005649.1  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.2  
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.1  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.1  
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.1  
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.4  
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.2  
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4.4  
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.5  
; OTHER INFORMATION: SWISSPROT HIT: Q63086, EVALU8 8.00e-03  
; OTHER INFORMATION: NT HIT: g11439486, EVALU8 0.00e+00

OTHER INFORMATION: EST\_HUMAN HIT: A1752561.1, EVALU8 0.00e+00  
US-09-864-761-23175

Query Match  
Best Local Similarity 99.8%; Score 493.4; DB 9; Length 495;  
Matches 494; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 273 CTGAACCTAGTGGGCCCCCTTTCACAGAGCAGACTTCAACCCCTCCGCTGGGGCA 332  
DB 495 CTGAACCTAGTGGGCCCCCTTTCACAGAGCAGACTTCAACCCCTCCGCTGGGGCA 436

QY 333 GAGACTTGGCCAGGGCCACTGTGACTTGGAGGTGTGGCAAGCTCAATGACAACTG 392  
DB 435 AAGACTTGGCCAGGGCCACTGTGACTTGGAGGTGTGGCAAGCTCAATGACAACTG 376

QY 353 CGGCTGACCCAGAACTAGAGGCGCTACAGCCACCTTGTGTACTTGGCGGCTCAAC 452  
DB 375 CGGCTGACCCAGAACTAGAGGCGCTACAGCCACCTTGTGTACTTGGCGGCTCAAC 316

QY 453 CGTCAGGCTGACACTGTGAGCTGGCGCGCAGCCTGGCCACTTGTGACAGCCTCCAG 512  
DB 315 CGTCAGGCTGACACTGTGAGCTGGCGCGCAGCCTGGCCACTTGTGACAGCCTCCAG 256

QY 513 GGCCTGCTGGGCGAGCATTGGGGCGCTCATGGCACTTGGGCTACCACTGCCCCAGCG 572  
DB 255 GGCCTGCTGGGCGAGCATTGGGGCGCTCATGGCACTTGGGCTACCACTGCCCCAGCG 196

QY 573 CTGCTGAGGACTGAACCCACTTGAATCTTGGCCCTGGCCACAGTACTTCTCCAGAG 632  
DB 195 CTGCTGAGGACTGAACCCACTTGAATCTTGGCCCTGGCCACAGTACTTCTCCAGAG 136

QY 633 ATGACGACTTCTGGCTCTGAAGAGCTGAGACTGTGGCGCTGGCCAGAGAC 692  
DB 135 ATGACGACTTCTGGCTCTGAAGAGCTGAGACTGTGGCGCTGGCCAGAGAC 76

QY 753 TTCAACCGGCTCAAGAAAGATGAGCTTCACAGCTGAGTACCTTCACCTGGGG 752  
DB 75 TTCAACCGGCTCAAGAAAGATGAGCTTCACAGCTGAGTACCTTCACCTGGGG 16

QY 753 GCTCATGGCTTCTGA 767  
DB 15 GCTCATGGCTTCTGA 1

RESULT 6  
US-09-864-761-6462/c  
; Sequence 6462, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharon G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY  
; FILE REFERENCE: Aecmca-X-1  
; CURRENT FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00662  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00661  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00670  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: US 60/234,687  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: US 09/608,408  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 09/774,203  
PRIOR FILING DATE: 2001-01-29  
NUMBER OF SEQ ID NOS: 49117  
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
SEQ ID NO 6462  
LENGTH: 492  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO AC005849.1  
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.2  
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.1  
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.1  
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.1  
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.4  
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.2  
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4.4  
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.5  
US-09-864-761-6462

Query Match 46.3%; Score 369; DB 9; Length 492;  
Best Local Similarity 100.0%; Pred. No. 2.5e-89;  
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
427 TTCTGTTACTTGGCGGCTCAACCGTACGAGCTGCTGAGCTGGCGGAGCC 486  
492 TTCTGTTACTTGGCGGCTCAACCGTACGAGCTGCTGAGCTGGCGGAGCC 433  
487 TGGCCACTTCTGACACGAGCTCCAGGAGCTGCTGAGGAGCATTTGGGAGCTGAGGAG 546  
432 TGGCCACTTCTGACACGAGCTCCAGGAGCTGCTGAGGAGCATTTGGGAGCTGAGGAG 373  
547 CTCTGGAGCTTACCACTGCGCCAGCCGCTGCTGGAGCTGAGACCACTTGGAGCTTGGCC 606  
372 CTCTGGAGCTTACCACTGCGCCAGCCGCTGCTGGAGCTGAGACCACTTGGAGCTTGGCC 313  
607 CTGGCCAGAGTGACTTCTTCCAGAGATGAGACATTTGGGAGCTGAGGAGAGCTGAGGAG 666  
312 CTGGCCAGAGTGACTTCTTCCAGAGATGAGACATTTGGGAGCTGAGGAGAGCTGAGGAG 253  
667 CTTGGCTGAGGAGCTGAGGAGAGATTTCAACCGGCTCAAGAGAGAGATGAGAGCTCCAG 726  
252 CTTGGCTGAGGAGCTGAGGAGAGATTTCAACCGGCTCAAGAGAGAGATGAGAGCTCCAG 193  
727 CAGCTGAGTCACTGAGGAGCTGAGGAGAGATTTCAACCGGCTCAAGAGAGAGATGAGAGCT 786  
192 CAGCTGAGTCACTGAGGAGCTGAGGAGAGATTTCAACCGGCTCAAGAGAGAGATGAGAGCT 133  
787 CGCTCCCC 795  
132 CGCTCCCC 124

RESULT 7

US-09-765-231A-75  
Sequence 75, Application US/09765231A  
Patent No. US20020119452A1  
GENERAL INFORMATION:  
APPLICANT: Searle/Monsanto  
APPLICANT: Phippard, Deborah  
APPLICANT: Vasanthakumari, Geetha  
APPLICANT: Dotson, Stanton  
APPLICANT: Ma, Xiao-Jun  
TITLE OF INVENTION: Osteoarthritis tissue-derived nucleic acids, polypeptides,  
FILE REFERENCE: SO-3221 PR  
CURRENT APPLICATION NUMBER: US/09/765,231A  
CURRENT FILING DATE: 2001-01-18  
NUMBER OF SEQ ID NOS: 82  
SEQ ID NO 75  
LENGTH: 283  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-765-231A-75

Query Match 33.8%; Score 269.4; DB 10; Length 283;  
Best Local Similarity 99.3%; Pred. No. 1.2e-62;  
Matches 281; Conservative 0; Mismatches 1; Indels 1; Gaps 1;  
37 CTCGGCAGAGCTCCGGAG 96  
1 CTCGGCAGAGCTCCGGAG 60  
97 TCCGAG 155  
61 TCCGAG 120  
156 CTTGAG 215  
121 CTTGAG 180  
216 ACCATGAG 275  
181 ACCATGAG 240  
276 AACTAGCTGAG 318  
241 AACTAGCTGAG 283

RESULT 8  
US-10-027-632-134702  
Sequence 134702, Application US/10027632  
Publication No. US20030204075A9  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
TITLE OF INVENTION: Polymorphisms in the Human Genome  
FILE REFERENCE: 108827.129  
CURRENT APPLICATION NUMBER: US/10/027,632  
CURRENT FILING DATE: 2002-04-30  
PRIOR APPLICATION NUMBER: US 60/218,006  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 60/198,676  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: US 60/193,483  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: US 60/185,218  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/167,363  
PRIOR FILING DATE: 1999-11-23  
PRIOR APPLICATION NUMBER: US 60/156,358  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: US 60/146,002  
PRIOR FILING DATE: 1999-08-09  
NUMBER OF SEQ ID NOS: 325720  
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 134702  
LENGTH: 809  
TYPE: DNA  
ORGANISM: Human  
US-10-027-632-134702

Query Match 22.1%; Score 175.8; DB 13; Length 809;  
Best Local Similarity 86.9%; Pred. No. 1.7e-37;  
Matches 192; Conservative 1; Mismatches 28; Indels 0; Gaps 0;

QY 66 CCGGCGCGGCGCCAGCCCGCCATGAGACCTCCGAGAGGGAGCTCCGGGGAGTTA 125  
DB 17 CCGGCGCGGCGCTCATGCTTCTCTGTCATCTGCGCCAGGGGACTCGTGGGGAGTTA 76  
QY 126 GGGTGGCTGTGACGGTGTCTGTGGACCTCCCTGACGATCGACTCTCAATGACAGAGG 185  
DB 77 GGGTGGCTGTGACGGTGTCTGTGGACCTCCCTGACGATCGACTCTCAATGACAGAGG 136  
QY 186 GACCCAGGGGCTGGCCCTTCCTCATCCAGAAACCTATGACCTCACCGGCTACCTGAGAC 245  
DB 137 GACCCAGGGGCTGGCCCTTCCTCATCCAGAAACCTATGACCTCACCGGCTACCTGAGAC 196  
QY 246 CAATCCGAGCTGTGGCTGGGACCTATGACTGACTGGG 286  
DB 197 CAATCCGAGCTGTGGCTGGGACCTATGACTGACTGAGCG 237

RESULT 9  
US-10-027-632-134702

Sequence 134702, Application US/10027632  
GENERAL INFORMATION:

APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
FILE REFERENCE: 108827,129  
CURRENT APPLICATION NUMBER: US/10/027,632

PRIOR FILING DATE: 2002-04-30  
PRIOR APPLICATION NUMBER: US 60/218,006  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 60/198,676  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: US 60/193,483  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: US 60/185,218  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/167,363  
PRIOR FILING DATE: 1999-11-23  
PRIOR APPLICATION NUMBER: US 60/156,358  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: US 60/146,002  
PRIOR FILING DATE: 1999-08-09  
NUMBER OF SEQ ID NOS: 325720  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 134702  
LENGTH: 809  
TYPE: DNA  
ORGANISM: Human  
US-10-027-632-134702

Query Match 22.1%; Score 175.8; DB 14; Length 809;  
Best Local Similarity 86.9%; Pred. No. 1.7e-37;  
Matches 192; Conservative 1; Mismatches 28; Indels 0; Gaps 0;

QY 66 CCGGCGCGGCGCCAGCCCGCCATGAGACCTCCGAGAGGGAGCTCCGGGGAGTTA 125  
DB 17 CCGGCGCGGCGCTCATGCTTCTCTGTCATCTGCGCCAGGGGACTCGTGGGGAGTTA 76  
QY 126 GGGTGGCTGTGACGGTGTCTGTGGACCTCCCTGACGATCGACTCTCAATGACAGAGG 185  
DB 77 GGGTGGCTGTGACGGTGTCTGTGGACCTCCCTGACGATCGACTCTCAATGACAGAGG 136  
QY 186 GACCCAGGGGCTGGCCCTTCCTCATCCAGAAACCTATGACCTCACCGGCTACCTGAGAC 245  
DB 197 CAATCCGAGCTGTGGCTGGGACCTATGACTGACTGAGCG 237

DB 137 GACCCAGGGGCTGGCCCTTCCTCATCCAGAAACCTATGACCTCACCGGCTACCTGAGAC 196  
QY 246 CAATCCGAGCTGTGGCTGGGACCTATGACTGACTGAGCG 286  
DB 197 CAATCCGAGCTGTGGCTGGGACCTATGACTGACTGAGCG 237

RESULT 10  
US-10-212-793-7

Sequence 7, Application US/10212793  
Publication No. US20030087935A1

GENERAL INFORMATION:

APPLICANT: Shi, et al.  
TITLE OF INVENTION: Cardiotrophin-like Cytokine  
FILE REFERENCE: P385D1C1

CURRENT APPLICATION NUMBER: US/10/212,793  
CURRENT FILING DATE: 2002-08-07  
PRIOR APPLICATION NUMBER: US 09/438,299  
PRIOR FILING DATE: 1999-11-12  
PRIOR APPLICATION NUMBER: US 09/106,182  
PRIOR FILING DATE: 1998-06-29  
PRIOR APPLICATION NUMBER: US 60/051,311  
PRIOR FILING DATE: 1997-06-30  
NUMBER OF SEQ ID NOS: 24  
SEQ ID NO 7

LENGTH: 396

TYPE: DNA

ORGANISM: homo sapiens

FEATURE:

NAME/KEY: Site

LOCATION: (199)

OTHER INFORMATION: n equals any nucleotide

FEATURE:

NAME/KEY: Site

LOCATION: (293)

OTHER INFORMATION: n equals any nucleotide

FEATURE:

NAME/KEY: Site

LOCATION: (306)

OTHER INFORMATION: n equals any nucleotide

FEATURE:

NAME/KEY: Site

LOCATION: (360)

OTHER INFORMATION: n equals any nucleotide

FEATURE:

NAME/KEY: Site

LOCATION: (371)

OTHER INFORMATION: n equals any nucleotide

FEATURE:

NAME/KEY: Site

LOCATION: (377)

OTHER INFORMATION: n equals any nucleotide

FEATURE:

NAME/KEY: Site

LOCATION: (383)

OTHER INFORMATION: n equals any nucleotide

US-10-212-793-7

Query Match 10.1%; Score 80.2; DB 15; Length 396;  
Best Local Similarity 96.5%; Pred. No. 7e-12;  
Matches 82; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 711 AAGATGACGCTTCCAGACGCTGACGACCTTCGACACCTGGGGGCTCAATGAGCTTGAATT 770  
DB 4 AAGAGGAGGCTTCCAGACGCTGACGACCTTCGACACCTGGGGGCTCAATGAGCTTGAATT 63  
QY 771 CTGACCTTCTCTCTGCTGCTCCCC 795  
DB 64 CTGACCTTCTCTCTGCTGCTCCCC 88

RESULT 11  
US-09-908-975-29446

```

; Sequence 29446, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLIC
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 29446
; LENGTH: 65
; TYPE: DNA
; ORGANISM: Mus musculus
; US-09-908-975-29446

```

```

Query Match
Best Local Similarity 7.4%; Score 58.6; DB 13; Length 65;
Matches 61; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

```

Qy 651 CTGAAGAGCTGCAGACTGCTGTGCGCTGCGCCAGACTTCAACGGCTCAAGAG 710
Db 1 CTGAAGAGCTGCAGACTGCTGTGCGCTGCGCCAGACTTCAACGGCTTAAAGAG 60

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Qy 711 AAGAT 715
Db 61 AAGAT 65

```

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RESULT 12
US-10-102-806-266
; Sequence 266, Application US/10102806
; Publication No. US20030054421A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA103P1C1
; CURRENT APPLICATION NUMBER: US/10/102,806
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 09/925,298
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05881
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 846
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 266
; LENGTH: 2320
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-102-806-266

```

```

Query Match
Best Local Similarity 5.9%; Score 46.8; DB 15; Length 2320;
Matches 156; Conservative 0; Mismatches 182; Indels 0; Gaps 0;

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Qy 11 CGCGGAGCGCGGCTGCGCTCCACTCGCGAGCGCTCGGAGAGCGGACCGGG 70
Db 64 CGGAGGCTGTGCGAGCCGCGCGCGGCGGCGGAGAGCGGCGCGGACCGCTCCG 123
Qy 71 CGGCGGAGCGCGGCTGCGCTCCACTCGCGAGCGGAGAGCGGAGAGCGGAG 130
Db 124 CCGGCGCGCGGCGGCTGCGCTCCACTCGCGAGCGGAGAGCGGAGAGCGGAG 183

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Qy 131 CTGTGACAGGCTGCTGTGACCTCTGACAGTGCAGCTCTCAATGACAGGGAGCC 190
Db 184 TGCGCTCGGCTTTTACGCCCCCGAGAGAGTTCGCTGTGCTGCCCCCAAGCC 243
Qy 191 AGGGCTGAGCCCTTCATTCAGAAAACCTATGACTCAACCGCTTACGAGACCACT 250
Db 244 AAGAGGATTCCTTCGCGCGCGGAGAGCGAGCTTCCCGGAGACCGGCGGCGG 303
Qy 251 CGGAGCTTGTGAGGAGCTTATCTGACTTACCTGAGCCCCCTTCAAGAGCGAGCTT 310
Db 304 GACAGAGTGGCGGGGTGGGAGATTCCTCCGCGCGCGCGGAGAGCTTTCCTGCT 363
Qy 311 CAACCTCCCGCGCGGAGAGAGCTGCGCGAGG 348
Db 364 CCACTTCCCTTGTGAGGATGCGAGCATGACAGAGG 401

```

```

RESULT 13
US-10-014-717-1
; Sequence 1, Application US/10014717
; Publication No. US20020192778A1
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Ligon, James
; APPLICANT: Molnar, Jervan
; APPLICANT: Zirkle, Ross
; APPLICANT: Cyr, Devon
; APPLICANT: Goerlach, Joern
; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
; FILE REFERENCE: 4-30582A
; CURRENT APPLICATION NUMBER: US/10/014,717
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US/09/335,409
; PRIOR FILING DATE: 1999-06-17
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 68750
; TYPE: DNA
; ORGANISM: Sorangium cellulosum
; US-10-014-717-1

```

```

Query Match
Best Local Similarity 5.0%; Score 44.8; DB 14; Length 68750;
Matches 112; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

```

```

Qy 456 CAGGCTGCACTGTGAGCTGCGCGGAGAGCTGCGGCACTTCTGACAGAGCTCCAGGGC 515
Db 57992 CAGGAGGAGTGGGAGAGCGGAGAGAGTCCGCGGCTTCCGATTCAGCGCGGCG 58051
Qy 516 CTGCTGGGAGCATTTGCGGGCGTCTATGAGCACTGAGCTGAGCCAGCGCGCTG 575
Db 58052 GTGCTGCGCGGAGTGGCGGCGTCTGAGAGCCCGGAGAGTCAACTGCGCGCTGCGC 58111
Qy 576 CTTGGGAGTGAACCTTGAATCTGCGCTGCGGCTGCGGCAAGTATCTCCAGAAAGT 635
Db 58112 GCCGCTTCAATGCGCGGCGTCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTG 58171
Qy 636 GACGACTTCTGAGCTGAGAGAGAGCTGAGAGAGCTGAGAGAGCTGAGAGAG 679
Db 58172 CTTCAATACGCGCGGCGGCTTGGCGGGGCTTCCGCGAGCTGTGCGG 58215

```

```

RESULT 14
US-10-295-027-1127
; Sequence 1127, Application US/10295027
; Publication No. US2003023250A1
; GENERAL INFORMATION:
; APPLICANT: Afari, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.

```

APPLICANT: Glyme, Richard  
APPLICANT: Hevazi, Peter A.  
APPLICANT: Mack, David H.  
APPLICANT: Murray, Richard  
APPLICANT: Watson, Susan R.  
APPLICANT: Eos Biotechnology, Inc.  
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and  
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer  
FILE REFERENCE: 018501-012500US  
CURRENT APPLICATION NUMBER: US/10/295,027  
PRIOR FILING DATE: 2002-11-13  
PRIOR APPLICATION NUMBER: US 09/663,733  
PRIOR FILING DATE: 2000-09-15  
PRIOR APPLICATION NUMBER: US 60/350,666  
PRIOR FILING DATE: 2001-11-13  
PRIOR APPLICATION NUMBER: US 60/335,394  
PRIOR FILING DATE: 2001-11-15  
PRIOR APPLICATION NUMBER: US 60/332,464  
PRIOR FILING DATE: 2001-11-21  
PRIOR APPLICATION NUMBER: US 60/347,393  
PRIOR FILING DATE: 2001-11-29  
PRIOR APPLICATION NUMBER: US 60/340,376  
PRIOR FILING DATE: 2001-12-14  
PRIOR APPLICATION NUMBER: US 60/347,211  
PRIOR FILING DATE: 2002-01-08  
PRIOR APPLICATION NUMBER: US 60/347,349  
PRIOR FILING DATE: 2002-01-10  
PRIOR APPLICATION NUMBER: US 60/355,250  
PRIOR FILING DATE: 2002-02-08  
PRIOR APPLICATION NUMBER: US 60/356,714  
PRIOR FILING DATE: 2002-02-13  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 1386  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO: 1127  
LENGTH: 3195  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-295-027-1127

Query Match 5.5%; Score 43.6; DB 12; Length 3195;  
Best Local Similarity 44.3%; Pred. No. 0.053; Indels 0; Gaps 0;  
Matches 178; Conservative 0; Mismatches 224; Indels 0; Gaps 0;  
QY 320 CCGCTGGGGGAGAGACTTGGCCAGGCGCACTGTGACTTGAAGTGTGGGAAGCT 379  
DB 1328 CCACCTGGCCGGGTGGCTTGTGCGCAGGTCAAGTCATCGGGGTGCTGGCCTCAGCTC 1387  
QY 380 CAATGACAACTGGGGCTGAGCCAGAACTAGAGGCTTACAGCCACTTGTGTACTT 439  
DB 1388 GGTGACGGCGACCCGGGTGGCGGAGCATCTGCTACGTGGGCAACGAGCCTGGAACAACCT 1447  
QY 440 GCGTGGCTCAACCGTCAAGGCTGCGACTGTAGTGGGCGGCGAGCCCTGGCCACTTGTG 499  
DB 1448 GCGGGCTTCTGCTGGGCGCGCTGTATCTTCACTTTCATGGCAACATGTTCTCTCT 1507  
QY 500 CACCACTTCAGGAGCTGTGGGAGCATGCGGGCTCATGAGGCTTGTGGTACCC 559  
DB 1508 GCGGGCTTCTGCTGGGAGCATGCGGGCTCATGAGGCTTGTGGTACCC 559  
QY 560 ACTGCGCCAGCGGCTGTGGGAGCATGAACTTGAAGTCTGTGGCCTTGTGGCCACAGTGA 619  
DB 1568 CAAGACGCAAGCTGAGAGAACTGATGATCGGCTGGGCTGTTCACGCTCTTACAC 1627  
QY 620 CTTCCTCAGAAAGATGAGACATTTGTGCTGTGAAGAGCTGAGACTGTGGTGGCG 679  
DB 1628 GGTGCGCGCGGGGTGGTGGTGGCTGTCTTTCATCAGAGCAACAACCGCCGCGCTG 1687  
QY 680 CTCGGCCAGAGACTTCAACCGGCTCAAGAAAGATGAGCC 721  
DB 1688 GAGGCGCAAGCAACTGCGCTGTGGGAGCTTGGAGCC 1729

RESULT 15  
US-10-285-976-54  
Sequence 54, Application US/10285976  
Publication No. US20030165500A1  
GENERAL INFORMATION:  
APPLICANT: Rhee, Chae-Seo  
APPLICANT: Malini, Sen  
APPLICANT: Wu, Christina  
APPLICANT: Leoni, Lorenzo M.  
APPLICANT: Corr, Maripat  
APPLICANT: Carson, Dennis A.  
TITLE OF INVENTION: The Regents of the University of California  
TITLE OF INVENTION: Wnt and Frizzled Receptors as Targets for Immunotherapy  
FILE REFERENCE: 023070-130320US  
CURRENT APPLICATION NUMBER: US/10/285,976  
PRIOR FILING DATE: 2002-11-01  
PRIOR APPLICATION NUMBER: US 60/287,995  
PRIOR FILING DATE: 2001-05-01  
PRIOR APPLICATION NUMBER: WO PCT/US02/13802  
PRIOR FILING DATE: 2002-05-01  
NUMBER OF SEQ ID NOS: 232  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO: 54  
LENGTH: 3195  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: human frizzled8 (Fzd8)  
US-10-285-976-54

Query Match 5.5%; Score 43.6; DB 13; Length 3195;  
Best Local Similarity 44.3%; Pred. No. 0.053; Indels 0; Gaps 0;  
Matches 178; Conservative 0; Mismatches 224; Indels 0; Gaps 0;  
QY 320 CCGCTGGGGGAGAGACTTGGCCAGGCGCACTGTGACTTGAAGTGTGGGAAGCT 379  
DB 1328 CCACCTGGCCGGGTGGCTTGTGCGCAGGTCAAGTCATCGGGGTGCTGGCCTCAGCTC 1387  
QY 380 CAATGACAACTGGGGCTGAGCCAGAACTAGAGGCTTACAGCCACTTGTGTACTT 439  
DB 1388 GGTGACGGCGACCCGGGTGGCGGAGCATCTGCTACGTGGGCAACGAGCCTGGAACAACCT 1447  
QY 440 GCGTGGCTCAACCGTCAAGGCTGCGACTGTAGTGGGCGGCGAGCCCTGGCCACTTGTG 499  
DB 1448 GCGGGCTTCTGCTGGGCGCGCTGTATCTTCACTTTCATGGCAACATGTTCTCTCT 1507  
QY 500 CACCACTTCAGGAGCTGTGGGAGCATGCGGGCTCATGAGGCTTGTGGTACCC 559  
DB 1508 GCGGGCTTCTGCTGGGAGCATGCGGGCTCATGAGGCTTGTGGTACCC 559  
QY 560 ACTGCGCCAGCGGCTGTGGGAGCATGAACTTGAAGTCTGTGGCCTTGTGGCCACAGTGA 619  
DB 1568 CAAGACGCAAGCTGAGAGAACTGATGATCGGCTGGGCTGTTCACGCTCTTACAC 1627  
QY 620 CTTCCTCAGAAAGATGAGACATTTGTGCTGTGAAGAGCTGAGACTGTGGTGGCG 679  
DB 1628 GGTGCGCGCGGGGTGGTGGTGGCTGTCTTTCATCAGAGCAACAACCGCCGCGCTG 1687  
QY 680 CTCGGCCAGAGACTTCAACCGGCTCAAGAAAGATGAGCC 721  
DB 1688 GAGGCGCAAGCAACTGCGCTGTGGGAGCTTGGAGCC 1729

Search completed: February 9, 2004, 09:36:12  
Job time: 369.674 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using SW model

Run on: February 9, 2004, 06:10:20 / Search time 65.1015 Seconds  
(without alignments)  
5403.600 Million cell updates/sec

Title: US-09-931-704-1

Perfect score: 797

Sequence: 1 attaaagctcgcgagcc.....ctcctcttcgctccccc 797

Scoring table: IDENTITY\_NUC

Gapop 10.0, Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

Issued Patents NA:  
1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:\*  
2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/2/ina/PTUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/2/ina/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	797	100.0	797	1	US-08-792-019B-1
2	797	100.0	797	3	US-08-988-819-1
3	797	100.0	797	3	US-09-016-534-1
4	749.4	94.0	1710	3	US-09-106-182-1
5	669.4	84.0	819	3	US-08-792-019B-4
6	669.4	84.0	819	3	US-08-988-819-4
7	669.4	84.0	819	3	US-09-016-534-4
8	523.4	65.7	5087	1	US-08-792-019B-3
9	523.4	65.7	5087	3	US-08-988-819-3
10	523.4	65.7	5087	3	US-09-016-534-3
11	80.2	10.1	396	3	US-09-106-182-7
12	44.8	5.6	68750	3	US-09-335-409-1
13	44.8	5.6	68750	4	US-09-568-102-1
14	44.8	5.6	68750	4	US-09-567-969-1
15	44.8	5.6	68750	4	US-09-568-480-1
16	44.8	5.6	68750	4	US-09-568-486-1
17	44.8	5.6	68750	4	US-09-568-472-1
18	44.8	5.6	68750	4	US-09-567-899-1
19	42.2	5.3	1590	4	US-09-252-991A-10070
20	42.2	5.3	1878	4	US-09-252-991A-9765
21	38.6	4.8	6858	4	US-09-252-991A-1219
22	38.4	4.8	71989	4	US-09-443-501A-2
23	38	4.8	223	1	US-08-383-761-1
24	38	4.8	223	1	US-08-824-277-1
25	37.8	4.7	3129	3	US-09-387-695-1
26	37.8	4.7	49272	1	US-08-614-770A-1
27	37.6	4.7	1071	4	US-09-252-991A-14206

C 28	37.6	4.7	2388	4	US-09-252-991A-14064	Sequence 14064, A
29	37.4	4.7	900	4	US-09-252-991A-9282	Sequence 9282, Ap
30	37.4	4.7	3729	4	US-09-252-991A-9272	Sequence 9272, Ap
C 31	37.2	4.7	1242	4	US-09-252-991A-9668	Sequence 9668, Ap
32	37.2	4.7	1521	4	US-09-252-991A-9746	Sequence 9746, Ap
33	37.2	4.7	2511	4	US-09-252-991A-9494	Sequence 9494, Ap
C 34	37.2	4.7	3583	4	US-09-252-991A-9541	Sequence 9541, Ap
C 35	37.2	4.7	3984	4	US-09-016-434-1199	Sequence 1199, Ap
C 36	37	4.6	468	4	US-09-252-991A-3528	Sequence 3528, Ap
37	37	4.6	1449	4	US-09-252-991A-3558	Sequence 3558, Ap
38	37	4.6	1698	4	US-09-252-991A-3551	Sequence 3551, Ap
C 39	37	4.6	2196	4	US-09-252-991A-3536	Sequence 3536, Ap
C 40	36.8	4.6	336	4	US-09-252-991A-12979	Sequence 12979, A
41	36.8	4.6	1059	4	US-09-252-991A-12662	Sequence 12662, A
42	36.8	4.6	1308	4	US-08-937-067-18	Sequence 18, Appl
43	36.8	4.6	2075	4	US-09-087-031E-2	Sequence 2, Appl
44	36.8	4.6	2078	4	US-09-087-031E-1	Sequence 1, Appl
45	36.8	4.6	2124	4	US-09-087-031E-26	Sequence 26, Appl

#### ALIGNMENTS

RESULT 1  
US-08-792-019B-1  
Sequence 1, Application US/08792019B  
Patent No. 5741772  
GENERAL INFORMATION:  
APPLICANT: CHANG, MING-SHI  
TITLE OF INVENTION: THE NEUROTROPIC FACTOR NNT-1  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: AMGEN INC.  
STREET: 1640 DEHAVILLAND DRIVE  
CITY: THOUSAND OAKS  
STATE: CA  
COUNTRY: USA  
ZIP: 91320  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/792,019B  
FILING DATE: 03-FEB-1997  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: COOK, ROBERT R.  
REGISTRATION NUMBER: 31,602  
REFERENCE/DOCKET NUMBER: A-442  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 797 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 90..764  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 171..764  
FEATURE:  
NAME/KEY: sig\_peptide  
LOCATION: 90..170  
US-08-792-019B-1

Query Match 100.0%; Score 797; DB 1; Length 797;  
Best Local Similarity 100.0%; Pred. No. 4,7e-181;  
Matches 797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATTAAGCTTCGCGGAGCCGCGGCTCGCCCTCCCACTCCGCCAGCCTCCGGAGAGAG 60  
DB 1 ATTAAGCTTCGCGGAGCCGCGGCTCGCCCTCCCACTCCGCCAGCCTCCGGAGAGAG 60  
QY 61 CCGGACCCCGGCGGAGCCGCGGCTCGCCCTCCCACTCCGCCAGCCTCCGGAGAGAG 120  
DB 61 CCGGACCCCGGCGGAGCCGCGGCTCGCCCTCCCACTCCGCCAGCCTCCGGAGAGAG 120  
QY 121 TGTAGCGTGTGCTGCAAGGCTGCTGCAAGCCTCCGCTGCAAGGCTGCTGCAAGG 180  
DB 121 TGTAGCGTGTGCTGCAAGGCTGCTGCAAGCCTCCGCTGCAAGGCTGCTGCAAGG 180  
QY 181 CAGGGAGCCGAGGCTGCGGCTCGCCCTCCCACTCCGCCAGCCTCCGGAGAGAG 240  
DB 181 CAGGGAGCCGAGGCTGCGGCTCGCCCTCCCACTCCGCCAGCCTCCGGAGAGAG 240  
QY 241 AGCAGCACTTCGCGGAGCCGCGGCTCGCCCTCCCACTCCGCCAGCCTCCGGAGAG 300  
DB 241 AGCAGCACTTCGCGGAGCCGCGGCTCGCCCTCCCACTCCGCCAGCCTCCGGAGAG 300  
QY 301 AGCAGCACTTCGCGGAGCCGCGGCTCGCCCTCCCACTCCGCCAGCCTCCGGAGAG 360  
DB 301 AGCAGCACTTCGCGGAGCCGCGGCTCGCCCTCCCACTCCGCCAGCCTCCGGAGAG 360  
QY 361 TGGAGGTGTGCGGAGCCGCGGCTCGCCCTCCCACTCCGCCAGCCTCCGGAGAG 420  
DB 361 TGGAGGTGTGCGGAGCCGCGGCTCGCCCTCCCACTCCGCCAGCCTCCGGAGAG 420  
QY 421 GCGACCTTGTGTGCTGCAAGGCTGCTGCAAGCCTCCGCTGCAAGGCTGCTGCAAGG 480  
DB 421 GCGACCTTGTGTGCTGCAAGGCTGCTGCAAGCCTCCGCTGCAAGGCTGCTGCAAGG 480  
QY 481 GCGACCTTGTGTGCTGCAAGGCTGCTGCAAGCCTCCGCTGCAAGGCTGCTGCAAGG 540  
DB 481 GCGACCTTGTGTGCTGCAAGGCTGCTGCAAGCCTCCGCTGCAAGGCTGCTGCAAGG 540  
QY 541 TGGAGGTGTGCGGAGCCGCGGCTCGCCCTCCCACTCCGCCAGCCTCCGGAGAG 600  
DB 541 TGGAGGTGTGCGGAGCCGCGGCTCGCCCTCCCACTCCGCCAGCCTCCGGAGAG 600  
QY 601 TGGAGGTGTGCGGAGCCGCGGCTCGCCCTCCCACTCCGCCAGCCTCCGGAGAG 660  
DB 601 TGGAGGTGTGCGGAGCCGCGGCTCGCCCTCCCACTCCGCCAGCCTCCGGAGAG 660  
QY 661 TGGAGGTGTGCGGAGCCGCGGCTCGCCCTCCCACTCCGCCAGCCTCCGGAGAG 720  
DB 661 TGGAGGTGTGCGGAGCCGCGGCTCGCCCTCCCACTCCGCCAGCCTCCGGAGAG 720  
QY 721 CTGCAAGCTGCAAGGCTGCTGCAAGGCTGCTGCAAGGCTGCTGCAAGGCTGCTG 780  
DB 721 CTGCAAGCTGCAAGGCTGCTGCAAGGCTGCTGCAAGGCTGCTGCAAGGCTGCTG 780  
QY 781 CCTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 797  
DB 781 CCTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 797

## RESULT 2

US-08-988-819-1  
; Sequence 1 Application US/08988819  
; Patent No. 6054294  
; GENERAL INFORMATION:  
; APPLICANT: CHANG, MING-SHI  
; TITLE OF INVENTION: NEUROTROPIC FACTOR NNT-1  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: AMGEN INC.  
; STREET: ONE AMGEN CENTER DRIVE  
; CITY: THOUSAND OAKS  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 91320  
; COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/988, 819  
FILING DATE: 12-DEC-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/792,019  
FILING DATE: 03-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: COOK, ROBERT R.  
REGISTRATION NUMBER: 31,602  
REFERENCE/DOCKET NUMBER: A-442A  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 797 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 90..764  
FEATURE:  
NAME/KEY: mat peptide  
LOCATION: 171..764  
FEATURE:  
NAME/KEY: sig peptide  
LOCATION: 90..170  
US-08-988-819-1

Query Match 100.0%; Score 797; DB 3; Length 797;  
Best Local Similarity 100.0%; Pred. No. 4,7e-181;  
Matches 797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATTAAGCTTCGCGGAGCCGCGGCTCGCCCTCCCACTCCGCCAGCCTCCGGAGAGAG 60  
DB 1 ATTAAGCTTCGCGGAGCCGCGGCTCGCCCTCCCACTCCGCCAGCCTCCGGAGAGAG 60  
QY 61 CCGGACCCCGGCGGAGCCGCGGCTCGCCCTCCCACTCCGCCAGCCTCCGGAGAGAG 120  
DB 61 CCGGACCCCGGCGGAGCCGCGGCTCGCCCTCCCACTCCGCCAGCCTCCGGAGAGAG 120  
QY 121 TGTAGCGTGTGCTGCAAGGCTGCTGCAAGCCTCCGCTGCAAGGCTGCTGCAAGG 180  
DB 121 TGTAGCGTGTGCTGCAAGGCTGCTGCAAGCCTCCGCTGCAAGGCTGCTGCAAGG 180  
QY 181 CAGGGAGCCGAGGCTGCGGCTCGCCCTCCCACTCCGCCAGCCTCCGGAGAGAG 240  
DB 181 CAGGGAGCCGAGGCTGCGGCTCGCCCTCCCACTCCGCCAGCCTCCGGAGAGAG 240  
QY 241 AGCAGCACTTCGCGGAGCCGCGGCTCGCCCTCCCACTCCGCCAGCCTCCGGAGAG 300  
DB 241 AGCAGCACTTCGCGGAGCCGCGGCTCGCCCTCCCACTCCGCCAGCCTCCGGAGAG 300  
QY 301 AGCAGCACTTCGCGGAGCCGCGGCTCGCCCTCCCACTCCGCCAGCCTCCGGAGAG 360  
DB 301 AGCAGCACTTCGCGGAGCCGCGGCTCGCCCTCCCACTCCGCCAGCCTCCGGAGAG 360  
QY 361 TGGAGGTGTGCGGAGCCGCGGCTCGCCCTCCCACTCCGCCAGCCTCCGGAGAG 420  
DB 361 TGGAGGTGTGCGGAGCCGCGGCTCGCCCTCCCACTCCGCCAGCCTCCGGAGAG 420  
QY 421 GCGACCTTGTGTGCTGCAAGGCTGCTGCAAGCCTCCGCTGCAAGGCTGCTGCAAGG 480  
DB 421 GCGACCTTGTGTGCTGCAAGGCTGCTGCAAGCCTCCGCTGCAAGGCTGCTGCAAGG 480  
QY 481 GCGACCTTGTGTGCTGCAAGGCTGCTGCAAGCCTCCGCTGCAAGGCTGCTGCAAGG 540  
DB 481 GCGACCTTGTGTGCTGCAAGGCTGCTGCAAGCCTCCGCTGCAAGGCTGCTGCAAGG 540



QY 541 TGGCAGCTCTGGGCTACCACTGCGCCGACGCGCTGCTGGGACTGACCACTTGGAGCTC 600  
DB 541 TGGCAGCTCTGGGCTACCACTGCGCCGACGCGCTGCTGGGACTGACCACTTGGAGCTC 600  
QY 601 CTGGCCCTGCGCCACAGTGAATCTCTCCAGAGATGAGCAGCTTCTGGCTGCTGAAGAGC 660  
DB 601 CTGGCCCTGCGCCACAGTGAATCTCTCCAGAGATGAGCAGCTTCTGGCTGCTGAAGAGC 660  
QY 661 TGCAGACCTGGCTGCTGGGCTGCGCCGACGAGCTTCAACCGGCTCAAGAGAGATGAGCAGC 720  
DB 661 TGCAGACCTGGCTGCTGGGCTGCGCCGACGAGCTTCAACCGGCTCAAGAGAGATGAGCAGC 720  
QY 721 CTCGACAGCTGACGATCACTGCTGCACTTGGGAGCTGATGAGCTTCTGACTTCTGACTTCT 780  
DB 721 CTCGACAGCTGACGATCACTGCTGCACTTGGGAGCTGATGAGCTTCTGACTTCTGACTTCT 780  
QY 781 CCTCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 797  
DB 781 CCTCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 797

## RESULT 3

US-09-016-534-1

Sequence 1, Application us/09016534

Patent No. 6143874

GENERAL INFORMATION:

APPLICANT: CHANG, MING-SHI

APPLICANT: ELIOTT, GARY S.

APPLICANT: SARMIENTO, ULIA

APPLICANT: SERALDI, GIORGIO

TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: AMGEN INC.

STREET: ONE AMGEN CENTER

CITY: THOUSAND OAKS

STATE: CA

COUNTRY: USA

ZIP: 91320

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/016,534

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/792,019

FILING DATE: 03-FEB-1997

ATTORNEY/AGENT INFORMATION:

NAME: COOK, ROBERT R.

REGISTRATION NUMBER: 31,602

REFERENCE/DOCKET NUMBER: A-442B

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 797 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 90..764

FEATURE:

NAME/KEY: mat\_peptide

LOCATION: 171..764

FEATURE:

NAME/KEY: sig\_peptide

LOCATION: 90..170

US-09-016-534-1

Query Match 100.0%; Score 797; DB 3; Length 797;  
Best Local Similarity 100.0%; Pred. No. 4,7e-181;  
Matches 797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATTAAGCTTGGCGGAGCGCGGCTGCGCTCCCACTCCGCGCAGCTCCGCGAGAGAG 60  
DB 1 ATTAAGCTTGGCGGAGCGCGGCTGCGCTCCCACTCCGCGCAGCTCCGCGAGAGAG 60  
QY 61 CCGACCCCGGCG 120  
DB 61 CCGACCCCGGCG 120  
QY 121 TGTAGCGTGTGCTGAGCGGTGCTGTGCGACCTCCCTGAGTGCAGCTTCAATCGCA 180  
DB 121 TGTAGCGTGTGCTGAGCGGTGCTGTGCGACCTCCCTGAGTGCAGCTTCAATCGCA 180  
QY 181 CAGGGGACCCAGGGGCTGCGCGCTGCGCATCGAGAAACCTATGACTCAACCGCTACG 240  
DB 181 CAGGGGACCCAGGGGCTGCGCGCTGCGCATCGAGAAACCTATGACTCAACCGCTACG 240  
QY 241 AGCACCACTCCGAGCTTGGCTGGAGCTATCTGAACTACTGAGGCGCGCTTCAACG 300  
DB 241 AGCACCACTCCGAGCTTGGCTGGAGCTATCTGAACTACTGAGGCGCGCTTCAACG 300  
QY 301 AGCCAGCTTCAACCTCCCGCGCTGCGGCGGAGAGACTCTGCCAGGCGCACTGTGACT 360  
DB 301 AGCCAGCTTCAACCTCCCGCGCTGCGGCGGAGAGACTCTGCCAGGCGCACTGTGACT 360  
QY 361 TGGAGGTGCGGAGAGCTCAATGACAACTGCGGCTGAGCCAGAGACTAGAGGCTTCA 420  
DB 361 TGGAGGTGCGGAGAGCTCAATGACAACTGCGGCTGAGCCAGAGACTAGAGGCTTCA 420  
QY 421 GCCACTTCTGTGTACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480  
DB 421 GCCACTTCTGTGTACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480  
QY 481 GAGGCTGCGGCACTTCTGACAGAGCTGCGGCGGCTGCGGCGGCTGCGGCGGCTGCG 540  
DB 481 GAGGCTGCGGCACTTCTGACAGAGCTGCGGCGGCTGCGGCGGCTGCGGCGGCTGCG 540  
QY 541 TGGCAGCTCTGGGCTACCACTGCGCCGACGCGCTGCTGGGACTGACCACTTGGAGCTC 600  
DB 541 TGGCAGCTCTGGGCTACCACTGCGCCGACGCGCTGCTGGGACTGACCACTTGGAGCTC 600  
QY 601 CTGGCCCTGCGCCACAGTGAATCTCTCCAGAGATGAGCAGCTTCTGGCTGCTGAAGAGC 660  
DB 601 CTGGCCCTGCGCCACAGTGAATCTCTCCAGAGATGAGCAGCTTCTGGCTGCTGAAGAGC 660  
QY 661 TGCAGACCTGGCTGCTGGGCTGCGCCGACGAGCTTCAACCGGCTCAAGAGAGATGAGCAGC 720  
DB 661 TGCAGACCTGGCTGCTGGGCTGCGCCGACGAGCTTCAACCGGCTCAAGAGAGATGAGCAGC 720  
QY 721 CTCGACAGCTGACGATCACTGCTGCACTTGGGAGCTGATGAGCTTCTGACTTCTGACTTCT 780  
DB 721 CTCGACAGCTGACGATCACTGCTGCACTTGGGAGCTGATGAGCTTCTGACTTCTGACTTCT 780  
QY 781 CCTCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 797  
DB 781 CCTCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 797

## RESULT 4

US-09-106-182-1

Sequence 1, Application us/09106182

Patent No. 6046035

GENERAL INFORMATION:

APPLICANT: Shi, Yangu

APPLICANT: Ruben, Steve

TITLE OF INVENTION: Cardiotrophin-Like Cytokine

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc

STREET: 9410 Key West Ave

CITY: Rockville  
STATE: MD  
COUNTRY: US  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/106,182  
FILING DATE: Herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/051,053  
FILING DATE: 30-JUN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Brookes, A. Anders  
REGISTRATION NUMBER: 36,373  
REFERENCE/DOCKET NUMBER: PF385  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-309-8504  
TELEFAX: 301-309-8439  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1710 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 46..720  
FEATURE:  
NAME/KEY: sig\_peptide  
LOCATION: 46..126  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 127..720  
US-09-106-182-1

Query Match 94.0%; Score 749.4; DB 3; Length 1710;  
Best Local Similarity 99.9%; Pred. No. 1.2e-169;  
Matches 750; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

45 GCTCCGGAGAGAGAGCCGACCCGCGCCGAGCCGACCCGATGAGCTTCGAGCA 104  
1 GCTCCGGAGAGAGAGCCGACCCGCGCCGAGCCGACCCGATGAGCTTCGAGCA 60  
105 GGGAGACTCGTGGGGGATGTTAGAGTCTGTGCAAGGTCTGTGACCTCCCTGACATG 164  
61 GGGAGACTCGTGGGGGATGTTAGAGTCTGTGCAAGGTCTGTGACCTCCCTGACATG 120  
165 CCAAGCTCTCAATGCAAGAGGAGCCAGAGGCTGCGCCCTCATCCAGAAAAGCTATGAC 224  
121 CCAAGCTCTCAATGCAAGAGGAGCCAGAGGCTGCGCCCTCATCCAGAAAAGCTATGAC 180  
225 CTCACCCGCTACCTGAGAGCAACCACTCCGACCTTGGCTGGAGACCTATCTGAATACCTG 284  
181 CTCACCCGCTACCTGAGAGCAACCACTCCGACCTTGGCTGGAGACCTATCTGAATACCTG 240  
285 GACCCCTTTCAACAGAGCCAGACTTCAACCTCCCGCTGGGGGAGAGACTGCGCC 344  
241 GACCCCTTTCAACAGAGCCAGACTTCAACCTCCCGCTGGGGGAGAGACTGCGCC 300  
345 AGGGCACTGTGACTTGGAGGTGTGGCAAGGCTCAATGACAACTGGCGGTGACCCAG 404  
301 AGGGCACTGTGACTTGGAGGTGTGGCAAGGCTCAATGACAACTGGCGGTGACCCAG 360  
405 AACTAGAGAGGCTTCAAGCACTTCTGTGTACTTGTGCGTGGCTCAACCTGAGGCTGCC 464  
361 AACTAGAGAGGCTTCAAGCACTTCTGTGTACTTGTGCGTGGCTCAACCTGAGGCTGCC 420

465 ACTGCTGAGCTGCGCCGAGAGCTTGAGCCCACTTCTGACACAGGCTCAGAGGCTGTGGGC 524  
421 ACTGCTGAGCTGCGCCGAGAGCTTGAGCCCACTTCTGACACAGGCTCAGAGGCTGTGGGC 480  
525 AGCATTTGGGGGCTGATGAGGAGCTTGGAGCTTACCACTGACCCGCTGCTGGAGCT 584  
481 AGCATTTGGGGGCTGATGAGGAGCTTGGAGCTTACCACTGACCCGCTGCTGGAGCT 540  
595 GAACCCACTTGGAGCTTGGAGGCTTGAGCCCAAGTACCTTCTGACAGAGTGGAGGACTTC 644  
541 GAACCCACTTGGAGCTTGGAGGCTTGAGCCCAAGTACCTTCTGACAGAGTGGAGGACTTC 600  
645 TGGCTGTGAAGAGAGCTGAGAGCTTGTGGCTGAGGCTGAGGAGACTTCAACCGGCTC 704  
601 TGGCTGTGAAGAGAGCTGAGAGCTTGTGGCTGAGGCTGAGGAGACTTCAACCGGCTC 660  
705 AAGAGAAAGATGACAGCTTCAAGAGCTGAGTACCTTGTGACCTGAGGAGGCTTATGCTTC 764  
661 AAGAGAAAGATGACAGCTTCAAGAGCTGAGTACCTTGTGACCTGAGGAGGCTTATGCTTC 720  
765 TGACTTGTGACCTTCTCTCTTCTGCTGCTCCGCC 795  
721 TGACTTGTGACCTTCTCTCTTCTGCTGCTCCGCC 751

RESULT 5  
US-08-792-019B-4  
Sequence 4, Application US/08792019B  
Patent No. 5741772  
GENERAL INFORMATION:  
APPLICANT: CHANG, MING-SHI  
TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: AMGEN INC.  
STREET: 1840 DEHAVILLAND DRIVE  
CITY: THOUSAND OAKS  
STATE: CA  
COUNTRY: USA  
ZIP: 91320  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/792,019B  
FILING DATE: 03-FEB-1997  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: COOK, ROBERT R.  
REGISTRATION NUMBER: 31,602  
REFERENCE/DOCKET NUMBER: A-442  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 819 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 95..769  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 176..769  
FEATURE:  
NAME/KEY: sig\_peptide  
LOCATION: 95..175  
US-08-792-019B-4

Query Match 84.0%; Score 669.4; DB 1; Length 819;  
Best Local Similarity 92.0%; Pred. No. 1.1e-150;

Matches 717; Conservative 0; Mismatches 61; Indels 1; Gaps 1;

QY 1 ATTAAGCTTGGCGGAGCGGCGCTGCGCTCCCACTCCGCGAGCTCCGGAGAGAG 60  
DB 5 ATTAAGCTTGGCGGAGCGGCGCTGCGCTCCCACTCCGCGAGCTCCGGAGAGAG 64

QY 61 CCGCAGCCGCGCGCGCGAG-CGCCAGGCCCATGAGACTCCGAGGAGGAGACTGCGGAG 119  
DB 65 CCGGCG 124

QY 120 ATGTAGGCTGCTGTGCAAGCTGCTGTGCAAGCTGCTGTGCAAGCTGCTGTGCA 179  
DB 125 ATGTAGGCTGCTGTGCAAGCTGCTGTGCAAGCTGCTGTGCAAGCTGCTGTGCA 184

QY 180 ACAGGAGGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 239  
DB 185 ACAGGAGGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 244

QY 240 GAGCAGCACTCCGCGAGCTGCTGCGAGCTGCTGCAAGCTGCTGCGAGCGCGCTTCA 239  
DB 245 GAGCAGCACTCCGCGAGCTGCTGCGAGCTGCTGCAAGCTGCTGCGAGCGCGCTTCA 304

QY 300 GAGCAGCACTTCAACCTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 359  
DB 305 GAGCAGCACTTCAACCTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 364

QY 360 TTGGAAGTGTGCGGAGCGCTCAATGAACTGCGGTGACCGAGAACTGCGGCGCTAC 419  
DB 365 TTGGAAGTGTGCGGAGCGCTCAATGAACTGCGGTGACCGAGAACTGCGGCGCTAC 424

QY 420 AGCAGCCTTGTGTTACTTGTGCGCTGCAAGCTGCAAGCTGCAAGCTGCAAGCTG 479  
DB 425 AGCAGCCTTGTGTTACTTGTGCGCTGCAAGCTGCAAGCTGCAAGCTGCAAGCTG 484

QY 480 CGCAGCTGCG 539  
DB 485 CGCAGCTGCG 544

QY 540 ATGAGCAGCTGCG 599  
DB 545 ATGAGCAGCTGCG 604

QY 600 CTTGCG 659  
DB 605 CTTGCG 664

QY 660 CTTGCG 719  
DB 665 CTTGCG 724

QY 720 CTTGCG 778  
DB 725 CTTGCG 783

RESULT 6  
US-08-988-819-4  
Sequence 4, Application US/0898819  
Patent No. 6054294

GENERAL INFORMATION:  
APPLICANT: CHANG, MING-SHI  
TITLE OF INVENTION: NEUROTROPHIC FACTOR NNT-1  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: AMGEN INC.  
STREET: ONE AMGEN CENTER DRIVE  
CITY: THOUSAND OAKS  
STATE: CA  
COUNTRY: USA  
ZIP: 91320  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/988,819  
FILING DATE: 12-DEC-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/792,019  
FILING DATE: 03-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: COOK, ROBERT R.  
REGISTRATION NUMBER: 31,602  
REFERENCE/DOCKET NUMBER: A-442A  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 819 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 95..769  
FEATURE:  
NAME/KEY: mac\_peptide  
LOCATION: 176..769  
FEATURE:  
NAME/KEY: big\_peptide  
LOCATION: 95..175  
US-08-988-819-4

Query Match 84.0%; Score 669.4; DB 3; Length 819;  
Best Local Similarity 92.0%; Pred. No. 1.1e-150;  
Matches 717; Conservative 0; Mismatches 61; Indels 1; Gaps 1;

QY 1 ATTAAGCTTGGCGGAGCGGCGCTGCGCTCCCACTCCGCGAGCTCCGGAGAGAG 60  
DB 5 ATTAAGCTTGGCGGAGCGGCGCTGCGCTCCCACTCCGCGAGCTCCGGAGAGAG 64

QY 61 CCGCAGCCGCGCGCGCGCGAG-CGCCAGGCCCATGAGACTCCGAGGAGGAGACTGCGGAG 119  
DB 65 CCGGCG 124

QY 120 ATGTAGGCTGCTGTGCAAGCTGCTGTGCAAGCTGCTGTGCAAGCTGCTGTGCA 179  
DB 125 ATGTAGGCTGCTGTGCAAGCTGCTGTGCAAGCTGCTGTGCAAGCTGCTGTGCA 184

QY 180 ACAGGAGGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 239  
DB 185 ACAGGAGGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 244

QY 240 GAGCAGCACTCCGCGAGCTGCTGCGAGCTGCTGCAAGCTGCTGCGAGCGCGCTTCA 239  
DB 245 GAGCAGCACTCCGCGAGCTGCTGCGAGCTGCTGCAAGCTGCTGCGAGCGCGCTTCA 304

QY 300 GAGCAGCACTTCAACCTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 359  
DB 305 GAGCAGCACTTCAACCTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 364

QY 360 TTGGAAGTGTGCGGAGCGCTCAATGAACTGCGGTGACCGAGAACTGCGGCGCTAC 419  
DB 365 TTGGAAGTGTGCGGAGCGCTCAATGAACTGCGGTGACCGAGAACTGCGGCGCTAC 424

QY 420 AGCAGCCTTGTGTTACTTGTGCGCTGCAAGCTGCAAGCTGCAAGCTGCAAGCTG 479  
DB 425 AGCAGCCTTGTGTTACTTGTGCGCTGCAAGCTGCAAGCTGCAAGCTGCAAGCTG 484

QY 480 CGCAGCTGCG 539  
DB 485 CGCAGCTGCG 544

QY 540 ATGAGCAGCTGCG 599

Db 545 ATGGCAGCCTTGGCTAACCCACTGCCCCAGCCTCTGCGAGGGACTGAGCCAGCCTGGGCC 604  
Qy 600 CTGGCCCTGCCCAAGTAGTCTTCTCCAGAAAGATGAGACTTGTGGCTGTGAAGAG 659  
Db 605 CTGGCCCTGCCCAAGTAGTCTTCTCCAGAAAGATGAGACTTGTGGCTGTGAAGAG 664  
Qy 660 CTGCAGACCTGGCTGTGGCGCTGGCGCAAGACTTCAACCGGCTCAAGAAAGATGAG 719  
Db 665 CTGCAGACCTGGCTGTGGCGCTGGCGCAAGACTTCAACCGGCTTAAAGAAAGATGAG 724  
Qy 720 CTTCAGCAGCTGCTGACTTCACTTGCACCTGGGGGCTCATGGCTTGTGACTTGTGACTT 778  
Db 725 CTTCAGCAGCTTGTGACTTCACTTGCACCTGGAGGCAATGTTTGTGACTTGTGACTT 783

RESULT 7  
US-09-016-534-4  
Sequence 4, Application US/09016534  
GENERAL INFORMATION:  
PATENT No. 613874  
APPLICANT: CHANG, MING-SHI  
APPLICANT: ELLIOTT, GARY S.  
APPLICANT: SARMIENTO, ULLA  
APPLICANT: SENALDI, GIORGIO  
TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: AMGEN INC.  
STREET: ONE AMGEN CENTER  
CITY: THOUSAND OAKS  
STATE: CA  
COUNTRY: USA  
ZIP: 91320  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/016,534  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/792,019  
FILING DATE: 03-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: COOK, ROBERT R.  
REGISTRATION NUMBER: 31,602  
REFERENCE/DOCKET NUMBER: A-442B  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 819 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 95..769  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 176..769  
FEATURE:  
NAME/KEY: sig\_peptide  
LOCATION: 95..175  
US-09-016-534-4

Query Match 84.0%; Score 669.4; DB 3; Length 819;  
Best Local Similarity 92.0%; Pred. No. 1.1e-150;  
Matches 717; Conservative 0; Mismatches 61; Indels 1; Gaps 1;

Qy 1 ATTAAGCTTCGCCGAGCGCGGCTGCGCTCCCACTCCGCGCAGCTCCGAGAGAGAG 60  
|||||

Db 5 ATTAAGCTTCGCCGAGCGCGGCTGCGCTCCCACTCCGCGCAGCTTCGAGAGAGAG 64  
Qy 61 CGGACCCGCGCGCGCCAG-CCCGAGCCCAATGACCTCCGAGGAGGAGACTCGTGGGG 119  
Db 65 CCGCGCCGCGCGCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCC 124  
Qy 120 ATGTTAGCTGTGCTGTGACGAGTGTGCTGTGACACTTCCGTGAGTGCAGCTTCAATGC 179  
Db 125 ATGTTAGCTGTGCTGTGACGAGTGTGCTGTGACACTTCCGTGAGTGCAGCTTCAATGC 184  
Qy 180 ACAGGAGACCCAGGCGCTGGCCCTTCATCCAGAAACCTTATGACTTACCTGACTG 239  
Db 185 ACAGGAGATCCAGGCGCTGGCCCTTCATCCAGAAACCTTATGACTTACCTGACTG 244  
Qy 240 GAGCACAACCTCCGAGCTGGGCTGGGACTATGAACTACCTGGGCCCCCTTCAAC 299  
Db 245 GAGCATCACTCCGAGCTTGAAGTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCT 304  
Qy 300 GAGCAGACTTCAACCTTCCCGCTGGGCGGAGAGACTTGGCCCGGAGGAGGAGGAG 359  
Db 305 GAGCTGACTTCAATCTCTGCTGACTGGGGGAGAGAACTTGGCCCGGAGGAGGAGGAG 364  
Qy 360 TTGAGGCTGGGCGGAGCTTCAATGACAACTGCGGCTGAGCCAGAACTAGAGGCTTAC 419  
Db 365 TTGAGAGTGTGCGAAGCTTCAATGACAGGCTGCGGCTGAGCCAGAACTATGAGGCTTAC 424  
Qy 420 AGCAGCTTGTGTTACTTGTGAGGCTCAACGCTGAGGCTGAGGCTGAGGCTGAGGCT 479  
Db 425 AGTCACTTGTGTTACTTGTGAGGCTCAACGCTGAGGCTGAGGCTGAGGCTGAGGCT 484  
Qy 480 CGCAGCTTGTGTTACTTGTGAGGCTCAACGCTGAGGCTGAGGCTGAGGCTGAGGCT 539  
Db 485 CGTACCTTGTGTTACTTGTGAGGCTCAACGCTGAGGCTGAGGCTGAGGCTGAGGCT 544  
Qy 540 ATGCACTTGTGTTACTTGTGAGGCTCAACGCTGAGGCTGAGGCTGAGGCTGAGGCT 599  
Db 545 ATGCACTTGTGTTACTTGTGAGGCTCAACGCTGAGGCTGAGGCTGAGGCTGAGGCT 604  
Qy 600 CTGGCCCTGGCCCAAGTAGTCTTCCAGAAAGATGAGACTTGTGGCTGTGAAGAG 659  
Db 605 CTGGCCCTGGCCCAAGTAGTCTTCCAGAAAGATGAGACTTGTGGCTGTGAAGAG 664  
Qy 660 CTGCAGACCTGGCTGTGGCGCTGGCGCAAGACTTCAACCGGCTCAAGAAAGATGAG 719  
Db 665 CTGCAGACCTGGCTGTGGCGCTGGCGCAAGACTTCAACCGGCTTAAAGAAAGATGAG 724  
Qy 720 CTTCAGCAGCTGCTGACTTCACTTGCACCTGGGGGCTCATGGCTTGTGACTTGTGACTT 778  
Db 725 CTTCAGCAGCTTGTGACTTCACTTGCACCTGGAGGCAATGTTTGTGACTTGTGACTT 783

RESULT 8  
US-08-792-019B-3  
Sequence 3, Application US/08792019B  
PATENT No. 5741772  
GENERAL INFORMATION:  
APPLICANT: CHANG, MING-SHI  
TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: AMGEN INC.  
STREET: 1840 DEHAVILLAND DRIVE  
CITY: THOUSAND OAKS  
STATE: CA  
COUNTRY: USA  
ZIP: 91320  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/792,019B





## RESULT 12

US-09-335-409-1  
Sequence 1, Application US/09335409  
Patent No. 6121029  
GENERAL INFORMATION:  
APPLICANT: Schupp, Thomas  
APPLICANT: Ligon, James  
APPLICANT: Molnar, Istvan  
APPLICANT: Zirkle, Ross  
APPLICANT: Cyr, Devon  
APPLICANT: Goelach, Joern  
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES  
FILE REFERENCE: 4-30582A  
CURRENT APPLICATION NUMBER: US/09/335.409  
CURRENT FILING DATE: 1999-06-17  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1  
LENGTH: 68750  
TYPE: DNA  
ORGANISM: Sorangium cellulosum  
US-09-335-409-1

Query Match 5.6%; Score 44.8; DB 3; Length 68750;  
Best Local Similarity 50.0%; Pred. No. 0.16;  
Matches 112; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

QY 456 CAGGCTGCCACTGTGAGTCGCGCCGACGCTTGCCACTTGTGACACGAGCTCCAGAGGC 515  
DB 57992 CAGGTAGCGAGTCGGAGCGGGGAGAACGTGCGCCCTTCGGATTCACGCGCGCGC 58051  
QY 516 CTGCTGGGAGCATTTGCGGCGCTCATGAGCTCTGGGCTACCACTGCCCGCGCTG 575  
DB 58052 GTGCTGCGCGGATGCGGCGCTCGAGACCCCGCGAGTCCAACTCGCGCGCTGCGC 58111  
QY 576 CTTGGAGCTGAACCCACTTGGACTCTGCGCCCTGCCACAGTAGTCTCTCCAGAGATG 635  
DB 58112 GCCCGCTTCATAGCCGCGCTGCGCGCTGCTATCTATGCTGCTCGCGCGAGATGGGG 58171  
QY 636 GACGACTTGTGCTGTGTAAGAGCTGCAGACTGCTGTGCGC 679  
DB 58172 CTTCAATACGCGCGCGGCTGCGGGGGCTGCGCGAGCTGTGGCG 58215

## RESULT 13

US-09-568-102-1  
Sequence 1, Application US/09568102  
Patent No. 6346404  
GENERAL INFORMATION:  
APPLICANT: Schupp, Thomas  
APPLICANT: Ligon, James  
APPLICANT: Molnar, Istvan  
APPLICANT: Zirkle, Ross  
APPLICANT: Cyr, Devon  
APPLICANT: Goelach, Joern  
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES  
FILE REFERENCE: 4-30582A  
CURRENT APPLICATION NUMBER: US/09/568.102  
CURRENT FILING DATE: 2000-05-10  
PRIOR APPLICATION NUMBER: 09/335.409  
PRIOR FILING DATE: 1999-06-17  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1  
LENGTH: 68750  
TYPE: DNA  
ORGANISM: Sorangium cellulosum  
US-09-568-102-1

Query Match 5.6%; Score 44.8; DB 4; Length 68750;  
Best Local Similarity 50.0%; Pred. No. 0.16;  
Matches 112; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

QY 456 CAGGCTGCCACTGTGAGTCGCGCCGACGCTTGCCACTTGTGACACGAGCTCCAGAGGC 515  
DB 57992 CAGGTAGCGAGTCGGAGCGGGGAGAACGTGCGCCCTTCGGATTCACGCGCGCGC 58051  
QY 516 CTGCTGGGAGCATTTGCGGCGCTCATGAGCTCTGGGCTACCACTGCCCGCGCTG 575  
DB 58052 GTGCTGCGCGGATGCGGCGCTCGAGACCCCGCGAGTCCAACTCGCGCGCTGCGC 58111  
QY 576 CTTGGAGCTGAACCCACTTGGACTCTGCGCCCTGCCACAGTAGTCTCTCCAGAGATG 635  
DB 58112 GCCCGCTTCATAGCCGCGCTGCGCGCTGCTATCTATGCTGCTCGCGCGAGATGGGG 58171  
QY 636 GACGACTTGTGCTGTGTAAGAGCTGCAGACTGCTGTGCGC 679  
DB 58172 CTTCAATACGCGCGCGGCTGCGGGGGCTGCGCGAGCTGTGGCG 58215

## RESULT 14

US-09-567-969-1  
Sequence 1, Application US/09567969  
Patent No. 6355457  
GENERAL INFORMATION:  
APPLICANT: Schupp, Thomas  
APPLICANT: Ligon, James  
APPLICANT: Molnar, Istvan  
APPLICANT: Zirkle, Ross  
APPLICANT: Cyr, Devon  
APPLICANT: Goelach, Joern  
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES  
FILE REFERENCE: 4-30582A  
CURRENT APPLICATION NUMBER: US/09/567.969  
CURRENT FILING DATE: 2000-05-10  
PRIOR APPLICATION NUMBER: 09/335.409  
PRIOR FILING DATE: 1999-06-17  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1  
LENGTH: 68750  
TYPE: DNA  
ORGANISM: Sorangium cellulosum  
US-09-567-969-1

Query Match 5.6%; Score 44.8; DB 4; Length 68750;  
Best Local Similarity 50.0%; Pred. No. 0.16;  
Matches 112; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

QY 456 CAGGCTGCCACTGTGAGTCGCGCCGACGCTTGCCACTTGTGACACGAGCTCCAGAGGC 515  
DB 57992 CAGGTAGCGAGTCGGAGCGGGGAGAACGTGCGCCCTTCGGATTCACGCGCGCGC 58051  
QY 516 CTGCTGGGAGCATTTGCGGCGCTCATGAGCTCTGGGCTACCACTGCCCGCGCTG 575  
DB 58052 GTGCTGCGCGGATGCGGCGCTCGAGACCCCGCGAGTCCAACTCGCGCGCTGCGC 58111  
QY 576 CTTGGAGCTGAACCCACTTGGACTCTGCGCCCTGCCACAGTAGTCTCTCCAGAGATG 635  
DB 58112 GCCCGCTTCATAGCCGCGCTGCGCGCTGCTATCTATGCTGCTCGCGCGAGATGGGG 58171  
QY 636 GACGACTTGTGCTGTGTAAGAGCTGCAGACTGCTGTGCGC 679  
DB 58172 CTTCAATACGCGCGCGGCTGCGGGGGCTGCGCGAGCTGTGGCG 58215

## RESULT 15

US-09-568-480-1  
Sequence 1, Application US/09568480  
Patent No. 6355458  
GENERAL INFORMATION:  
APPLICANT: Schupp, Thomas  
APPLICANT: Ligon, James  
APPLICANT: Molnar, Istvan  
APPLICANT: Zirkle, Ross

; APPLICANT: Cyr, Devon  
 ; APPLICANT: Goerlach, Joern  
 ; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES  
 ; FILE REFERENCE: 4-30582A  
 ; CURRENT APPLICATION NUMBER: US/09/568,480  
 ; CURRENT FILING DATE: 2000-05-10  
 ; PRIOR APPLICATION NUMBER: 09/335,409  
 ; PRIOR FILING DATE: 1999-06-17  
 ; NUMBER OF SEQ ID NOS: 30  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 1  
 ; LENGTH: 68750  
 ; TYPE: DNA  
 ; ORGANISM: Sorangium cellulosum  
 ; US-09-568-480-1

Query Match 5.6%; Score 44.8; DB 4; Length 68750;  
 Best Local Similarity 50.0%; Pred. No. 0.16; Indels 0; Gaps 0;  
 Matches 112; Conservative 0; Mismatches 112; Indels 0; Gaps 0;  
 QY 456 CAGGCTGCCACTGCTGAGCTGCGCCGACGCTGAGCCCTTCTGACAGAGCTCCAGAGGC 515  
 DB 57992 CAGGTAGCGAGTCGGAGCGCGGGGAGACGTGCGCGCCCTTCCGAGTCACAGCGCGCGGC 58051  
 QY 516 CTGCTGGGCGAGATTGCGGCGCTCATGTGCGAGCTTGCGCTACCCACTGCGCCGAGCGCTG 575  
 DB 58052 GTGCTGCGCGGATCGGGCGCGCTCGAGACCCCGCGAGGTGGAACCTCGCGCGCTGCGGC 58111  
 QY 576 CCTGGGACTGAACCCACTTGAAGCTGCTGCGCCCTGCGCCAGAGTACTTCTCCAGAGATG 635  
 DB 58112 GCCCGGCTTCATGCGCGCGCTGCGCGCTGCGCTATCTATGTGCGCTGCGCGAGATGGG 58171  
 QY 636 GACGACTTCTGCTGCTGAAGAGCTGACAGACTGCGCTGAGG 679  
 DB 58172 CTTCAATAGCGCGCGCGCTTGGCGGGGCTCGCGAGACTGTGGG 58215

Search completed: February 9, 2004, 06:13:03  
 Job time : 78.1015 secs



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OM protein - protein search, using SW model

Run on: February 9, 2004, 06:14:57 ; Search time 36 Seconds  
(without alignments)  
1612.829 Million cell updates/sec

Title: US-09-931-704-2

Perfect score: 1226  
Sequence: 1 MDLRAGDSWGMGLACTVLM.....KKKMPAAAVTLHGAGGF 225

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SP\_ARCHAEA:\*  
2: SP\_BACTERIA:\*  
3: SP\_FUNGI:\*  
4: SP\_HUMAN:\*  
5: SP\_INVERTEBRATE:\*  
6: SP\_MAMMAL:\*  
7: SP\_MHC:\*  
8: SP\_ORGANELLE:\*  
9: SP\_PHAGE:\*  
10: SP\_PLANT:\*  
11: SP RODENT:\*  
12: SP\_VIRUS:\*  
13: SP\_VERTEBRATE:\*  
14: SP\_UNCLASSIFIED:\*  
15: SP\_VIRINUS:\*  
16: SP\_BACTERIAP:\*  
17: SP\_ARCHAEP:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1226	100.0	225	4	Q9UBD9
2	1193	97.3	225	11	Q9QZM3
3	150.5	12.3	215	13	Q9PUJ1
4	150.5	12.3	215	13	Q9PUJ0
5	150.5	12.3	215	13	Q9PUJ2
6	148.5	12.1	215	13	Q9PUJ9
7	97.5	8.0	318	4	Q9E1S2
8	97.5	8.0	530	3	Q8XUE9
9	97	7.9	8601	2	Q8GM87
10	96.5	7.9	243	4	Q8NEV9
11	96.5	7.9	455	11	Q9CMV7
12	94	7.7	287	4	Q8N358
13	93	7.6	392	2	Q8KXK2
14	92	7.5	332	10	Q9MAU1
15	91.5	7.5	716	16	Q8PI99
16	89.5	7.3	771	2	Q9S3Q9

17	89	7.3	733	16	Q91664	Q91664 pseudomonas
18	88	7.2	392	11	Q8B113	Q8B113 mus musculu
19	88	7.2	422	11	Q8BGR5	Q8BGR5 mus musculu
20	87	7.1	955	11	Q88287	Q88287 mus musculu
21	87	7.1	1561	11	Q88286	Q88286 mus musculu
22	86.5	7.1	379	2	Q8KRX4	Q8KRX4 streptomyce
23	86.5	7.1	640	16	Q54153	Q54153 streptomyce
24	85.5	7.0	522	7	Q8HWH4	Q8HWH4 mus musculu
25	85.5	7.0	1154	11	Q921R2	Q921R2 mus musculu
26	85	6.9	476	11	Q8R363	Q8R363 mus musculu
27	85	6.9	727	11	Q88841	Q88841 mus musculu
28	84.5	6.9	294	11	Q9CPZ1	Q9CPZ1 mus musculu
29	84.5	6.9	389	17	Q9YA71	Q9YA71 aeropyrum p
30	84	6.9	200	16	Q8YB81	Q8YB81 bruceella me
31	84	6.9	232	16	Q8FX31	Q8FX31 bruceella su
32	84	6.9	294	4	Q9NXX5	Q9NXX5 homo sapien
33	84	6.9	411	16	Q9RVF3	Q9RVF3 deinococcus
34	84	6.9	559	16	Q83432	Q83432 treponema p
35	84	6.9	655	11	Q8BY35	Q8BY35 mus musculu
36	84	6.9	876	4	Q9P210	Q9P210 homo sapien
37	83.5	6.8	310	4	Q9S159	Q9S159 homo sapien
38	83.5	6.8	5990	2	Q9RLP6	Q9RLP6 mycobacteri
39	83	6.8	222	2	Q9LS84	Q9LS84 streptococ
40	83	6.8	4782	11	Q8K1G6	Q8K1G6 mus musculu
41	82.5	6.7	310	4	Q9UID0	Q9UID0 homo sapien
42	82.5	6.7	542	16	Q9HTB5	Q9HTB5 pseudomonas
43	82.5	6.7	1122	10	Q8GV08	Q8GV08 oryza sativ
44	82	6.7	283	2	Q9ZB87	Q9ZB87 pseudomonas
45	82	6.7	468	16	Q8DHQ5	Q8DHQ5 synchococ

## ALIGNMENTS

### RESULT 1

ID	Q9UBD9	PRELIMINARY;	PRT;	225 AA.
AC	Q9UBD9			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-OCT-2002 (TREMBLrel. 22, Last annotation update)			
DE	Neurotrophin-1/B-cell stimulating factor-3 (Cardiotrophin-like cytokine) (Similar to cardiotrophin-like cytokine, neurotrophin-1/B-cell stimulating factor-3).			
DE	cell stimulating factor-3).			
GN	CLC.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
NC	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99432254; PubMed=10500198;			
RA	Senaldi G., Varnum B.C., Sarmiento U., Starnes C., Lile J., Scully S., Guo J., Elliott G., McNinch J., Shaklee C.L., Freeman D., Mann F., Simonet W.S., Boone T., Chang M.-S.;			
RA	"Novel neurotrophin-1/B cell-stimulating factor-3: A cytokine of the IL-6 family."			
RT	Proc. Natl. Acad. Sci. U.S.A. 96:11458-11463(1999).			
RT	[2]			
RN	SEQUENCE FROM N.A.			
RX	MEDLINE=99382254; PubMed=10448081;			
RA	Shi Y., Wang W., Yourey P.A., Gohari S., Zukauskas D., Zhang J., Ruben S., Alderson R.F.;			
RA	"Computational EST database analysis identifies a novel member of the neurotrophin-like cytokine family."			
RT	biochem. Biophys. Res. Commun. 262:132-138(1999).			
RT	[3]			
RN	SEQUENCE FROM N.A.			
RA	Hu X., Xu Y., Zhang B., Peng X., Yuan J., Qiang B.;			
RA	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.			
RT	[4]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Kidney;			

RA Strausberg R.;  
 Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF176912; AAF00992.1; -;  
 DR EMBL; AF172854; AAD54284.1; -;  
 DR EMBL; AF176911; AAF00991.1; -;  
 DR EMBL; AY049779; AAL15436.1; -;  
 DR EMBL; BC012939; AAL12939.1; -;  
 SQ SEQUENCE 225 AA; 25176 MW; E2DD4B6280833B55 CRC64;

Query Match 100.0%; Score 1226; DB 4; Length 225;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-106; Indels 0; Gaps 0;  
 Matches 225; Conservative 0; Mismatches 0;

QY 1 MDLRAGDSWGMKLACTVIMHLPAVPALNRTGDPGPGPSIQTYDLTRYLHQSLAGT 60  
 DB 1 MDLRAGDSWGMKLACTVIMHLPAVPALNRTGDPGPGPSIQTYDLTRYLHQSLAGT 60  
 QY 61 YLNYLGPPEPNEPDPFPRIGAEFTLPRAVTVLEWMSLNDKRLTONYEAYSHLCLYRGL 120  
 DB 61 YLNYLGPPEPNEPDPFPRIGAEFTLPRAVTVLEWMSLNDKRLTONYEAYSHLCLYRGL 120  
 QY 121 NROAATAEIRSLAHCSTSLQGLSIGVMAALGYPPLPGTEPTTPGPAHSDFIQ 180  
 DB 121 NROAATAEIRSLAHCSTSLQGLSIGVMAALGYPPLPGTEPTTPGPAHSDFIQ 180  
 QY 181 KMDDFWLKELQTWLMRSKDFNRLKKKQPPAAAVTLHGAHGF 225  
 DB 181 KMDDFWLKELQTWLMRSKDFNRLKKKQPPAAAVTLHGAHGF 225

## RESULT 2

Q9QZM3 PRELIMINARY; PRT; 225 AA.

AC Q9QZM3; 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE Neurotrophin-1/B-cell stimulating factor-3.  
 GN BSF3.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99432254; PubMed=10500198;  
 RA Senaldi G., Varnum B.C., Sarmiento U., Starnes C., Lile J., Scully S.,  
 RA Guo J., Elliott G., McNinch J., Shaklee C.L., Freeman D., Mann F.,  
 RA Simonet W.S., Boone T., Chang M.-S.;  
 RT "Novel neurotrophin-1/B cell-stimulating factor-3: a cytokine of the  
 RT IL-6 family."  
 RL Proc. Natl. Acad. Sci. U.S.A. 96:11458-11463(1999).  
 DR EMBL; AF176913; AAF00993.1; -;  
 DR MGD; MGI:1930088; Bsf3.  
 SQ SEQUENCE 225 AA; 25261 MW; 68B1FEAAB7F1A950 CRC64;

Query Match 97.3%; Score 1193; DB 11; Length 225;  
 Best Local Similarity 96.9%; Pred. No. 5e-105; Indels 0; Gaps 0;  
 Matches 218; Conservative 3; Mismatches 4;

QY 1 MDLRAGDSWGMKLACTVIMHLPAVPALNRTGDPGPGPSIQTYDLTRYLHQSLAGT 60  
 DB 1 MDLRAGDSWGMKLACTVIMHLPAVPALNRTGDPGPGPSIQTYDLTRYLHQSLAGT 60  
 QY 61 YLNYLGPPEPNEPDPFPRIGAEFTLPRAVTVLEWMSLNDKRLTONYEAYSHLCLYRGL 120  
 DB 61 YLNYLGPPEPNEPDPFPRIGAEFTLPRAVTVLEWMSLNDKRLTONYEAYSHLCLYRGL 120  
 QY 121 NROAATAEIRSLAHCSTSLQGLSIGVMAALGYPPLPGTEPTTPGPAHSDFIQ 180  
 DB 121 NROAATAEIRSLAHCSTSLQGLSIGVMAALGYPPLPGTEPTTPGPAHSDFIQ 180  
 QY 181 KMDDFWLKELQTWLMRSKDFNRLKKKQPPAAAVTLHGAHGF 225  
 DB 181 KMDDFWLKELQTWLMRSKDFNRLKKKQPPAAAVTLHGAHGF 225

DB 181 KMDDFWLKELQTWLMRSKDFNRLKKKQPPAAAVTLHGAHGF 225

## RESULT 3

Q9PUJ1 PRELIMINARY; PRT; 215 AA.

AC Q9PUJ1; 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)  
 DE Receptivity factor isoform 2 precursor.  
 GN PRF.  
 OS Plethodon jordanii (Salamander).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Caudata; Salamandroides; Plethodontidae;  
 OC Plethodon.  
 OX NCBI\_TaxID=8336;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99420364; PubMed=10489368;  
 RA Rollmann S.M., Houck L.D., Feidhoff R.C.;  
 RT "Proteinaceous pheromone affecting female receptivity in a terrestrial  
 RT salamander."  
 RL Science 285:1907-1909(1999).  
 DR EMBL; AF181481; AAF01026.1; -;  
 KM Signal.  
 FT SIGNAL 1 23 POTENTIAL.  
 SQ SEQUENCE 215 AA; 24080 MW; B341BB7B4E28438 CRC64;

Query Match 12.3%; Score 150.5; DB 13; Length 215;  
 Best Local Similarity 26.2%; Pred. No. 3e-06; Indels 7; Gaps 3;  
 Matches 42; Conservative 31; Mismatches 80;

QY 56 SLAGTYLNYLGPPEPNEPDPFPRIGAEFTLPRAVTVLEWMSLNDKRLTONYEAYSHLCL 115  
 DB 55 SLPLTYLNFQGAFLSDPPYOLPHIVANLPTRAMDYDFPMQOTBETRLNNMLYFYSALVE 114  
 QY 116 YLR-GLNRQ---AATAELRSLAHCSTSLQGLSIGVMAALGYPPLPGTEPTTPGPAHSDFIQ 170  
 DB 115 FLKEMTQEDINPRLSLKAKFEEMANSNLTSKISDINTOMKMSVTLTP--KLIV 172  
 QY 171 PGPAHSDFIQKMDDFWLKELQTWLMRSKDFNRLKKKQPPAAAVTLHGAHGF 210  
 DB 173 PGPAHSDFIQKMDDFWLKELQTWLMRSKDFNRLKKKQPPAAAVTLHGAHGF 212

## RESULT 4

Q9PUJ0 PRELIMINARY; PRT; 215 AA.

AC Q9PUJ0; 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)  
 DE Receptivity factor isoform 3 precursor.  
 GN PRF.  
 OS Plethodon jordanii (Salamander).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Caudata; Salamandroides; Plethodontidae;  
 OC Plethodon.  
 OX NCBI\_TaxID=8336;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99420364; PubMed=10489368;  
 RA Rollmann S.M., Houck L.D., Feidhoff R.C.;  
 RT "Proteinaceous pheromone affecting female receptivity in a terrestrial  
 RT salamander."  
 RL Science 285:1907-1909(1999).  
 DR EMBL; AF181482; AAF01027.1; -;  
 KM Signal.  
 FT SIGNAL 1 23 POTENTIAL.  
 SQ SEQUENCE 215 AA; 24024 MW; 6EB6E64AD93A1343 CRC64;



Db 235 LFGSRSTPSTPYES 249

## RESULT 8

Q8X0E9 PRELIMINARY; PRT; 530 AA.  
AC Q8X0E9;  
DT 01-MAR-2002 (TREMBlrel. 20, Created)  
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)  
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
DE Hypothetical 59.4 kDa protein.  
GN B14a6.080.  
OS Neurospora crassa.  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
OC Sordariales; Sordariaceae; Neurospora.  
OK NCBI\_Taxid=5141;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Schulte U., Allyn V., Hohnsels J., Brandt P., Fartmann B., Holland R.,  
RA Nyakatura G., Mewes H.W., Mannhaupt G.;  
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA German Neurospora genome project;  
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AL670007; CAD21310.1; -  
DR InterPro; IPR001810; F-box.  
DR PROSITE; PS50181; FBOX; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 530 AA; 59352 MW; 70382EB15F71BB9D CRC64;

Query Match 8.0%; Score 97.5; DB 3; Length 530;  
Best Local Similarity 24.8%; Pred. No. 1;  
Matches 41; Conservative 22; Mismatches 65; Indels 37; Gaps 6;  
QY 64 YLGPFPNEDFPNPRIGAEITLPPRA-TVDELVRSINDKRLTONYEAVSHLCYLRGLNR 122  
DB 236 FLVPPYLPEDFLPYLAGLKKHLVLDADLATRHDEIQVLRKKFLALTPNLTWLR----- 291  
QY 123 QAATBELRSLAHFCTSLQGLGSIAGVMAALGYPLPQPLPPT-----EPTWTPGP 173  
DB 292 ----VNFERSISHY-----GKKEALKWLASLSRPGTWSPPGLINADPSRLPP 336  
QY 174 AHSDFLOKMDFWLKELOTWLMRSKDNRLKXKQPPAAAVTL 218  
DB 337 VEPDLEQD---IGQLDV---SANTLYRLFNKFSSTLKATSL 373

## RESULT 9

Q8GM87 PRELIMINARY; PRT; 8601 AA.  
AC Q8GM87;  
DT 01-MAR-2003 (TREMBlrel. 23, Created)  
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE Mixed type I polyketide synthase/nonribosomal peptide synthetase.  
GN PEDP.  
OS symbiont bacterium of Paederus fuscipes.  
OC Bacteria.  
OK NCBI\_Taxid=176282;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=22294974; PubMed=12381784;  
RA Piel J.;  
RT "A polyketide synthase-peptide synthetase gene cluster from an  
RT uncultured bacterial symbiont of Paederus beetles";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:14002-14007(2002).  
DR EMBL; AY059471; AAL27851.1;  
SQ SEQUENCE 8601 AA; 948046 MW; C498ACB80B5082C7 CRC64;

Query Match 7.9%; Score 97; DB 2; Length 8601;  
Best Local Similarity 25.6%; Pred. No. 43;

Matches 51; Conservative 37; Mismatches 69; Indels 42; Gaps 12;

QY 58 AGTYINLYGPPNEDFPNPRIGAEITLPPRAVDLEVMRSINDKRLTONYEAVSHLCYLR 117  
DB 5078 SGTNVLVVEEFVRSNSDPRLVDVSSSTAQPEL-TILSTQDAERLS---EVLNNLAHFV 5133  
QY 118 RGLNRQAATAELRSLAHFCTSLQ-----LIGSIAGVMAALGYPLPQPLPSTE 166  
DB 5134 RQAQNPADLE-RLSLADLATYLTQTRGRAMQRVALVIGDLAGLLEALS-ALREERPCPV 5191  
QY 167 PWT-----PGPAH-----SDPLQKMDFFVL-----LKEI-QTWLMRSADFNRLK 206  
DB 5192 SVWSGVRVPGPSRGAETVNAQPAELLQRIPO-WIARCADELAAQAVVAGAPIDWCQLR 5250  
QY 207 KMKQPPAAAVTLHLGANGF 225  
DB 5251 RR-RPPR--RVHLPSYPF 5265

## RESULT 10

Q8NEV9 PRELIMINARY; PRT; 243 AA.  
AC Q8NEV9;  
DT 01-OCT-2002 (TREMBlrel. 22, Created)  
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE IL-27 p28 subunit.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OK NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Pfanz S., Timans J., Cheung J., Rosales R., Kanzler H., Gilbert J.,  
RA Hibbert L., Churakova T., Travis M., Vatsberg E., Blumenschein W.,  
RA Matsson J., Wagner J., To W., Zurawski S., McClanahan T., Gorman D.,  
RA Bazan F., de Waal Malefyt R., Renwick D., Kastelein R.;  
RT "IL-27 p28 subunit sequences";  
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY099296; AAM34498.1; -  
SQ SEQUENCE 243 AA; 27476 MW; 2FA8A8EB6CF61A88 CRC64;

Query Match 7.9%; Score 96.5; DB 4; Length 243;  
Best Local Similarity 23.7%; Pred. No. 0.46;  
Matches 58; Conservative 26; Mismatches 104; Indels 57; Gaps 9;

QY 1 MDLRAGD-SWGMALCLCTVL-----WHLPAVPALNRTGDPGPSIQ-----TYDL 46  
DB 1 MGQTAGDGLGMRSLSLPLPLLVQAGVWGFPRRPG-----RPQLSLQELRRREFVSLHL 53  
QY 47 TRYLEHQRLSLAGTYLN-----YLGPFPNEDFPNPRIGAEITLPPRAVDLEVMRSIN 98  
DB 54 ARKLSEVRGAHRAESHLPGVNLVLLP-----LG-RQLPVSILTFQAWRLS 101  
QY 99 DKLRLTONYEAVSHLCYLRGLNRQAATAELRR-SLAHFTSLQGLSAGVMAALGY 157  
DB 102 DPERLCFTSTLQPPHAPLGLGIGQKRWTKERNQMLAMRLDLKDQHLARFQVLAAGFN 161  
QY 158 LPQP-----LPTEPTWTPGPAHSDFLQKMDFWLKELOTWLMRSADNF 202  
DB 162 LPPEEEEBEERBEERKGLPLGALGSMALQGAQVSWPQLSTYRLHLSLELVLSAVAL 221  
QY 203 NRLKK 207  
DB 222 LLLSK 226

## RESULT 11

Q9CWV7 PRELIMINARY; PRT; 455 AA.  
AC Q9CWV7;  
DT 01-JUN-2001 (TREMBlrel. 17, Created)  
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)  
 DE 2410003H12RIK protein.  
 GN 2410003H12RIK.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CS7B/6J; TISSUE=Embryonic stem cells;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA Kawai T., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Akawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamamoto I.,  
 RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,  
 RA Kodera K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,  
 RA Kuehl P., Lewis S., Matsumoto Y., Nikaido I., Pesole G., Quackenbush J.,  
 RA Schirml L.M., Staudl P., Suzuki R., Tomita M., Wagner L., Maehio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barah G.,  
 RA Blake J., Beffelli D., Bojunga N., Carlini P., de Bonaldo M.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Wetz C., Whitaker C., Wilming L.,  
 RA Wyeth-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohzuki S.,  
 RA Hayashizaki Y.,  
 RT "Functional annotation of a full-length mouse cDNA collection."  
 RL Nature 409:685-690(2001).  
 DR EMBL; AK010358; BAB26878.1;  
 DR MGD; MGI:1919221; 2410003H12RIK.  
 SO SEQUENCE 455 AA; 51481 MW; 201868B14EB9CF CRC64;

Query Match 7.9%; Score 96.5; DB 11; Length 455;  
 Best Local Similarity 22.4%; Pred. No. 1;  
 Matches 59; Conservative 24; Mismatches 89; Indels 91; Gaps 12;

QY 7 DSGMGLACTCTVLM-HLPAVPALNRGDPG-----RGSIOKTYDITRYLEHQLNS 56  
 DB 29 DARNYOSCFWQDIPAFHPEVFLFHRITNPRGKYLTPYLVGPRVQVQEGPLARAV----- 82  
 QY 57 LAGTYLVNLGGRPNE-----PDENPRRLGAEITLPRATVDEWRSINDKRLRL 104  
 DB 83 -----YFAIPFNEDARGIAQMPQVFKFNP-----AMERVNTIL--- 116  
 QY 105 QNVEAYSHLCYLRGLNRQAATAELRSIAHFTSLQGLIGSIAGVMAALGYPLQP--- 161  
 DB 117 ----VDPHFL-LPFTLMEFPFTLEVLISAFHICKFLQKGYQL-----PLEQPVQR 162  
 QY 162 ----LPGEPFTWPCPAH-----SDPLQKMDFWLKEIQTWI---WRSADKF 202  
 DB 163 LLLSSLOSTGCSATAGTAKRLTYLLNNCIPSSRLPELHSHMLND-RIMLHWRSRAS 221  
 QY 203 NRLKKMGPPAPAAVTLHLGAGF 225  
 DB 222 SKYFQSLMAHILSOPFGTTPF 244

RESULT 12  
 OGN358 PRELIMINARY; PRT; 287 AA.  
 AC OGN358;  
 DT 01-OCT-2002 (TReMBLrel. 22, Created)  
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)  
 DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)  
 DE Hypochemical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC Tissue=Blood;  
 RA Strausberg R.;  
 RL Submitted (Apr-2002) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; BC028076; AAH28076.1; -  
 KW Hypothetical protein.  
 SO SEQUENCE 287 AA; 32156 MW; 6E571BCA0328E74E CRC64;

Query Match 7.7%; Score 94; DB 4; Length 287;  
 Best Local Similarity 22.3%; Pred. No. 0.99;  
 Matches 47; Conservative 18; Mismatches 62; Indels 84; Gaps 9;

QY 15 LCTVLMHLPAVPALNRGDPGSPSIQTYD-----LTRY---LEHOL--RSLAG 59  
 DB 132 LPLVWLRF-----PDGPTLNLTLQCPGSRQSPGYLRFHNLQMLHVLTGAFIN 181  
 QY 60 TYLVN---LGPPEPDENPRRLGAEITLPRATVDEWRSINDKRLTONYBAYSHLC 115  
 DB 182 TYLFYGAAYVGP-----ESSSVYSIRLA 204  
 QY 116 YLRGLNRQAATAELRSIAHFTSLQGLIGSI-----GVMAALGYPLQPLPTEPTW 169  
 DB 205 YL-----LSPLACLLLCFCGTLHQLSTLASGPGAGPWAHPACPLPGULPRLQ 256  
 QY 170 TEGPAHSDPLQKM-----DDFWLKEIQTWI 196  
 DB 257 LPPPHIAQVLRAGAMGSDTWGRSGFLPWGW 287

RESULT 13  
 O8KNF2 PRELIMINARY; PRT; 392 AA.  
 AC O8KNF2;  
 DT 01-OCT-2002 (TReMBLrel. 22, Created)  
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)  
 DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)  
 DE Calg.  
 GN CALG.  
 OS Micromonospora echinospora (Micromonospora purpurea).  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Micromonosporaceae; Micromonosporaceae; Micromonospora.  
 OX NCBI\_TaxID=1877;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NRL 15839;  
 RA Ahlert J., Shepard E., Lomovskaya N., Zazopoulos E., Staffa A.,  
 RA Bachmann B.O., Huang K., Fomstein L., Czisny A., Whitwam R.E.,  
 RA Farnet C.M., Thorson J.S.;  
 RT "The calicheamicin gene cluster and its iterative type I PKS."  
 RL Science 0-0-0(2002).  
 DR EMBL; AF497482; AAM70336.1; -  
 DR InterPro; IPR000890; Acetate\_kin.  
 DR PROSITE; PS01076; ACETATE KINASE 2; 1.  
 SO SEQUENCE 392 AA; 41151 MW; 8D298611281E065E CRC64;

Query Match 7.6%; Score 93; DB 2; Length 392;  
 Best Local Similarity 26.4%; Pred. No. 1.9;  
 Matches 43; Conservative 15; Mismatches 61; Indels 44; Gaps 7;

QY 45 DITRYLEHQLRSLA-----GTLYLVNLGPPPEPDP--NPPLGAEITLPR 86  
 DB 146 DITRSIEEYVRGLAQRLGIDLPGRIDRGNGNFIDIFPSLOEPFRARPRHLERPVF 205  
 QY 87 ATV-DLEWRSINDKRLRLTONYBAYSHLCYLRGLNRQAATAELRSIAHFTSLQGLIG 145  
 DB 206 AAGGDLPAVLSSRDYAR-----PLVYLTLTGSSGTEYVRA-----AIDGLAG 249  
 QY 146 SIAGVMAALGYPLQPLPTEP-----TWTGPA---HSDPL 179  
 DB 250 LDADVLVASGSLDIVSGLGEVPANVRLBSWVQALLPVDLV 292

RESULT 14

Q9MAU1 PRELIMINARY; PRT; 332 AA.  
 AC Q9MAU1: 01-OCT-2000 (TREMblrel. 15, Created)  
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)  
 DT 01-OCT-2002 (TREMblrel. 22, Last annotation update)  
 DE F13M7.8 protein (Hypothetical protein).  
 GN F13M7.8.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OC NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RA Vysotskaia V.S., Schwartz J.R., Toriumi M., Yu G., Kwan A., Liu, S.,  
 Li J., Kremetskaia I., Luros J., Araujo R., Au M., Bredel V.,  
 Buehler E., Conway A., Dewar K., Feng J., Kim C., Kurtz D., Li Y.,  
 Palm C., Shinn P., Sun H., Davis J., Ecker J., Federspiel N.,  
 RA Theologis A.;  
 RT "The sequence of BAC F13M7 from Arabidopsis thaliana chromosome 1.";  
 RL Submitted (JUN-1998) to the EMBL/Genbank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RA Theologis A.;  
 RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Haas B.J., Volkovskiy N., Town C.D., Troukhan M., Alexandrov N.,  
 RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;  
 RT "Full-length messenger RNA sequences greatly improve genome  
 RT annotation.";  
 RL Genome Biol. 0:0-0(2002).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,  
 RA Feldmann K.;  
 RT "Full-length cDNA from Arabidopsis thaliana.";  
 RL Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; AC004809; AAF4044.1; -;  
 DR EMBL; AY085490; AAM62716.1; -;  
 DR InterPro; IPR002965; P rich exten. -;  
 DR PRINTS; PR01217; PRICHEXTENSN.  
 KW Hypothetical protein.  
 SO SEQUENCE 332 AA; 36793 MW; 18E867141A070F4 CRC64;

Query Match 7.5%; Score 92; DB 10; Length 332;  
 Best Local Similarity 26.4%; Pred. No. 1.9;  
 Matches 58; Conservative 24; Mismatches 72; Indels 66; Gaps 13;

QY 23 PAVPALNRTGDPGPGPSIQKTYDLTRYLEHQLRSLAGTYLVN----- 64  
 DB 113 PSVAGNLSGYV-PRPSF--TYDPGPEYQWESLQOFIRERNQIRPLRLGLGSPVG 169  
 QY 65 LGPPNEEDFNPRLGAEFTLRATVDLEWRSINDKRLTQNYEAYSHLCTYGLNQA 124  
 DB 170 LGPIRASQFTQPRVAP--PTSIID---TSRNKAR-----SKGALAVVRG--RKV 215  
 QY 125 ATAEIIRSL-----AHFCTSLQGLSLGVAALGYPLPPLP--GTEPTWT 170  
 DB 216 RITGSSSLVLSLGNKGNH-----GIQPRSGIMK-----PLPKPLPVDLTTEISVP 266  
 QY 171 PGPAHSDFLQKMDFWMLKELQTLWRSAGKPNRLKXKM 210  
 DB 267 DDPDESADKDEKDEAVKQL-----SEKDL--LKRHIE 298

RESULT 15  
 ID Q8P199 PRELIMINARY; PRT; 716 AA.  
 AC Q8P199; 08P199;  
 AC Q8P199;

DT 01-OCT-2002 (TREMblrel. 22, Created)  
 DT 01-OCT-2002 (TREMblrel. 22, Last sequence update)  
 DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)  
 DE Peptidase.  
 GN XAC2999.  
 OS Xanthomonas axonopodis (pv. citri).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;  
 OC Xanthomonadaceae; Xanthomonas.  
 OC NCBI\_TaxID=92829;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=306 / ATCC 13902 / XV 101;  
 RX MEDLINE=22022145; PubMed=12024217;  
 RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furian L.R.,  
 RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,  
 RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.B.A.,  
 RA Camarotte G., Cammaran F., Cardozo J., Chabergo F., Clapina L.P.,  
 RA Ciccarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,  
 RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,  
 RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,  
 RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,  
 RA Locall E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,  
 RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,  
 RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,  
 RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,  
 RA Spindola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,  
 RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,  
 RA Setubal J.C., Kitaajima J.P.;  
 RT "Comparison of the genomes of two Xanthomonas pathogens with differing  
 RT host specificities.";  
 RL Nature 417:459-463(2002).  
 DR EMBL; AE011942; AAM37844.1; -;  
 DR InterPro; IPR006025; Zn MTpeptidse.  
 DR PROSITE; PS00142; ZINC\_PROTEASE; 1.  
 KW Complete proteome.  
 SO SEQUENCE 716 AA; 79145 MW; 0C6D18875E07DDCD CRC64;

Query Match 7.5%; Score 91.5; DB 16; Length 716;  
 Best Local Similarity 25.7%; Pred. No. 5.6;  
 Matches 54; Conservative 18; Mismatches 63; Indels 75; Gaps 13;

QY 22 LPAPVALNRTGDPGPGPSI---QKTYDLTRYLEHQLRSLAG---TYLVNLYGPPNEEDF 74  
 DB 101 LPDAPNMYRSGSGVPGAFWQNRADYLSASIDPATHTLSGEAAITYNH-----SPD 153  
 QY 75 NPRLGAEFTLRATVDLEWRSINDKRLTQNYEAYSHLCTYGLNLR-----QAATA 127  
 DB 154 -----TLDV-LW-----LQDQNIYRVDAARAASRPLRKKEFTDGMQIASV 193  
 QY 128 EL-----RRSLAHFCTSLQGLSLGVAALGYPLPPLP-----TEP-TW 169  
 DB 194 EIDGGGRROSHFIVD-----DTRNRVDLPPLAGQKALTVHIRYRTITIGTW 242  
 QY 170 TPGPASDFLQKMDFWMLKELQTLWRS 199  
 DB 243 GGRTAVS--ASKQDIY---EIAQWYPRMA 267

Search completed: February 9, 2004, 06:19:05  
 Job time : 41 secs

[illegible]

PD	21-APR-1998.
XX	03-FEB-1997; 97US-0792019.
PF	03-FEB-1997; 97US-0792019.
PR	03-FEB-1997; 97US-0792019.
XX	(AMGE-) AMGEN INC.
PA	
XX	Chang M;
PI	
DR	WPI; 1998-260526/23.
DR	P-PSDB; AAW56142.
PT	Neurotrophic factor NNT-1 polypeptide and related nucleic acids -
PT	useful for stimulating growth of motor and sympathetic neurons
XX	
XX	Disclosure; Fig 4; 41bp; English.
CC	The present sequence encodes a murine neurotrophic factor, designated
CC	NNT-1, which is capable of stimulating growth of motor or sympathetic
CC	neurons. The NNT-1 protein is useful in the treatment of neurological
CC	diseases characterized by the degeneration and death of particular
CC	classes of neurons. These diseases specifically include Parkinson's
CC	disease, amyotrophic lateral sclerosis (ALS), Alzheimer's disease,
CC	stroke and various degenerative disorders affecting vision.
XX	
SQ	Sequence 819 BP; 156 A; 288 C; 218 G; 157 T; 0 other;
	Query Match 84.0%; Score 669.4; DB 19; Length 819;
	Best Local Similarity 92.0%; Pred. No. 6.2e-147;
	Matches 717; Conservative 0; Mismatches 61; Indels 1; Gaps 1
OY	1 ATTAAAGCTTGC CGGAGCGGGAGCTCGCCTCCACTCCGCCAGCCTCCGGAGAGAG 60
Dd	5 ATTTAAGCTTC CGGAGCGGGAGCTCGCCTCCACTCCGCCAGCCTTCGGAGAGAG 64
OY	61 CCGCAACCCGGCGGGCCAG-CCCAGCCCCATGAGACTCCGAGAGGGGACTGTGGGG 119
Dd	65 CCCCGCCCGCGGGCCCGCCCCCAGCCCATGAGACTCCGAGAGGGGACTGTGGGG 124
OY	120 ATGTAGCGTGCTGTGACGCGGTGTCTGGGACCTCCCTGAGAGGCCAGCTTCATCGC 179
Dd	125 ATTTAGCTTGCTTAGCACGGGTGTGTGGACCTCTCTGCAGTGCCAGCTTTAATCGC 184
OY	180 ACAGGGGACCAGGGGCTGGCCCTCCATCCAGAAAATTATGACTTACCCGTA CTG 239
Dd	185 ACAGGAGATCCAGGCGCTGGCCCTCCATCCAGAAAATTATGACTTACCCGTA CTG 244
OY	240 GAGCAACAATCCGACGTTGGTGGGACTTATGTGAATACTGGGCCCCCTTTCAAC 299
Dd	245 GAGCATCAACTCCGACGTTAGCTGGGACTTACCTGAATCACTGGGGCCCCCTTTCAAC 304
OY	300 GAGCCGACTTCAACCTTCCCCTGGGGGACAGACTCTGCCAGGGGCACTGTGAC 355
Dd	305 GAGCCGACTTCAATCTCTCTGACTGGGGGACAGAACTTGGCCAGGGCCAAGTCAAC 364
OY	360 TTGGAGGTGTGGAGAAGCCTCAATGACAACTGGGCTGACCCAGAACTACGAGGCTTAC 419
Dd	365 TTGGAGGTGTGGAGAAGCCTCAATGACAACTGGGCTGACCCAGAACTATGAGGCTTAC 424
OY	420 AGCCACTTCTGTGTACTTGGTGGGCTCAACCGTCAAGGTGCACTGTGAGCTGCGC 479
Dd	425 AGTCACTCTGTGTACTTGGTGGGCTCAACCGTCAAGGTGCAAGCTGAATCTCGA 484
OY	480 CGAGGCTTGGCCACTTCTGACACAGCTCCAGGGGCTGTGGGACAGATTGGCGGGCTC 539
Dd	485 CGTAGGCTTGGCCACTTCTGTACAGGCTCCAGGGGCTGTGGGACAGATTGGCGGGCTC 544
OY	540 ATGGGAGCTGTGGGCTAACCACTGGCCAGCGCTGCTGGGAGCTGAACCACTTGGACT 599
Dd	545 ATGGGAGCTGTGGGCTAACCACTGGCCAGCGCTGCTGGGAGCTGAACCACTTGGAGC 604
OY	600 CCTGGGCTTGGCCACAGTGAATTTCTCCAGGAAGATGACGACTTGTGGCTGTAAGAG 659









GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: February 9, 2004, 06:10:21 ; Search time 274.709 Seconds  
(without alignments)  
7831.763 Million cell updates/sec

Title: US-09-931-704-1

Perfect score: 797  
Sequence: 1 attaaagcttcgscgagcc.....tctctctcgtctccccc 797

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq.19Jun03.\*

1:	/SIDSI/gcgdata/geneeq/geneeqn-emb1/NA1980.DAT.*
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25:	/SIDSI/gcgdata/geneeq/geneeqn-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	797	100.0	797	19	AAV47510 Human neurotrophic
2	797	100.0	797	19	AAV22652 CDNA encoding huma
3	797	100.0	797	21	AAAJ9481 Human NNT-1 CDNA.
4	797	100.0	797	24	ABK11647 Human CDNA encodin
5	793.4	99.5	881	22	AAH74484 Nucleotide sequenc
6	793.4	99.5	1790	21	AAH88546 Human interleukin-
7	759.2	95.3	768	22	AAH9772 Human protein enco
8	749.4	94.0	1710	20	AAH16161 Human cardiocroph

9	710	89.1	729	22	AAD04201 Human cardiocroph
10	694.8	87.2	1008	22	AAK51548 Human polynucleoti
11	669.4	84.0	819	19	AAV47512 Mouse neurotrophic
12	669.4	84.0	819	19	AAV22654 CDNA encoding mur
13	669.4	84.0	819	21	AAAJ9483 Murine NNT-1 CDNA.
14	669.4	84.0	819	24	ABK11649 Mouse CDNA encodin
15	668.4	83.9	968	22	ABA09140 Human cardiocroph
16	668.4	83.9	968	22	AAK52532 Human polynucleoti
17	558.4	70.1	648	21	AAH8547 Mouse interleukin-
18	523.4	65.7	5087	21	AAAJ9482 Human NNT-1 DNA.
19	523.4	65.7	5087	24	ABK11648 Human novel neurot
20	523.4	65.7	5088	19	AAV47511 Human neurotrophic
21	523.4	65.7	5088	19	AAV22653 Human genomic DNA
22	493.4	61.9	495	22	ABA17773 Human foetal liver
23	493.4	61.9	495	22	ABA37855 Probe #16321 for g
24	493.4	61.9	495	22	AAK20142 Human brain expres
25	493.4	61.9	495	22	AAK46202 Human bone marrow
26	493.4	61.9	495	22	AAI25564 Probe #15497 for g
27	493.4	61.9	495	22	AAI52108 Probe #20794 used
28	493.4	61.9	495	23	ABSA5921 Human liver single
29	493.4	61.9	495	24	ABS20512 Human genome-deriv
30	369	46.3	492	22	ABA59256 Human foetal liver
31	369	46.3	492	22	ABA27996 Probe #6462 for ge
32	369	46.3	492	22	AAK07469 Human brain expres
33	369	46.3	492	22	AAK3253 Human bone marrow
34	369	46.3	492	22	AAI16384 Probe #6317 for ge
35	369	46.3	492	22	AAI38047 Human liver single
36	369	46.3	492	23	ABSS3003 Human genome-deriv
37	369	46.3	492	24	ABS08085 Osteoarthritis tis
38	269.4	33.8	283	22	AAH21145 Human cardiocroph
39	80.2	10.1	396	20	AAH16162 Oligonucleotide fo
40	73.6	9.2	1260	24	ABQ16902 Oligonucleotide fo
41	73.6	9.2	1260	24	ABQ16903 Human DNK interle
42	58.6	7.4	65	24	ABNS6698 Oligonucleotide fo
43	49	6.1	627	20	AAH60797 Human DNK interle
44	46.8	5.9	1260	24	ABQ16904 Oligonucleotide fo
45	46.8	5.9	1260	24	ABQ16905

## ALIGNMENTS

RESULT 1  
ID AAV47510 standard; CDNA, 797 BP.

ID	AAV47510	Location/Qualifiers
AC	AAV47510;	
XX		
XX		
DT	09-NOV-1998 (first entry)	
XX		
XX		
DE	Human neurotrophic factor NNT-1 CDNA.	
XX		
KW	NNT-1; neurotrophic factor; human; antiinflammatory; adjuvant;	
KW	Alzheimer's disease; Parkinson's disease; Huntington's disease;	
KW	amyotrophic lateral sclerosis; Charcot-Marie-Tooth syndrome;	
KW	peripheral neuropathy; dystrophy; neural retina degeneration;	
KW	common variable immunodeficiency; CVID; selective Iga deficiency;	
KW	hypergammaglobulinaemia; X-linked agammaglobulinaemia; antihepatic;	
KW	therapy; se.	
XX		
OS	Homo sapiens.	
XX		
XX		
FH	Key	
FT	CDS	90..767
FT		/*tag= a
FT	sig_peptide	90..170
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FT	mat_peptide	171..764
FT		/*tag= c
XX		
XX		
XX		
PD	WO9833922-A1.	
	06-AUG-1998.	

XX 02-FEB-1998; 98WO-US02363.  
 PF  
 XX 30-JAN-1998; 98US-0016534.  
 PR 03-FEB-1997; 97US-0792019.  
 XX  
 XX (AMGE-) AMGEN INC.  
 XX  
 PI Chang M, Elliot GS, Sarmiento U, Senaldi G;  
 XX  
 DR WPI: 1998-437475/37.  
 DR P-PSDB; AAM29715.  
 PT  
 PT Newly isolated nucleic acid encoding human or murine neurotrophic  
 PT immunological diseases or inflammation, also as vaccine adjuvant  
 XX  
 PS Claim 3, Fig 1; 120p; English.

CC This newly isolated human cDNA sequence (deposited at ATCC 98295)  
 CC codes for a novel neurotrophic factor, designated NNT-1 (see  
 CC AAM29715), that is a growth factor for neurons and for B or T cells.  
 CC It was obtained from a T-cell lymphoma cDNA library by expressed  
 CC sequence tag analysis on the basis of homology to CNTF. The  
 CC isolated NNT-1 cDNA was used as probe to isolated NNT-1 genomic  
 CC DNA (see AAV47511). Vectors containing the cDNA or genomic DNA and  
 CC host cells are provided for use in the production of NNT-1  
 CC polypeptides. These are used to treat: (i) neurological or  
 CC immunological diseases, specifically Alzheimer's, Parkinson's or  
 CC Huntington's diseases, amyotrophic lateral sclerosis,  
 CC Charcot-Marie-Tooth syndrome, peripheral neuropathy, dystrophy and  
 CC degeneration of the neural retina, or conditions characterised by T  
 CC or B cell defects, e.g. common variable immunodeficiency (CVID),  
 CC selective IgA deficiency, hypogammaglobulinemia and X-linked  
 CC agammaglobulinemia (claimed), but many others disclosed; and (ii)  
 CC inflammation. NNT-1 is also able to boost immunoreactivity and  
 CC antibody production following vaccination, and, since it inhibits  
 CC tumour necrosis factor production, it may also be useful for  
 CC treating sepsis. NNT-1 nucleic acid fragments are also used as  
 CC hybridisation probes in diagnostic assays. In addition, cells that  
 CC have been engineered to express NNT-1 can be implanted, or nucleic  
 CC acids are delivered in gene therapy vectors.

XX Sequence 797 BP; 139 A; 297 C; 218 G; 143 T; 0 other;

XX Query Match 100.0%; Score 797; DB 19; Length 797;

XX Best Local Similarity 100.0%; Pred. No. 9.5e-177;

XX Matches 797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATTTAAAGCTTCCGCGAGGCGGCGCTCGCCCTCCCACTCCGCGAGCTCCGGAGAGGAG 60  
 DB 1 ATTTAAAGCTTCCGCGAGGCGGCGCTCGCCCTCCCACTCCGCGAGCTCCGGAGAGGAG 60  
 QY 61 CCGCAACCCGCGCGCGCCAGCCCGCATGAGACTCCGAGCAGGGAGCTGTGGGGGA 120  
 DB 61 CCGCAACCCGCGCGCGCCAGCCCGCATGAGACTCCGAGCAGGGAGCTGTGGGGGA 120  
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 DB 121 TGTTAGCGCTGTGCGAGGCTGTGCACTCCCTGCACTCCGCAATGCGCA 180  
 QY 181 CAGGGGACCCAGGGGCTGGCCCTCATCAGAAAACTATACCTCAACCGCTACCTGG 240  
 DB 181 CAGGGGACCCAGGGGCTGGCCCTCATCAGAAAACTATACCTCAACCGCTACCTGG 240  
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 DB 301 AGCCGAGCTTCAACCTCCCGCTGGGGGCGAGACTTGGCCAGGGGCACTGTTGACT 360

QY 361 TGGAGTGTGGGGAAGCTCAATGACAACTGCGGCTGACCCAGAACTACGAGGCTTACA 420  
 DB 361 TGGAGTGTGGGGAAGCTCAATGACAACTGCGGCTGACCCAGAACTACGAGGCTTACA 420  
 QY 421 GCCACTTCTGTGTACTTGGTGGCTTCAACCGTCAAGGCTGCCACTGAGCTGGGCC 480  
 DB 421 GCCACTTCTGTGTACTTGGTGGCTTCAACCGTCAAGGCTGCCACTGAGCTGGGCC 480  
 QY 481 GCAAGCTGGCCCACTTTCGACACAGCTCCGAGGGCTGCGGAGCAATGGCGGCTCA 540  
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 DB 541 TGGCAGCTCTGGGGCTAACCCACTGCGCCGCGCTGCGGAGTGAACCACTTGGACTC 600  
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 DB 721 CTCCAGCAGCTGCAAGTCACTGCACTGGGGGCTCATAGCTTGTGACTTGAACCTTCT 780  
 QY 781 CCTCTTGGCTCCCGCC 797  
 DB 781 CCTCTTGGCTCCCGCC 797

# RESULT 2

AAV22652  
 ID AAV22652 standard; cDNA; 797 BP.

AAV22652;

13-JUL-1998 (first entry)

cDNA encoding human neurotrophic factor NNT-1.

Human; neurotrophic factor; NNT-1; growth; motor; sympathetic; neuron;  
 treatment; neurological disease; degeneration; Parkinson's disease;  
 amyotrophic lateral sclerosis; ALS; Alzheimer's disease; stroke; ss.

Homo sapiens.

Key	Location/Qualifiers
CDS	90..767
FT	/*tag= a
FT	sig_peptide 90..170
FT	/*tag= b
FT	mat_peptide 171..764
FT	/*tag= c

US5741772-A.

21-APR-1998.

03-FEB-1997; 97US-0792019.

03-FEB-1997; 97US-0792019.

(AMGE-) AMGEN INC.

Chang M;

WPI: 1998-260526/23.

P-PSDB; AAM56141.

Neurotrophic factor NNT-1 polypeptide and related nucleic acids -

PT useful for stimulating growth of motor and sympathetic neurons  
 XX  
 PS Disclosure; Fig 1; 41pp; English.

CC The present sequence encodes a human neurotrophic factor, designated  
 CC NNT-1, which is capable of stimulating growth of motor or sympathetic  
 CC neurons. The NNT-1 protein is useful in the treatment of neurological  
 CC diseases characterized by the degeneration and death of particular  
 CC classes of neurons. These diseases specifically include Parkinson's  
 CC disease, amyotrophic lateral sclerosis (ALS), Alzheimer's disease,  
 CC stroke and various degenerative disorders affecting vision.

XX Sequence 797 BP; 139 A; 297 C; 218 G; 143 T; 0 other;

Query Match 100.0%; Score 797; DB 19; Length 797;  
 Best Local Similarity 100.0%; Pred. No. 9.5e-177;  
 Matches 797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATTAAGCTTCCGCGAGCGCGGCTCGCCCTCCCACTCCGCGAGCTCCGGAGAGAG 60
DB 1 ATTAAGCTTCCGCGAGCGCGGCTCGCCCTCCCACTCCGCGAGCTCCGGAGAGAG 60
QY 61 CCGCACCCGCGCGCGCCAGCCCGCATGAGCTCCGAGCAGGGGACTGCGGGGGA 120
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DB 181 CAGGGGACCCAGGGGCTGGCCCTCCATGCAAAAAAATATGACCTCAACCCGCTACTG 240
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DB 241 AGCACCACTCCGAGCTTGGAGCTTGAATCTGAACTAGCTGGGCCCCCTTTCAAG 300
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DB 361 TGGAGGTGGGAGGCTCAATGACAACTGCGGTGACCCAGACTGACAGGCTTACA 420
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DB 601 CTGGGCTTGGCCCACTTTCGACACAGCTTTCGAGAGATTCGCTGCTGAGAGAGC 660
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DB 661 TGCACACCTGGGCTGCGCTGGGCGAGAGATTCGAGCTTCAAGAGAGAGAGAGC 720
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DB 721 CTCGACAGCTGACAGCTGACAGCTGAGGAGCTTCAAGCTTTCGAGCTTCT 780
QY 781 CCTTCTGCTCCCGCC 797
DB 781 CCTTCTGCTCCCGCC 797

```

# RESULT 3

```

ID AAA39481
AC AAA39481;
DT 24-AUG-2000 (first entry)
DE Human NNT-1 cDNA.
KW NNT-1; human; neurotrophic factor; neuroprotective; treatment;
KW anticonvulsant; antiparkinsonian; antidiabetic; ophthalmological;
KW nervous system degeneration; Alzheimer's disease; Parkinson's disease;
KW amyotrophic lateral sclerosis; Charcot-Marie-Tooth syndrome;
KW Huntington's disease; peripheral neuropathy; neural retina degeneration;
KW retinopathy; immune disorder; hematopoietic disorder; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 90..767
FT /tag= a
FT /product= "NNT-1"
PN US6054294-A.
PD 25-APR-2000.
PF 12-DEC-1997; 97US-0988819.
PR 03-FEB-1997; 97US-0792019.
PA (AMGE-) AMGEN INC.
PI Chang M;
PI P-PSDB; AA187813.
DR MPI. 2000-338492/29.
DR P-PSDB; AA187813.
PT New nucleic acids encoding neurotrophic factors useful for stimulating
PT growth of motor or sympathetic neurons for treating neuron cell damage
PT
PS Claim 1a; Fig 1; 42pp; English.
XX
XX This invention describes a novel nucleic acid molecule (I) encoding a
XX novel neurotrophic factor (NNT-1) (II) which has neurotrophic,
XX neuroprotective, anticonvulsant, antiparkinsonian, antidiabetic and
XX ophthalmological activity. (I) is useful for producing NNT-1
XX polypeptides which are useful for treating patients in whom various
XX cells of the central, autonomic, or peripheral nervous system have
XX degenerated and/or have been damaged by congenital disease, trauma,
XX mechanical damage, surgery, stroke, ischemia, infection, metabolic
XX disease, nutritional deficiency, malignancy and/or toxic agents. NNT-1
XX proteins are used to treat diseases like Alzheimer's, Parkinson's,
XX amyotrophic lateral sclerosis, Charcot-Marie-Tooth syndrome, Huntington's
XX disease, peripheral neuropathy induced by diabetes or other metabolic
XX disorders, and/or dystrophies or degeneration of the neural retina such
XX as retinitis pigmentosa, drug-induced retinopathies, stationary forms of
XX night blindness, progressive cone-rod degeneration, immune disorders and
XX hematopoietic disorders. (I) is effective in treating neurological
XX conditions and promotes neuron regeneration. Neural functions are
XX effectively restored in patients suffering from various neurological
XX disorders. This sequence encodes the human NNT-1 protein described in the
XX method of the invention.
SQ Sequence 797 BP; 139 A; 297 C; 218 G; 143 T; 0 other;
Query Match 100.0%; Score 797; DB 21; Length 797;
Best Local Similarity 100.0%; Pred. No. 9.5e-177;
Matches 797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 1 ATTTAAAGCTTGGCGGAGCGCGGCTGGCCCTCCACTCCGACAGCTCCGGAGAGAG 60  
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 DB 61 CCGGACCCGGCGCGGCGCGGCTGGCCCTCCACTCCGACAGCTCCGGAGAGAG 120  
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 DB 121 TGTATGCGGCTGTGACGAGGCTGTGACCTCTCCAGGCTGCACTCAATCGCA 180  
 QY 181 CAGGGAGACCGGCGGCTGGCCCTCCACTCCGACAGCTCCGGAGAGAG 240  
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 DB 241 AGCAGCACTCCGAGCTGGCTGGAGCTATCTGAATCACTGGGCGGCTTCAGG 300  
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 QY 361 TGGAGGCTGGCGGAGCTCAATGACAACTGGGCTGACCGAGACTGAGGCTTACA 420  
 DB 361 TGGAGGCTGGCGGAGCTCAATGACAACTGGGCTGACCGAGACTGAGGCTTACA 420  
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 DB 421 GGCACCTTGTGTATCTTGGCTGAGCTGACCGTCAAGCTGCTGAGCTGCGCC 480  
 QY 481 GAGGCTGGCGGAGCTTGGACAGCTTCCAGGCTGCTGGGCGAGCTTGGGCGGCTA 540  
 DB 481 GAGGCTGGCGGAGCTTGGACAGCTTCCAGGCTGCTGGGCGAGCTTGGGCGGCTA 540  
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 DB 541 TGGGAGCTTGGGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 600  
 QY 601 CTGGGCTGGCGGAGCTTCTTCCAGAGAGTGAAGCTTGGCTGAGAGAGAG 660  
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 QY 661 TGGGAGCTTGGGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 720  
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 QY 721 CTGGGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTTCT 780  
 DB 721 CTGGGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTTCT 780  
 QY 781 CCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 797  
 DB 781 CCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 797  
 RESULT 4  
 ABK11647  
 ID ABK11647 standard; cDNA; 797 BP.  
 AC ABK11647;  
 XX  
 DT 05-JUN-2002 (first entry)  
 DE Human cDNA encoding novel neurotrophic factor NNT1.  
 XX  
 KW Human; ss; gene; NNT1; neurotrophic factor; IGF-related disease; Type I allergic disease; allergic rhinitis; eczema; dermatitis; pollinosis; asthma; immune disease; cancer; arteriosclerosis; vascular restenosis; rheumatoid arthritis; psoriatic arthritis; inflammatory arthritis; osteoarthritis; inflammatory joint disease;

KW autoimmune disease; multiple sclerosis; lupus; diabetes; endometriosis; inflammatory bowel disease; transplant rejection; reproductive disorder; graft versus host disease; infertility; miscarriage; preterm labour.  
 OS Homo sapiens.  
 XX  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 90..767  
 FT /tag= a  
 FT /product= "NNT1"  
 PN WO200215977-A2.  
 XX  
 PD 28-FEB-2002.  
 XX  
 PF 17-AUG-2001; 2001WO-US25906.  
 XX  
 PR 18-AUG-2000; 2000US-226436P.  
 PR 16-AUG-2001; 2001US-0931704.  
 XX  
 PA (AMGE-) AMGEN INC.  
 PI Senaldi G;  
 DR WPI; 2002-280867/32.  
 DR P-PSDB; AAU78176.  
 PT Treating Immunoglobulin E-related disease, modulating IGF levels in a patient, preventing IGF-related disease and treating allergic diseases, involves administering NNT-1 inhibitor to a patient  
 PS Claim 2; Fig 1; 63pp; English.  
 XX  
 CC The invention relates to treating Immunoglobulin E (IGE)-related disease, modulating IGF levels in a patient, preventing an IGF-related disease, and treating allergic diseases, comprising administering a therapeutically effective amount of novel neurotrophic factor (NNT)-1 inhibitor to a patient. Also included are a method of diagnosing an IGF-related disease or susceptibility to an IGF-related disease, by determining the presence or amount of expression of an NNT1 polypeptide encoded by a NNT1 nucleotide sequence, its fragment or naturally occurring variant, and diagnosing an IGF-related disease or susceptibility of an IGF-related disease based on the presence or amount of expression of the polypeptide and a pharmaceutical composition for use in treating IGF-related disease, comprising the NNT1 inhibitor.  
 CC The NNT1 inhibitor is useful for preventing and treating IGF-related disease, modulating IGF levels, and treating allergic diseases e.g. Type I allergic disease, allergic rhinitis, eczema, dermatitis, pollinosis, asthma, immune diseases and disorders, diseases involving abnormal cell proliferation including cancer, arteriosclerosis and vascular restenosis, diseases and conditions relating to dysfunction of immune system including rheumatoid arthritis, psoriatic arthritis, inflammatory arthritis, osteoarthritis, inflammatory joint disease, autoimmune disease, multiple sclerosis, lupus, diabetes, inflammatory bowel disease, transplant rejection, and graft versus host disease, and reproductive diseases and disorders including infertility, miscarriage, preterm labour and delivery, and endometriosis. The present sequence encodes human NNT1.  
 CC  
 CC  
 SQ Sequence 797 BP; 139 A; 297 C; 218 G; 143 T; 0 other;  
 Query Match 100.0%; Score 797; DB 24; Length 797;  
 Best Local Similarity 100.0%; Pred. No. 9.5e-177;  
 Matches 797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ATTTAAAGCTTGGCGGAGCGCGGCTGGCCCTCCACTCCGACAGCTCCGGAGAGAG 60  
 DB 1 ATTTAAAGCTTGGCGGAGCGCGGCTGGCCCTCCACTCCGACAGCTCCGGAGAGAG 60  
 QY 61 CCGGACCCGGCGCGGCGCGGCTGGCCCTCCACTCCGACAGCTCCGGAGAGAG 120  
 DB 61 CCGGACCCGGCGCGGCGCGGCTGGCCCTCCACTCCGACAGCTCCGGAGAGAG 120

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OY 121 TGTAGCGTCTGTGACGAGTCTGTGACACCTCCCTGACAGTGCAGCTTCAATCGCA 180
DB 121 TGTAGCGTCTGTGACGAGTGTCTGTGACCTCCCTGACAGTGCAGCTTCAATCGCA 180
OY 181 CAGGGGACCCAGAGGCTGTGACCTCCCTGATCAGAAAACCTATGACTTACCCGCTTACCTG 240
DB 181 CAGGGGACCCAGAGGCTGTGACCTCCCTGATCAGAAAACCTATGACTTACCCGCTTACCTG 240
OY 241 AGCACAACCTCCGACAGTGTGCTGGGAGCTTATCTGAACTACCTGGGAGCCCTTTCACAG 300
DB 241 AGCACAACCTCCGACAGTGTGCTGGGAGCTTATCTGAACTACCTGGGAGCCCTTTCACAG 300
OY 301 AGCCAGACTTCAACCTCCCTGCTGGGAGAGACTGTGCTGACAGGAGCCACTGTGACT 360
DB 301 AGCCAGACTTCAACCTCCCTGCTGGGAGAGACTGTGCTGACAGGAGCCACTGTGACT 360
OY 361 TGGAGGTGTGGGAGAGCTCAATGACAACTGCGGCTGACCCAGAACTATGAGAGGCTTACA 420
DB 361 TGGAGGTGTGGGAGAGCTCAATGACAACTGCGGCTGACCCAGAACTATGAGAGGCTTACA 420
OY 421 GCCACCTTCTGTTACTTGTGCTGAGCTGACAGCTGACCTGCTGAGCTGCGCC 480
DB 421 GCCACCTTCTGTTACTTGTGCTGAGCTGACAGCTGACCTGCTGAGCTGCGCC 480
OY 481 GCAGCTGTGCTGCTTGTGACACAGCTGCTGAGGCTGCTGAGGAGCACTTGGGAGCTCA 540
DB 481 GCAGCTGTGCTGCTTGTGACACAGCTGCTGAGGCTGCTGAGGAGCACTTGGGAGCTCA 540
OY 541 TGGCAGCTTGTGGGCTTACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
DB 541 TGGCAGCTTGTGGGCTTACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
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DB 601 CTGGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
OY 661 TGCAGACCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
DB 661 TGCAGACCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
OY 721 CTTCAGACCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
DB 721 CTTCAGACCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
OY 781 CCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 797
DB 781 CCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 797

```

## RESULT 5

AAH74484

ID AAH74484 Standard; DNA, 881 BP.

15-OCT-2001 (first entry)

Nucleotide sequence of a human NNT-1 protein.

NNT-1; CLF-1; SCNTFralpha; nervous system; neuron; nervous system;  
 neuro-muscular function; tumour; immune system; haematopoietic system;  
 amyotrophic lateral sclerosis; Parkinson's disease; Huntington's disease;  
 muscular mass; paralysis; cancer; obesity; fertility; endometriosis;  
 blastocyst implantation; thrombosis; retinal disease;  
 retinal pigmentosis; ss.

Homo sapiens.

Key Location/Qualifiers  
 CDS 174..851  
 FT /tag= a  
 FT /product= "NNT-1"

```

XX XX WO20015172-A2.
PN 02-AUG-2001.
XX PD
XX PF
XX 26-JAN-2001; 2001WO-FR00253.
XX PR
XX 27-JAN-2000; 2000FR-0001035.
XX PR
XX 12-OCT-2000; 2000FR-0013089.
XX PA
XX (FABR ) FABRE MEDICAMENT SA PIERRE.
XX PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
XX PI
XX Elson G, Gauchat J, Plun-Favreau H, Chevalier S, Gascan H;
XX DR WPI, 2001-488773/53.
XX DR P-PSDB; AAG63543.
XX PT
XX A complex comprising a NNT-1 protein and a CLF-1 and/or SCNTFralpha
XX PT protein useful to treat neurodegenerative disease including Parkinson's
XX PT and Huntington's, obesity and cancer
XX PS
XX Disclosure; Page 57-58; 67pp; French.
XX CC
XX The present sequence encodes a human NNT-1 protein. The specification
XX CC describes a complex comprising a NNT-1 protein and a CLF-1 and/or
XX CC SCNTFralpha protein. The NNT-1/CLF-1 complex is used to modulate
XX CC activity of the SCNTFralpha/gp130/LiFrbeta receptor complex, or to
XX CC induce phosphorylation of the tyrosine of gp130 and LiFrbeta,
XX CC particularly where cells expressing the receptor complex are in the
XX CC central or peripheral nervous system, in neurons implicated in
XX CC neuro-muscular function or in skeletal muscle. The complex or
XX CC antibodies are also used to decrease the survival, growth or
XX CC proliferation of tumour cells or to facilitate the proliferation and/or
XX CC inhibit differentiation of cells stocks. The complex is also used to
XX CC modulate activity of the gp130/LiFrbeta receptor or cells expressing
XX CC that receptor, particularly those cells implicated in the immune,
XX CC haematopoietic, nervous or reproductive system, the liver or skeletal
XX CC muscle. Molecules of the invention may be used to prevent or treat
XX CC neurodegenerative diseases including amyotrophic lateral sclerosis,
XX CC Parkinson's and Huntington's disease, to repair or regenerate nervous
XX CC or muscular tissue or to maintain muscular mass in paralysis patients.
XX CC They may also be used to treat cancer, obesity and associated diseases,
XX CC and to improve fertility, particularly to avoid endometriosis and/or
XX CC assist blastocyst implantation, thrombosis, or retinal disease,
XX CC particular retinal pigmentosis.
XX SQ
XX Sequence 881 BP; 158 A; 318 C; 246 G; 159 T; 0 other;

```

Query Match 99.5%; Score 793.4; DB 22; Length 881;

Best Local Similarity 99.9%; Pred. No. 6.8e-176;

Matches 794; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

OY 1 ATTAAGCTTGGCCGAGCCCGGCTGCTCCCACTCCGCGAGCTCCGAGAGAGAG 60
DB 85 ATTAAGCTTGGCCGAGCCCGGCTGCTCCCACTCCGCGAGCTCCGAGAGAGAG 144
OY 61 CCGACCCGCGCGCCAGCCCGGCTGCTCCCACTCCGCGAGCTCCGAGAGAGAG 120
DB 145 CCGACCCGCGCGCCAGCCCGGCTGCTCCCACTCCGCGAGCTCCGAGAGAGAG 204
OY 121 TGTAGCTGTGCTGTGACAGTGTGCTGTGAGCACTTCCCTGACAGTGTGCACTTCAATCGCA 180
DB 205 TGTAGCTGTGCTGTGACAGTGTGCTGTGAGCACTTCCCTGACAGTGTGCACTTCAATCGCA 264
OY 181 CAGGGGACCCAGAGGCTGTGACCTCCCTGATCAGAAAACCTATGACTTACCCGCTTACCTG 240
DB 265 CAGGGGACCCAGAGGCTGTGACCTCCCTGATCAGAAAACCTATGACTTACCCGCTTACCTG 324
OY 241 AGCACAACCTCCGACAGTGTGCTGGGAGAGCTTATCTGAACTACCTGGGAGCCCTTTCACAG 300
DB 325 AGCACAACCTCCGACAGTGTGCTGGGAGAGCTTATCTGAACTACCTGGGAGCCCTTTCACAG 384

```

```

QY 301 AGCCAGACTTCAACCTCCCGCTGGGGGAGAGACTCTGCCCAGAGGCGCACTGTTGACT 360
DB 385 AGCCAGACTTCAACCTCCCGCTGGGGGAGAGACTCTGCCCAGAGGCGCACTGTTGACT 444
QY 361 TGGAGGTGGGGAAGCTTCAATGAGAACTGGCGCTGACCCAGAACTAGAGGCTTACA 420
DB 445 TGGAGGTGGGGAAGCTTCAATGAGAACTGGCGCTGACCCAGAACTAGAGGCTTACA 504
QY 421 GCCACCTTGTGTTACTTGGCTGGGCTCAACCGTCAAGGCTGCACTGCTGAGCTGGCGC 480
DB 505 GCCACCTTGTGTTACTTGGCTGGGCTCAACCGTCAAGGCTGCACTGCTGAGCTGGCGC 564
QY 481 GCAGCTGGGCGCCACTTCTGACACAGCTTCAGAGGCTGCTGGGCGAGCATTTGGGGGTCA 540
DB 555 GCAGCTGGGCGCCACTTCTGACACAGCTTCAGAGGCTGCTGGGCGAGCATTTGGGGGTCA 624
QY 541 TGGCAGCTTGGGCTTACCACTGCGCCAGCGCTGCTGGGAGTGAACCCACTTGGACTC 600
DB 625 TGGCAGCTTGGGCTTACCACTGCGCCAGCGCTGCTGGGAGTGAACCCACTTGGACTC 684
QY 601 CTGGCCCTGGCCCAAGTGACTTCTCCAGAGATGAGAGACTTCTGGGCTGTAAGGAGC 660
DB 685 CTGGCCCTGGCCCAAGTGACTTCTCCAGAGATGAGAGACTTCTGGGCTGTAAGGAGC 744
QY 661 TGCAGACTGGCTGGGCGCTGCGCCAGAGACTTCAACCGCTCAAGAGAGATGCGAGC 720
DB 745 TGCAGACTGGCTGGGCGCTGCGCCAGAGACTTCAACCGCTCAAGAGAGATGCGAGC 804
QY 721 CTCGAGCAGCTGAGTCACTGACCTGCGACCTTGGGGCTGATGCTTGTGACTTGTGACTTCT 780
DB 805 CTCGAGCAGCTGAGTCACTGACCTGCGACCTTGGGGCTGATGCTTGTGACTTGTGACTTCT 864
QY 781 CCTCTTGGCTGCCCC 795
DB 865 CCTCTTGGCTGCCCC 879

```

## RESULT 6

AAA88546  
ID AAA88546 standard; DNA; 1790 BP.

AAA88546;

22-JAN-2001 (first entry)

Human interleukin-B60 (IL-B60) gene.

Interleukin-B60; IL-B60; human; cytokine; chromosome 11;

cytokine-like factor-1; haematopoietic; inflammation;

antiflammatory; autoimmune disease; therapy; ds.

Homo sapiens.

Key Location/Qualifiers

FT CDS 162..809

FT sig\_peptide 162..212

FT mat\_peptide 213..806

FT tag= b

FT tag= c

FT tag= c

FT tag= c

FT tag= c

FT tag= c

DR WPI; 2000-587426/55.

DR P-PSDB; AAB19686.

PT Cytokine-like factor 1 (CLF-1) and interleukin (IL)-B60 complexes,

PT polypeptides, and nucleic acids, useful in research, diagnosis and for

PT treating inflammatory and autoimmune disorders -

PS Claim 17; Page 15-16; 97pp; English.

XX The present sequence is that of DNA encoding human interleukin-B60  
CC (IL-B60, see AAB19586), a novel, small soluble cytokine-like protein  
CC of 198 amino acids that exhibits structural motifs characteristic  
CC of a member of the long-chain cytokines, and which shows homology  
CC to granulocyte colony stimulating factor and interleukin-6. IL-60B  
CC may have either stimulatory or inhibitory effects on haematopoietic  
CC cells, including e.g. lymphoid cells, such as T-cells, B-cells,  
CC natural killer cells, macrophages, dendritic cells, haematopoietic  
CC progenitors, etc. Methods are provided for modulating the  
CC physiology or development of a cell or tissue culture cells by  
CC contacting the cell with an agonist or antagonist of IL-B60 or an  
CC agonist of antagonist of a complex of mature IL-B60 and its  
CC partner, cytokine-like factor-1 (CLF-1, see AAB19588). The  
CC IL-B60/CLF-1 cytokine serves as a key physiological factor in motor  
CC neuron development and regeneration. IL-60B, its agonists and  
CC antagonists may be used to treat inflammatory or autoimmune  
CC disorders and also for drug screening. The IL60B gene maps to  
CC human chromosome 11.

XX Sequence 1790 BP; 381 A; 560 C; 474 G; 375 T; 0 other:

Query Match 99.5%; Score 793.4; DB 21; Length 1790;

Best Local Similarity 99.9%; Pred. No. 7.9e-17;

Matches 794; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 ATTTAAAGCTTGGCGGAGCCCGGCTGCTCCCACTCCGCGAGCTCCGGAGAGAG 60
DB 43 ATTTAAAGCTTGGCGGAGCCCGGCTGCTCCCACTCCGCGAGCTCCGGAGAGAG 102
QY 61 CCGACCCCGGCGCGGCGCCAGCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120
DB 103 CCGACCCCGGCGCGGCGCCAGCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 162
QY 121 TGTAGCGTGTGCTGACGAGTGTGCTGAGCACTCCCTGACAGTGCAGCTTCAATGCA 180
DB 163 TGTAGCGTGTGCTGACGAGTGTGCTGAGCACTCCCTGACAGTGCAGCTTCAATGCA 222
QY 181 CAGGGAGCCAGGGGCTGGCCCTTCATCCAGAAAACCTATGACTACCCGCTAAGCTGG 240
DB 223 CAGGGAGCCAGGGGCTGGCCCTTCATCCAGAAAACCTATGACTACCCGCTAAGCTGG 282
QY 241 AGCACCAATCGCGAGCTGTGGGAGCTATGAACTACTGTGGGCGCCCTTCAAGC 300
DB 283 AGCACCAATCGCGAGCTGTGGGAGCTATGAACTACTGTGGGCGCCCTTCAAGC 342
QY 301 AGCCAGACTTCAACCTCCCGCTGGGGGAGAGACTCTGCCAGGGGCACTGTGACT 360
DB 343 AGCCAGACTTCAACCTCCCGCTGGGGGAGAGACTCTGCCAGGGGCACTGTGACT 402
QY 361 TGGAGGTGGGGAAGCTTCAATGAGAACTGGCGCTGACCCAGAACTAGAGGCTTACA 420
DB 403 TGGAGGTGGGGAAGCTTCAATGAGAACTGGCGCTGACCCAGAACTAGAGGCTTACA 462
QY 421 GCCACCTTGTGTTACTTGGCTGGGCTCAACCGTCAAGGCTGCACTGCTGAGCTGGCGC 480
DB 463 GCCACCTTGTGTTACTTGGCTGGGCTCAACCGTCAAGGCTGCACTGCTGAGCTGGCGC 522
QY 481 GCAGCTGGGCGCCACTTCTGACACAGCTTCAGAGGCTGCTGGGAGCATTTGGGGGTCA 540
DB 523 GCAGCTGGGCGCCACTTCTGACACAGCTTCAGAGGCTGCTGGGAGCATTTGGGGGTCA 582
QY 541 TGGCAGCTTGGGCTTACCACTGCGCCAGCGCTGCTGGGAGTGAACCCACTTGGACTC 600
DB 583 TGGCAGCTTGGGCTTACCACTGCGCCAGCGCTGCTGGGAGTGAACCCACTTGGACTC 642

```



QY 601 CTGGCCCTGCCAGTGAAGTCTTCTCCAGAGATGAGACGACTTCTGGCTGTGAAGAGC 660  
DB 643 CTGGCCCTGCCAGTGAAGTCTTCTCCAGAGATGAGACGACTTCTGGCTGTGAAGAGC 702  
QY 661 TGGCAGACTGGCTGTGGCGCTGGCCAGAGACTTCAACCGGCTCAAGAGAGATGACAC 720  
DB 703 TGGCAGACTGGCTGTGGCGCTGGCCAGAGACTTCAACCGGCTCAAGAGAGATGACAC 762  
QY 721 CTGCAGACTGAGTCAACCTTGCACCTTGGGGCTCAATGGCTTCACTTTCACCTTCT 780  
DB 763 CTGCAGACTGAGTCAACCTTGCACCTTGGGGCTCAATGGCTTCACTTTCACCTTCT 822  
QY 781 CCTTCTGGCTCCCGC 795  
DB 823 CCTTCTGGCTCCCGC 837

RESULT 7  
AAH9772  
ID AAH9772 standard; cDNA; 768 BP.  
XX AAH9772;  
XX  
XX 16-OCT-2001 (first entry)  
DE Human protein encoding cDNA sequence SEQ ID NO:607.  
XX  
XX Human; cancer; ulcer; HIV infection; human immunodeficiency virus;  
KW anti-inflammation; anti-rheumatic; anti-arthritic; immunosuppressive;  
KW anti-bacterial; endocrine; cardiac; central nervous system; virulence;  
KW anti-HIV; fungicide; antimutagen; cardiovascular; anti-nausea; anaemia;  
KW anti-aggregant; haemostatic; vulnery; antitumor; osteopathic; eczema;  
KW dermatological; anti-dermatitis; anti-dermatitis; cytostatic;  
KW neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;  
KW immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;  
KW antineoplastic; rheumatoid arthritis; septic shock; pancreatitis;  
KW cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;  
KW genetic disease; haematopoietic disorder; platelet disorder; asthma;  
KW thrombocytopenia; osteoporosis; severe combined immunodeficiency;  
KW allergic rhinitis; diabetes; multiple sclerosis; depression;  
KW Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;  
KW neurological disorder; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200153455-A2.  
XX  
XX 26-JUL-2001.  
XX  
XX 22-DEC-2000; 2000MO-US55017.  
XX  
XX 23-DEC-1999; 99US-0471275.  
XX 21-JAN-2000; 2000US-048725.  
XX 25-APR-2000; 2000US-0552317.  
XX  
XX (HYSE-) HYSE INC.  
XX  
XX Tang YT, Liu C, Drmanac RT;  
PI WPI; 2001-457603/49.  
XX  
XX P-PSDB; AAM25831.  
XX  
XX Isolated human polynucleotides encoding polypeptides, useful for the  
PT treatment and diagnosis of e.g. cancer, ulcers and HIV infection -  
XX  
XX Claim 1; Page 638; 1217pp; English.  
XX  
XX AAH99166 to AAH99904 encode the human proteins given in AAM25225 to  
CC AAM25963. The proteins can have activities based on the classes and  
CC cells they are expressed in, such as: anti-inflammatory; anti-neuritic;  
CC anti-arthritic; immunosuppressive; antibacterial; endocrine; cardiac;  
CC central nervous system; virulence; anti-HIV; fungicide; antimutagen;

CC cardiovascular; anti-nausea; anti-aggregant; haemostatic; vulnery;  
CC anti-tumor; osteopathic; dermatological; anti-arthritic; anti-neuritic;  
CC anti-bacterial; cytostatic; neuroprotective; antidepressant; nootropic;  
CC antiparkinsonian; and immunostimulant. The proteins and polynucleotides  
CC encoding them can be used in gene therapy, antisense therapy and vaccine  
CC production. The proteins and polynucleotides are useful for screening for  
CC agonists or antagonists of a protein and for the treatment and diagnosis  
CC of disorders associated with the activity of a protein e.g. inflammation,  
CC rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,  
CC neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal  
CC infections, autoimmunity, genetic diseases, haematopoietic disorders,  
CC anaemia, platelet disorders, thrombocytopenia, wounds, burns, ulcers,  
CC osteoporosis, severe combined immunodeficiency, eczema, allergic  
CC rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,  
CC Alzheimer's disease, Parkinson's disease, neurodegenerative and  
CC neurological disorders.

SQ Sequence 768 BP; 137 A; 278 C; 217 G; 136 T; 0 other;  
XX  
XX

Query Match 95.3%; Score 759.2; DB 22; Length 768;  
Best Local Similarity 99.6%; Pred. No. 6,4e-168;  
Matches 761; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATTAAGCTTGGCCGAGCCCGGCTCGCCCTCCGACTCCGCGACCTCCGGAGAGAG 60  
DB 5 ATTAAGCTTGGCCGAGCCCGGCTCGCCCTCCGACTCCGCGACCTCCGGAGAGAG 64  
QY 61 CCGCACCAGCCGCGCCGAGCCCGGCTCGCCCTCCGACTCCGCGACCTCCGGAGAGAG 120  
DB 65 CCGCACCAGCCGCGCCGAGCCCGGCTCGCCCTCCGACTCCGCGACCTCCGGAGAGAG 124  
QY 121 TGTAGCGGCTGTGACGAGGCTGTGACCTCCGAGTGCAGTGCAGTGCAGTGCAGTGCAG 180  
DB 125 TGTAGCGGCTGTGACGAGGCTGTGACCTCCGAGTGCAGTGCAGTGCAGTGCAGTGCAG 184  
QY 181 CAGGGAGCCAGAGGCTGTGACCTCCGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAG 240  
DB 185 CAGGGAGCCAGAGGCTGTGACCTCCGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAG 244  
QY 241 AGCACAACCTCCGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAG 300  
DB 245 AGCACAACCTCCGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAG 304  
QY 301 AGCACAACCTCCGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAG 360  
DB 305 AGCACAACCTCCGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAG 364  
QY 361 TGGAGGTGTGGAGAGCTCAATGACAACTGCGCTGACCCAGAGACTTACAGAGGCTTACA 420  
DB 365 TGGAGGTGTGGAGAGCTCAATGACAACTGCGCTGACCCAGAGACTTACAGAGGCTTACA 424  
QY 421 GCCACCTTGTGTGTAATGCTGCGCTGACCCGAGTGCAGTGCAGTGCAGTGCAGTGCAG 480  
DB 425 GCCACCTTGTGTGTAATGCTGCGCTGACCCGAGTGCAGTGCAGTGCAGTGCAGTGCAG 484  
QY 481 GCAAGCTGCGCACTTTCGACCAAGCTTCAGAGGCTGTGAGGAGCAATTGAGGAGCTTCA 540  
DB 485 GCAAGCTGCGCACTTTCGACCAAGCTTCAGAGGCTGTGAGGAGCAATTGAGGAGCTTCA 544  
QY 541 TGGCAGCTTGTGGCTTACCACTGCGCCAGGCTGCTGAGAGTGAATGCACTTGTGAGACT 600  
DB 545 TGGCAGCTTGTGGCTTACCACTGCGCCAGGCTGCTGAGAGTGAATGCACTTGTGAGACT 604  
QY 601 CTGGCCCTGCCAGTGAAGTCTTCTCCAGAGATGAGACGACTTCTGGCTGTGAAGAGC 660  
DB 605 CTGGCCCTGCCAGTGAAGTCTTCTCCAGAGATGAGACGACTTCTGGCTGTGAAGAGC 664  
QY 661 TGGCAGACTGGCTGTGGCGCTGGCCAGAGACTTCAACCGGCTCAAGAGAGATGACAC 720  
DB 665 TGGCAGACTGGCTGTGGCGCTGGCCAGAGACTTCAACCGGCTCAAGAGAGATGACAC 724  
QY 721 CTGCAGACTGAGTCAACCTTGCACCTTGGGGCTCAATGGCTTCACTTTCACCTTCT 764



PT /cag= C  
FT /Product= "Human mature cardiotrophin-like cytokine  
FT (CLC) protein"  
XX  
XX  
PN W0200127157-A1.  
XX  
PD 19-APR-2001.  
XX  
PF 06-OCT-2000; 2000WO-AV01216.  
XX  
PR 08-OCT-1999; 99AU-0003327.  
XX 12-MAY-2000; 2000AU-0007489.  
XX  
PA (AMRA-) AMRAD OPERATIONS PTY LTD.  
XX  
PI Nash A, Jachno KM, Pabri LJ, Reid K, Bartlett PR, Hilton DJ;  
PI Nakata Y, Haegawa M;  
DR MPI; 2001-281978/29.  
DR P-PSDB; AAE00828.  
XX  
XX New biologically active complex comprising NR6 and  
PT cardiotrophin-like cytokine, for facilitating proliferation,  
PT differentiation and/or survival of a cell -  
XX  
PS Claim 31; Page 112-114; 123pp; English.  
XX  
CC The present invention relates to a biologically active complex comprising  
CC a haemopoietin receptor, NR6 and cardiotrophin-like cytokine (CLC).  
CC The complex is useful in the manufacture of a medicament for the  
CC treatment and/or prophylaxis of a subject, as it is involved in  
CC facilitating proliferation, differentiation and/or survival of a cell.  
CC The complex or its components have neurotrophic activity. The present  
CC sequence is human cardiotrophin-like cytokine (CLC) cDNA.  
SQ Sequence 729 BP; 132 A; 261 C; 196 G; 140 T; 0 other;  
Query Match 89.1%; Score 710; DB 22; Length 729;  
Best Local Similarity 100.0%; Pred. No. 2e-156;  
Matches 710; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 86 CCCCATGAGACTTCGAGAGAGGAGCTGTGGGGAGATTAGCGCTGTGACGGTGTCT 145  
DB 7 CCCCATGAGACTTCGAGAGAGGAGCTGTGGGGAGATTAGCGCTGTGACGGTGTCT 66  
QY 146 CTGGCACTTCCTCGAGTGCAGACTCTCAATGCGACAGGGGAGCCAGGGGCTTGGCCCTTC 205  
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QY 206 CATCGAAGAAACCTATGACCTCACCAGCTACCTGAGGACCAACTCCGAGAGCTTGGCTGG 265  
DB 127 CATCGAAGAAACCTATGACCTCACCAGCTACCTGAGGACCAACTCCGAGAGCTTGGCTGG 186  
QY 266 GACCTATCTGAACTACTGTGGGCCCCCTTTCAAGAGAGCAAGTTCACCTCCCGGCT 325  
DB 187 GACCTATCTGAACTACTGTGGGCCCCCTTTCAAGAGAGCAAGTTCACCTCCCGGCT 246  
QY 326 GGGGGGAGAGACTCTGCGCCAGGGGCACTGTGACTTGAAGGTGTGGCGAAAGCTTCATAGA 385  
DB 247 GGGGGGAGAGACTCTGCGCCAGGGGCACTGTGACTTGAAGGTGTGGCGAAAGCTTCATAGA 306  
QY 386 CAAGCTGGGGCTGACCCAGAGAACTAGAGGCTTACAGCAACCTTCTGTGTTACTTGGGTGG 445  
DB 307 CAAGCTGGGGCTGACCCAGAGAACTAGAGGCTTACAGCAACCTTCTGTGTTACTTGGGTGG 366  
QY 446 CCTCAACCTGTAGCTGCGCACTGTGAGCTGCGCCAGCTTGGCCACCTTCTGACACAG 505  
DB 367 CCTCAACCTGTAGCTGCGCACTGTGAGCTGCGCCAGCTTGGCCACCTTCTGACACAG 426  
QY 506 CCTTCAGGGGCTGTGGGAGAGCAATTGGGGGCTTACATGAGCAAGCTTCTGGGCTACCACTGCC 565  
DB 427 CCTTCAGGGGCTGTGGGAGAGCAATTGGGGGCTTACATGAGCAAGCTTCTGGGCTACCACTGCC 486

QY 566 CCAGCCGCTGCTGGGAGATGAACCACTTGAATCTCTGCGCCCTGCGCACAGTGAATTCCT 625  
DB 487 CCAGCCGCTGCTGGGAGATGAACCACTTGAATCTCTGCGCCCTGCGCACAGTGAATTCCT 546  
QY 626 CCAGAGATGAGACGACTTCTGCTGCTGAGAGAGCTGACAGACCTTGGCGCTCGGC 685  
DB 547 CCAGAGATGAGACGACTTCTGCTGCTGAGAGAGCTGACAGACCTTGGCGCTCGGC 606  
QY 686 CAAGACTTCAACCGGCTCAAGAGAGATGAGAGCTGACAGAGCTGACAGCTGACCTGCA 745  
DB 607 CAAGACTTCAACCGGCTCAAGAGAGATGAGAGCTGACAGAGCTGACAGCTGACCTGCA 666  
QY 746 CTGGGGGCTGATGAGCTTCTGACTTGAACCTTCTCTCTTCTGCTGCTGCTGCTGCT 795  
DB 667 CTGGGGGCTGATGAGCTTCTGACTTCTGACTTCTCTCTCTTCTGCTGCTGCTGCTGCT 716  
RESULT 10  
AAKS1548  
ID AAKS1548 standard; cDNA; 1008 BP.  
XX  
XX AAKS1548;  
AC  
XX 06-NOV-2001 (first entry)  
DT  
XX  
DE Human polynucleotide SEQ ID NO 93.  
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;  
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;  
KW tissue growth factor; immunomodulatory; cancer; leukaemia;  
KW nervous system disorder; arthritis; inflammation; ss.  
OS Homo sapiens.  
XX  
XX W0200157190-A2.  
PN  
XX  
PD 09-AUG-2001.  
XX  
PF 05-FEB-2001; 2001WO-US04098.  
XX  
PR 03-FEB-2000; 2000US-0496914.  
XX 27-APR-2000; 2000US-0560875.  
PR 20-JUN-2000; 2000US-0598075.  
PR 19-JUL-2000; 2000US-0620325.  
PR 01-SEP-2000; 2000US-0654936.  
PR 15-SEP-2000; 2000US-0663561.  
PR 20-OCT-2000; 2000US-0693325.  
PR 30-NOV-2000; 2000US-0728422.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
XX Tang YT, Liu C, Dzmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;  
PI Zhao QA, Wang Y, Zhang J, Ren F, Chen R, Wang ZW;  
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;  
XX  
DR MPI: 2001-476283/51.  
XX P-PSDB; AAM78415.  
PT Nucleic acids encoding polypeptides with cytokine-like activities,  
XX useful in diagnosis and gene therapy -  
XX  
PS Claim 1; Page 711-712; 6221pp; English.  
XX  
XX The invention relates to polynucleotides (AAKS1456-AAKS3435) and the  
CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to  
CC cytokine, cell proliferation or cell differentiation or which may induce  
CC production of other cytokines in other cell populations. The  
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or  
CC peptide therapy. The polypeptides have various cytokine-like activities,  
CC e.g. stem cell growth factor activity, haematopoietic regulatory  
CC activity, tissue growth factor activity, immunomodulatory activating  
CC activity/inhibin activity and may be useful in the diagnosis and/or  
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and



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1..569
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="S13KMS5-40-G02"
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/cell_line="KMS-5"
/lab_host="Top10F"
/clone_lib="S13KMS5"
/notes="Vector: pCNS; Site_1: EcoRI; Site_2: NotI; The poly
(A) + RNA was dephosphorylated with bacterial alkaline
phosphatase (BAP) and then deapped with tobacco acid
pyrophosphatase (TAP). The deapped intact mRNA was
ligated with DNA-RNA linker including EcoRI site by
treatment of T4 RNA ligase and the first strand cDNA was
synthesized from oligo dt-selected mRNA by priming with
dt-tailed vector. The dt-tailed vector was adjusted to
have about 60nt. The cDNA vector was circularized with E.
coli DNA ligase after digestion of EcoRI which site is
also included in vector. An RNA strand converted to a DNA
strand by Okayama-Berg method. The obtained cDNA vectors
were used for transformation of competent cells E. coli
Top10F by electroporation method. The cDNA libraries
constructed by this method are full-length enriched cDNA
library."
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BASE COUNT 135 a 192 c 151 g 91 t

ORIGIN

Query Match 57.6%; Score 458.8; DB 12; Length 569;  
Best Local Similarity 99.6%; Pred. No. 2.1e-88;  
Matches 460; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 61 CCGCACCCCGCGCGCCAGCCAGCCCATGAACTCCAGACAGGGAGACTGCGGGGA 120  
DB 168 CCGCACCCCGCGCGCCAGCCAGCCCATGAACTCCAGACAGGGAGACTGCGGGGA 227  
QY 121 TGTAGCGTGTGACAGGTGCTGTGACCTCCCTGACGTGCCAGCTCAATCGCA 180  
DB 228 TGTAGCGTGTGACAGGTGCTGTGACCTCCCTGACGTGCCAGCTCAATCGCA 287  
QY 181 CAGGGGACCCAGGGGCTGGCCCTCATCAGAAAACTATGACCTCAACCCGCTACTGG 240  
DB 288 CAGGGGACCCAGGGGCTGGCCCTCATCAGAAAACTATGACCTCAACCCGCTACTGG 347  
QY 241 AGCACCAACTCCGACAGCTTGGGAACTATCTGAACCTAGGAGCCCTTTCAAG 300  
DB 348 AGCACCAACTCCGACAGCTTGGGAACTATCTGAACCTAGGAGCCCTTTCAAG 407  
QY 301 AGCCAGACTTCAACCTCCCGGCTGGGGGAGAGACTGTGCCAGGGGCACTGTGACT 360  
DB 408 AGCCAGACTTCAACCTCCCGGCTGGGGGAGAGACTGTGCCAGGGGCACTGTGACT 467  
QY 361 TGGAGTGTGGGAGAGCTCAATGACAACTGGGCTGACCCAGAACTACGAGGCTACA 420  
DB 468 TGGAGTGTGGGAGAGCTCAATGACAACTGGGCTGACCCAGAACTACGAGGCTACA 527  
QY 421 GCCACCTTCTGTGTTACTTGTGAGCTCAACCTGAGGCTG 462  
DB 528 GCCACCTTCTGTGTTACTTGTGAGCTCAACCTGAGGCTG 569

Search completed: February 9, 2004, 09:23:57  
Job time : 2160.8 secs

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RESULT 14  
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 ACCESSION BM847924.1 GI:19204323  
 VERSION  
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 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
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 1 (bases 1 to 529)  
 Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,  
 Oh,K.U., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and  
 Kim,Y.S.  
 21C Frontier Korean EST Project 2001  
 Unpublished  
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 Tel: +82-42-860-4470  
 Fax: +82-42-860-4409  
 Email: yongsung@mail.kr.ibm.re.kr  
 Plate: 57 row: A column: 03  
 High quality sequence stop: 529.  
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 pyrophosphatase (TAP). The deapped intact mRNA was  
 ligated with DNA-RNA linker including EcoR I site by  
 treatment of T4 RNA ligase and the first strand cDNA was  
 synthesized from oligo dt-selected mRNA by priming with  
 dt-tailed vector. The dt-tailed vector was adjusted to  
 have about 60nt. The cDNA vector was circularized with E.  
 coli DNA ligase after digestion of EcoRI which site is  
 also included in vector. An RNA strand converted to a DNA  
 strand by Okayama-Berg method. The obtained cDNA vectors  
 were used for transformation of competent cells E. coli  
 Top10F by electroporation method. The cDNA libraries  
 constructed by this method are full-length enriched cDNA

BASE COUNT 92 a 199 c 147 g 91 t  
 ORIGIN  
 Query Match 64.6%; Score 514.8; DB 12; Length 529;  
 Best Local Similarity 99.4%; Pred. No. 2e-100;  
 Matches 527; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 31 CTCCTCCGCGACCTCCGGGAGAGAGAGCCGAGCCGAGCCGAGCCGAGCCCA 90  
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 QY 91 TGAACCTCCGAGACAGAGAGATCTGTGGAGATTTAGTGTGCAAGTGTCTGTGC 150  
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RESULT 15  
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 DEFINITION mRNA sequence.  
 BM846748  
 ACCESSION BM846748.1 GI:19203147  
 VERSION  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
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 1 (bases 1 to 569)  
 Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,  
 Oh,K.U., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and  
 Kim,Y.S.  
 21C Frontier Korean EST Project 2001  
 Unpublished  
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 Korea Research Institute of Bioscience & Biotechnology  
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 Fax: +82-42-860-4409  
 Email: yongsung@mail.kr.ibm.re.kr  
 Plate: 40 row: G column: 02  
 High quality sequence stop: 569.  
 Location/Qualifiers



Db 566 ACTTCTGCTGCTGAAGAGAGCTGCAACTTGGCTGTGGCTGGCCCAAGACTTCMAAC 625  
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RESULT 11  
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K-EST0125376 S13KMS5s1 Homo sapiens cDNA clone S13KMS5s1-21-A09 5',  
mRNA sequence.  
BM846370  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS

1 (bases 1 to 532)  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,  
Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and  
Kim, Y.S.  
21C Frontier Korean EST Project 2001  
Unpublished  
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Korea Research Institute of Bioscience & Biotechnology  
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Tel: +82-42-860-4470  
Fax: +82-42-860-4409  
Email: yongsung@mail.kribb.re.kr  
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Location/Qualifiers

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(A)+ RNA was dephosphorylated with bacterial alkaline  
phosphatase (BAP) and then deaped with tabacco acid  
pyrophosphatase (TAP). The deapped intact mRNA was  
ligated with DNA-RNA linker including EcoRI site by  
treatment of T4 RNA ligase and the first strand cDNA was  
synthesized from oligo dt-selected mRNA by priming with  
dt-tailed vector. The dt-tailed vector was adjusted to  
have about 60nt. The cDNA vector was circularized with E.  
coli DNA ligase after digestion of EcoRI which site is  
also included in vector. An RNA strand converted to a DNA  
strand by Okayama-Berg method. The obtained cDNA vectors  
were used for transformation of competent cells E. coli  
Top10P by electroporation method. The cDNA libraries  
constructed by this method are full-length enriched cDNA  
library. After analyzing and sequencing about 2,000 ~  
3,000 colonies in original cDNA library, the abundant  
cDNAs were selected and amplified by PCR reaction using  
vector region primer including T7 promoter as 5' primer  
and N(dt)14 as 3' primer. The PCR products were used as  
template for synthesis of biotinylated single stranded RNA  
by in vitro transcription reaction. The synthesized RNA  
probes were hybridized with antisense single stranded  
cDNAs prepared from original library and incubated with  
avidin-gel. After removing DNA-RNA hybrids by centrifuge,  
the subtracted cDNA libraries were constructed by  
transformation of the remaining DNA into competent cells E.  
coli Top10P with electroporation method."

BASE COUNT 92 a 201 c 148 g 91 t

ORIGIN

Query Match 66.3%; Score 528.8; DB 12; Length 532;  
Best Local Similarity 99.6%; Pred. No. 2e-103; Indels 0; Gaps 0;  
Matches 530; Conservative 0; Mismatches 2;

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Qy 91 TGGACCTCCGAG 150  
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Qy 151 ACCCTCCGAG 210  
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Qy 211 AGAAACCTATGACCTCAACCCGCTACCTGAGAGAGAGAGAGAGAGAGAGAG 270  
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Qy 271 ATCTGAACCTACCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 330  
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Qy 331 CAGAGACTCTGAG 390  
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Qy 391 TGGGCTGAG 450  
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Qy 451 ACCGTGAG 510  
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mRNA sequence.  
BM841897  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS

1 (bases 1 to 522)  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,  
Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and  
Kim, Y.S.  
21C Frontier Korean EST Project 2001  
Unpublished  
Contact: Kim YS  
Genome Research Center  
Korea Research Institute of Bioscience & Biotechnology  
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea  
Tel: +82-42-860-4470  
Fax: +82-42-860-4409  
Email: yongsung@mail.kribb.re.kr  
Plate: 34 row: A column: 05  
High quality sequence stop: 522.  
Location/Qualifiers

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Db 668 CTGCAGACCTG 678

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LOCUS K-EST0118015 S13KMS5 Homo sapiens cDNA clone S13KMS5-35-D11 5',  
DEFINITION mRNA sequence.  
ACCESSION BM840863  
VERSION BM840863.1 GI:19197272  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 573)  
Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,  
Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and  
Kim, Y.S.  
21C Frontier Korean EST Project 2001  
JOURNAL Unpublished  
COMMENT Contact: Kim YS  
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Korea Research Institute of Bioscience & Biotechnology  
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Tel: +82-42-860-4470  
Fax: +82-42-860-4409  
Email: yongsung@mail.kribb.re.kr  
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pyrophosphatase (TAP). The deapped intact mRNA was  
ligated with DNA-RNA linker including EcoR I site by  
treatment of T4 RNA ligase and the first strand cDNA was  
synthesized from oligo dT-selected mRNA by priming with  
dT-tailed vector. The dT-tailed vector was adjusted to  
have about 60nt. The cDNA vector was circularized with E.  
coli DNA ligase after digestion of EcoRI which site is  
also included in vector. An RNA strand converted to a DNA  
strand by Okayama-Berg method. The obtained cDNA vectors  
were used for transformation of competent cells E. coli  
TOP10F<sup>+</sup> by electroporation method. The cDNA libraries  
constructed by this method are full-length enriched cDNA  
library."

BASE COUNT 98 a 217 c 160 g 98 t

Query Match 71.7%; Score 571.4; DB 12; Length 573;  
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QY 31 CTCCTCCAGCTCCGAGCTCCGAGAGAGAGCCGAGCCGAGCCGAGCCGAGCCCA 90  
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QY 91 TGGACCTCCGAGAGGGGAGCTGCTGGGGAGTGTAGCGTCTGTGACAGCGTCTGGC 150  
Db 61 TGGACCTCCGAGAGGGGAGCTGCTGGGGAGTGTAGCGTCTGTGACAGCGTCTGGC 120

QY 151 ACCTCCCTCAGTGCAGCTCTCAATGCGAGAGGAGCCAGGAGCCCTGCCTCATCC 210  
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QY 211 AGAAAACCTATGACTCTACCCGCTACCTGGAGACCAACTCCGAGCTTGGCTGGAGCT 270  
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Db 541 CGCTGCTGGGAGCTGAACCCACTTGTGACTCTG 573

RESULT 9  
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DEFINITION clone CS0D1004YML5 5-PRIME, mRNA sequence.  
ACCESSION AL543945  
VERSION AL543945.2 GI:31265790  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 1028)  
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
Full-length cDNA libraries and normalization  
JOURNAL Unpublished  
COMMENT On Feb 15, 2001 this sequence version replaced gi:12876424.  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: segre@genoscope.cns.fr, Web: www.genoscope.cns.fr  
Library was constructed by Life Technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 6127.r For  
more information about this cluster, see  
http://www.genoscope.cns.fr/  
cgi-bin/cluster.cgi?seq=CS0D1004AG080P1cluster=6127.r. Contact :  
Feng Liang Email: fliang@life.techn.com URL :  
http://fulllength.invitrogen.com/invitrogen Corporation 1600  
Faraday Avenue Genoscope sequence ID : CS0D1004AG080P1.  
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 Db 542 CGCTGCTGGAGCTGACCTGAGCTGCTGCTGCTG 580  
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**RESULT 7**  
 BY735168  
 LOCUS BY735168  
 DEFINITION BY735168 RIKEN full-length enriched, mammary gland RCB-0527 Jy9-MC(B) cDNA Mus musculus cDNA clone G930015G22 5', mRNA

**ACCESSION**  
 BY735168  
**VERSION**  
 BY735168  
**KEYWORDS**  
 EST  
**SOURCE**  
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 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

**REFERENCE**  
 AUTHORS  
 Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nishido, I., Otsu, N., Saito, R., Suzuki, H., Yamana, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Balderelli, R., Hill, D. P., Bult, C., Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Baccalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Bruscia, V., Chochia, C., Corbani, L. E., Cousine, S., Dalia, E., Dragani, T. A., Fletcher, C. P., Forrest, A., Frazer, K. S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Guellinich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A., Kawai, H., Kawasawa, Y., Kedziarski, R. M., Kling, B. L., Konagaya, A., Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W. J., Perlea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J. V., Qi, D., Ramchandran, S., Ravi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M., Sandelin, A., Schneider, C., Sempile, C. A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M., Verrado, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L. G., Wymshaw-Bois, A., Yanagisawa, M., Yang, L., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carinini, P., Hayatsu, N., Hirozane-Kobayashi, T., Kono, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Alzawa, K., Akakawa, T., Fukuda, S., Hara, A., Hasehizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shingawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S., Rogers, J., Birney, E., and Hayashizaki, Y.  
 Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
 Nature 420, 563-573 (2002)

**TITLE**  
 JOURNAL  
 MEDLINE  
 PUBMED  
 COMMENT

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 The Institute of Physical and Chemical Research (RIKEN)  
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 Tel: 81-45-503-9222  
 Fax: 81-45-503-9216  
 Email: genome-res@gsr.riken.go.jp,  
 URL: http://genome.gsc.riken.go.jp/  
 Adachi, J., Alzawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hasehizume, W., Hayashida, K., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Koyama, S., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Saito, R., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Takeda, Y., Waki, K., Watanabe, A., Muramatsu, M. and Hayashizaki, Y. Direct Substitution  
 Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)  
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)  
 RIKEN integrated sequence analysis (RISA) system--384-format

sequencing pipeline with 384 multipillar sequencer. Genome Res. 10 (11), 1757-1771 (2000)  
 Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
 Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

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SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
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AUTHORS	NIH-MGC <a href="http://mgc.ncl.nih.gov/">http://mgc.ncl.nih.gov/</a> .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished
COMMENT	Contact: Robert Strausberg, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: InCyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LINL at:  
<http://image.lnl.gov>  
Plate: LHM10246    row: m    column: 14  
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Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
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Note: this is a NIH_MGC library."
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REFERENCE  
AUTHORS  
1 (bases 1 to 594)  
Kim, N. S., Hahn, Y., Oh, J. H., Lee, J. Y., Ahn, H. Y., Chu, M. Y., Kim, M. F., Oh, K. J., Cheong, J. E., Sohn, H. Y., Kim, J. M., Park, H. S., Kim, S. and Kim, Y. S.

TITLE 21C Frontier Korean EST Project 2001  
JOURNAL Unpublished  
COMMENT Contact: Kim YS

**FEATURES**

Korea Research Institute of Bioscience & Biotechnology  
52, Boeun-dong, Yuseong-gu, Daejeon 305-333, South Korea  
Tel.: +82-42-860-4470  
Fax: +82-42-860-4409  
Email: [Yongsung@mail.kribb.re.kr](mailto:Yongsung@mail.kribb.re.kr)  
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ligated with DNA-RNA linker including EcoR I site by
treatment of T4 RNA ligase and the first strand cDNA was
synthesized from oligo dt-selected mRNA by priming with
dt-tailed vector. The dt-tailed vector was adjusted to
have about 60nt. The cDNA vector was circularized with E.
coli DNA ligase after digestion of EcoRI which site is
also included in vector. An RNA strand converted to a DNA
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[illegible]

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NotI; cDNA made by oligo-dT priming. Directionally cloned

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into EcoRI/XhoI sites using the following 5' adaptor:  
GGGACGAG(G). Library constructed by Ling Hong in the  
Laboratory of Gerald M. Rubin (University of California,  
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and  
Superscript II RT (Life Technologies). Note: this is a  
NIH-MGC Library."

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REFERENCE 1 (bases 1 to 1157)  
NIH-MGC http://mgc.ncl.nih.gov/.  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: cgabs-remail.nih.gov  
Tissue Procurement: Dr. James R. Lupski  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
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source

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Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor  
College of Medicine) and is available through Life  
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CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone Distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
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Qy 591 ACTTGGACTCTGCGCTGCGCCAGTGAATCTTCTCAGAGAGTGAAGCACTTCTGCGCTG 650  
Db ACTTGGACTCTGCGCTGCGCCAGTGAATCTTCTCAGAGAGTGAAGCACTTCTGCGCTG 1545

Qy 1486 ACTTGGACTCTGCGCTGCGCCAGTGAATCTTCTCAGAGAGTGAAGCACTTCTGCGCTG 1545  
Db ACTTGGACTCTGCGCTGCGCCAGTGAATCTTCTCAGAGAGTGAAGCACTTCTGCGCTG 1545

Qy 651 CTGAAGAGAGCTGAGACTTGGCTGTGGCTGCGCCAGAGACTTCAACCGGCTCAAGAG 710  
Db CTGAAGAGAGCTGAGACTTGGCTGTGGCTGCGCCAGAGACTTCAACCGGCTCAAGAG 1605

Qy 1546 CTGAAGAGAGCTGAGACTTGGCTGTGGCTGCGCCAGAGACTTCAACCGGCTCAAGAG 1605  
Db CTGAAGAGAGCTGAGACTTGGCTGTGGCTGCGCCAGAGACTTCAACCGGCTCAAGAG 1605

Qy 711 AAGATGAGAGCTTCAAGAGCTGAGTGAAGCTTGGAGGAGCTGAGTGAAGCTTCAAGAG 770  
Db AAGATGAGAGCTTCAAGAGCTGAGTGAAGCTTGGAGGAGCTGAGTGAAGCTTCAAGAG 1665

Qy 1606 AAGATGAGAGCTTCAAGAGCTGAGTGAAGCTTGGAGGAGCTGAGTGAAGCTTCAAGAG 1665  
Db AAGATGAGAGCTTCAAGAGCTGAGTGAAGCTTGGAGGAGCTGAGTGAAGCTTCAAGAG 1665

Qy 771 CTGACCTTCTCC 782  
Db CTGACCTTCTCC 1677

RESULT 14  
AR002596 AR002596 5087 bp DNA linear PAT 04-DEC-1998  
LOCUS Sequence 3 from patent US 5741772.  
DEFINITION  
ACCESSION AR002596  
VERSION AR002596.1 GI:3964150  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

Unclassified.  
REFERENCE 1 (bases 1 to 5087)  
AUTHORS Chang, M.-S.  
TITLE Neurotrophic factor NRT-1  
JOURNAL Patent: US 5741772-A 3 21-APR-1998;  
FEATURES  
source location/Qualifiers  
1..5087  
/organism="unknown"

Query Match 65.7%; Score 523.4; DB 6; Length 5087;  
Best Local Similarity 99.8%; Pred. No. 8.3e-97;  
Matches 524; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 271 ATCTGACTTACTGGGCGCCCTTTTCAAGAGCCAGACTTCAACCTCCCGCTGGGGG 330  
Db ATCTGACTTACTGGGCGCCCTTTTCAAGAGCCAGACTTCAACCTCCCGCTGGGGG 3422

Qy 331 CAGAGACTTGGCCAGAGGCGCACTGTGACTTGGAGGTGTGGAGAGCTCAATGACAAAC 390  
Db CAGAGACTTGGCCAGAGGCGCACTGTGACTTGGAGGTGTGGAGAGCTCAATGACAAAC 3482

Qy 3423 CAGAGACTTGGCCAGAGGCGCACTGTGACTTGGAGGTGTGGAGAGCTCAATGACAAAC 3482  
Db CAGAGACTTGGCCAGAGGCGCACTGTGACTTGGAGGTGTGGAGAGCTCAATGACAAAC 3542

Qy 391 TGGCGCTGACCCAGAGACTGAGGCTTCAAGAGCTTCTGTGTACTTGTGCTGAGCTTCA 450  
Db TGGCGCTGACCCAGAGACTGAGGCTTCAAGAGCTTCTGTGTACTTGTGCTGAGCTTCA 3542

Qy 3483 TGGCGCTGACCCAGAGACTGAGGCTTCAAGAGCTTCTGTGTACTTGTGCTGAGCTTCA 3542  
Db TGGCGCTGACCCAGAGACTGAGGCTTCAAGAGCTTCTGTGTACTTGTGCTGAGCTTCA 3542

Qy 451 ACCGTGAGGCTGCCAGCTGCTGAGCTGCGCGGAGCTTGGCCACTTCTGACACAGCTTCC 510  
Db ACCGTGAGGCTGCCAGCTGCTGAGCTGCGCGGAGCTTGGCCACTTCTGACACAGCTTCC 3602

Qy 3543 ACCGTGAGGCTGCCAGCTGCTGAGCTGCGCGGAGCTTGGCCACTTCTGACACAGCTTCC 3602  
Db ACCGTGAGGCTGCCAGCTGCTGAGCTGCGCGGAGCTTGGCCACTTCTGACACAGCTTCC 3602

Qy 511 AGGGCTGCTGGGAGAGCTTGGGCGGATGAGGAGCTTGGGCGGATGAGGAGCTTGGGCGG 570  
Db AGGGCTGCTGGGAGAGCTTGGGCGGATGAGGAGCTTGGGCGGATGAGGAGCTTGGGCGG 3662

Qy 3603 AGGGCTGCTGGGAGAGCTTGGGCGGATGAGGAGCTTGGGCGGATGAGGAGCTTGGGCGG 3662  
Db AGGGCTGCTGGGAGAGCTTGGGCGGATGAGGAGCTTGGGCGGATGAGGAGCTTGGGCGG 3722

Qy 571 CGTGCCTGAGGACTGAACCACTTGAATCTCTGCGCTTCCAGAGTGAATCTTCTCAGA 630  
Db CGTGCCTGAGGACTGAACCACTTGAATCTCTGCGCTTCCAGAGTGAATCTTCTCAGA 3722

Qy 3663 CGTGCCTGAGGACTGAACCACTTGAATCTCTGCGCTTCCAGAGTGAATCTTCTCAGA 630  
Db CGTGCCTGAGGACTGAACCACTTGAATCTCTGCGCTTCCAGAGTGAATCTTCTCAGA 3722

Qy 631 AGATGAGAGACTTCTGCTGCTGAGAGAGCTGAGAGCTTGGCTGTGGCTGCGCCAGAG 690  
Db AGATGAGAGACTTCTGCTGCTGAGAGAGCTGAGAGCTTGGCTGTGGCTGCGCCAGAG 3782

Qy 3723 AGATGAGAGACTTCTGCTGCTGAGAGAGCTGAGAGCTTGGCTGTGGCTGCGCCAGAG 3782  
Db AGATGAGAGACTTCTGCTGCTGAGAGAGCTGAGAGCTTGGCTGTGGCTGCGCCAGAG 3782

Qy 691 ACTTCAACCGGCTCAAGAGAGAGTGAAGCTTCAAGAGAGTGAAGCTTCAAGAGAGTGAAG 750  
Db ACTTCAACCGGCTCAAGAGAGAGTGAAGCTTCAAGAGAGTGAAGCTTCAAGAGAGTGAAG 3842

Qy 3783 ACTTCAACCGGCTCAAGAGAGAGTGAAGCTTCAAGAGAGTGAAGCTTCAAGAGAGTGAAG 3842  
Db ACTTCAACCGGCTCAAGAGAGAGTGAAGCTTCAAGAGAGTGAAGCTTCAAGAGAGTGAAG 3842

Qy 751 GGGCTCATGAGCTTGAATCTTGAATCTTCTGCTTCCCTTCCCTCC 795  
Db GGGCTCATGAGCTTGAATCTTGAATCTTCTGCTTCCCTTCCCTCC 3887

Qy 3843 GGGCTCATGAGCTTGAATCTTGAATCTTCTGCTTCCCTTCCCTCC 3887  
Db GGGCTCATGAGCTTGAATCTTGAATCTTCTGCTTCCCTTCCCTCC 3887

RESULT 15  
AX392088 AX392088 5087 bp DNA linear PAT 23-MAR-2002  
LOCUS Sequence 3 from Patent W00215977.  
DEFINITION  
ACCESSION AX392088  
VERSION AX392088.1 GI:19700576  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1  
Senaldi, G.  
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
TITLE Methods and compositions for treating ige-related disease using m  
c-1 inhibitors  
JOURNAL Patent: WO 0215977-A 3 28-FEB-2002;  
Amgen Inc. (US)  
FEATURES  
source location/Qualifiers  
1..5087  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"

Db 485 CTTAGCTGGCCCACTTTCTTACCAAGCTTCCAGGAGCTCTGCTGGCAGCATTTGCAAGTGTTC 544  
QY 540 ATGGCAGCTCTGGGCTACCCCACTGCCCCAGCCGCTGCTGGGACTGAACCCACTTGGACT 599  
Db 545 ATGGCAGCTCTGGGCTACCCCACTGCCCCAGCCGCTCTGCTGGGACTGAACCCACTTGGGCC 604  
QY 600 CTTGGGCTCTGGGCTACCCCACTGCCCCAGCCGCTCTGCTGGGACTGAACCCACTTGGGCC 659  
Db 605 CTTGGGCTCTGGGCTACCCCACTGCCCCAGCCGCTCTGCTGGGACTGAACCCACTTGGGCC 664  
QY 660 CTTGGGCTCTGGGCTACCCCACTGCCCCAGCCGCTCTGCTGGGACTGAACCCACTTGGGCC 719  
Db 665 CTTGGGCTCTGGGCTACCCCACTGCCCCAGCCGCTCTGCTGGGACTGAACCCACTTGGGCC 724  
QY 720 CTTGGGCTCTGGGCTACCCCACTGCCCCAGCCGCTCTGCTGGGACTGAACCCACTTGGGCC 778  
Db 725 CTTGGGCTCTGGGCTACCCCACTGCCCCAGCCGCTCTGCTGGGACTGAACCCACTTGGGCC 783

RESULT 12  
AF176913 819 bp mRNA linear ROD 04-OCT-1999  
LOCUS Mus musculus neurotrophin-1/B-cell stimulating factor-3 mRNA,  
DEFINITION complete cds.  
ACCESSION AF176913 GI:6007644  
VERSION AF176913  
KEYWORDS  
SOURCE Mus musculus (house mouse)  
ORGANISM  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 819)  
AUTHORS Senaldi, G., Varnum, B.C., Sarmiento, U., Lile, J., Starnes, C.,  
Scully, S., Guo, J., Elliott, G., McNinch, J., Freeman, D., Shakkie, C.L.,  
Freeman, D., Mann, F., Simmet, W.S., Boone, T. and Chang, M.S.  
TITLE Novel neurotrophin-1/B cell-stimulating factor-3: a cytokine of the  
IL-6 family  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (20), 11458-11463 (1999)  
MEDLINE 99432254  
PUBMED 10500198

REFERENCE 2 (bases 1 to 819)  
AUTHORS Senaldi, G., Varnum, B., Sarmiento, U., Lile, J., Starnes, C.,  
Scully, S., Guo, J., Elliott, G., McNinch, J., Freeman, D., Shakkie, C.,  
Mann, F., Simmet, W.S., Boone, T. and Chang, M.S.  
TITLE Direct Substitution  
JOURNAL Submitted (11-AUG-1999) Amgen, Inc., One Amgen Center Drive,  
Thousand Oaks, CA 91320, USA  
FEATURES  
source  
1. 819  
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CDS  
156 a 288 c 218 g 157 t

BASE COUNT 156 a 288 c 218 g 157 t  
ORIGIN  
Query Match 84.0%; Score 669.4; DB 10; Length 819;  
Best Local Similarity 92.0%; Pred. No. 1.8e-126;  
Matches 717; Conservative 0; Mismatches 61; Indels 1; Gaps 1;

QY 1 ATTTAAAGCTTGGCGGAGCGGCTGGCTCTGCTGGGACTGAACCCACTTGGGCC 60  
Db 5 ATTTAAAGCTTGGCGGAGCGGCTGGCTCTGCTGGGACTGAACCCACTTGGGCC 64

QY 61 CCGCAGCCGCGCGGCCAG-CCCGACGCCCATGAGCTTCGAGCAGAGGAGCTGTGGGG 119  
Db 65 CCGCAGCCGCGCGGCCAG-CCCGACGCCCATGAGCTTCGAGCAGAGGAGCTGTGGGG 124  
QY 120 ATTTAGCGTGGCTGTGACAGGTGTCTGTGGACCTTCCCTGCAATGCTCAATTCG 179  
Db 125 ATTTAGCGTGGCTGTGACAGGTGTCTGTGGACCTTCCCTGCAATGCTCAATTCG 184  
QY 180 ACAGGAGACCCAGAGGCGTGGCCCTTCATTCAGAAAACCTATGACTCAACCCGCTACCT 239  
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QY 240 GAGCAGCACTCCGAGCTTGTGGAGCTTATGAACTACCTGGGCCCCCTTTCAAC 299  
Db 245 GAGCAGCACTCCGAGCTTGTGGAGCTTATGAACTACCTGGGCCCCCTTTCAAC 304  
QY 300 GAGCAGCACTTCAACCTTCCCGCTGTGGGGGAGAGACTGTGCCAGGGGCACTGTTCAC 359  
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QY 420 AGCCAGCTTCTGTGTACTTGTGGGCTCAACCGTCAAGGCTGCTGAGCTGAGTGGCC 479  
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QY 480 CCGAGCTGGGCCAATCTTGTGACACAGGCTTCAGAGGCTGTGCTGGGAGCATTTGGGGGCTTC 539  
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QY 540 ATGGCAGCTCTGGGCTACCCCACTGCCCCAGCCGCTGCTGGGACTGAACCCACTTGGACT 599  
Db 545 ATGGCAGCTCTGGGCTACCCCACTGCCCCAGCCGCTGCTGGGACTGAACCCACTTGGACT 604  
QY 600 CTTGGGCTCTGGGCTACCCCACTGCCCCAGCCGCTCTGCTGGGACTGAACCCACTTGGGCC 659  
Db 605 CTTGGGCTCTGGGCTACCCCACTGCCCCAGCCGCTCTGCTGGGACTGAACCCACTTGGGCC 664  
QY 660 CTTGGGCTCTGGGCTACCCCACTGCCCCAGCCGCTCTGCTGGGACTGAACCCACTTGGGCC 719  
Db 665 CTTGGGCTCTGGGCTACCCCACTGCCCCAGCCGCTCTGCTGGGACTGAACCCACTTGGGCC 724  
QY 720 CTTGGGCTCTGGGCTACCCCACTGCCCCAGCCGCTCTGCTGGGACTGAACCCACTTGGGCC 778  
Db 725 CTTGGGCTCTGGGCTACCCCACTGCCCCAGCCGCTCTGCTGGGACTGAACCCACTTGGGCC 783

RESULT 13  
AX205060 1692 bp DNA linear PAT 30-AUG-2001  
LOCUS Sequence 19 from Patent WO0155219.  
DEFINITION AX205060  
ACCESSION AX205060  
VERSION AX205060.1 GI:15394299  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Elson, G. and Gauchat, J.F.  
TITLE Scentfr/mt-1 fusion protein  
JOURNAL Patent: WO 0155219-A 19 02-AUG-2001;  
PIERRE FABRE MEDICAMENT (FR)  
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SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 819)  
TITLE Chang, M.-B.  
JOURNAL Neurotrophic factor NNT-1  
Patent: US 5741772-A 4 21-APR-1998;  
FEATURES Location/Qualifiers  
source 1..819  
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BASE COUNT 156 a 288 c 218 g 157 t  
ORIGIN

Query Match 84.0%; Score 669.4; DB 6; Length 819;  
Best Local Similarity 92.0%; Pred. No. 1.8e-126;  
Matches 717; Conservative 0; Mismatches 61; Indels 1; Gaps 1;

QY 1 ATTTAAAGCTTGGCCGGAGCGCGGCTCGCCCTCCCACTCCGCGAGAGAGAG 60  
DB 5 ATTTAAAGCTTGGCCGGAGCGCGGCTCGCCCTCCCACTCCGCGAGAGAGAG 64  
QY 61 CCGCAACCGCGCGCGCGCGAG-CCCGAGCCCGCATGAGACCTCCGAGAGAGAGAG 119  
DB 65 CCGCGCCG 124  
QY 120 ATGTTAGCGTGGCTGTGCAAGGCTGTGCGACCTCCGCGAGTGCAGCTCTCAATCGC 179  
DB 125 ATGTTAGCTTGGCTGTGCAAGGCTGTGCGACCTCCGCGAGTGCAGCTCTCAATCGC 184  
QY 180 ACAGGAGACCGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 239  
DB 185 ACAGGAGATCCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 244  
QY 240 GAGCAACCACTCGGAGCTTGGCTGGAGCTTATGAACTACTGGGCGCGCGCGCGCG 299  
DB 245 GAGCAATCACTCGGAGCTTGGAGCTTACTGAACTACTGGGCGCGCGCGCGCGCG 304  
QY 300 GAGCGAGATTTCAACCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 359  
DB 305 GAGCGTGAATTTCAATCTCTCTGCACTGGGGGCGAGAACTCTGCCAGGCGCGCG 364  
QY 360 TTGGAAGTGTGGCGAAGCTCTCAATGACAACTGGCGCTGAGCCGAGAACTAGAGCGCTAC 419  
DB 365 TTGGAAGTGTGGCGAAGCTCTCAATGACAACTGGCGCTGAGCCGAGAACTAGAGCGCTAC 424  
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DB 425 AGTCACTCTGTGTGTTACTTGTGGTGGCTCAACCGTCAAGGCTGCGCACTGAGCTGGCG 484  
QY 480 CGCAGCTGGCG 539  
DB 485 CGTACCTGGCG 544  
QY 540 ATGGAGCTGTGGGCTACCCACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 599  
DB 545 ATGGAGAGCTTGGCTACCCACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 604  
QY 600 CCG 659  
DB 605 CCG 664  
QY 660 CTGCAAGCTTGGCTGTGGCGCTCGGCGAGAGACTTCAACCGGCTCAAGAGAGATGCGAG 719  
DB 665 CTGCAAGCTTGGCTGTGGCGCTCGGCGAGAGACTTCAACCGGCTTAAAGAGAGATGCGAG 724  
QY 720 CTTCAAGAGCTGTGAGTCAACCTTCAAGCTTGGGCGCTCATGCTTGTGACTTGTGACTT 778  
DB 725 CTTCAAGAGCTGTGAGTCAACCTTCAAGCTTGGGCGCTCATGCTTGTGACTTGTGACTT 783

RESULT 11  
AX392089  
LOCUS AX392089 819 bp DNA linear PAT 23-MAR-2002

DEFINITION Sequence 4 from Patent WO0215977.  
ACCESSION AX392089  
VERSION AX392089.1 GI:19700577  
KEYWORDS  
SOURCE  
ORGANISM Mus sp.  
REFERENCE 1  
AUTHORS Senaldi, G.  
TITLE Methods and compositions for treating ige-related disease using nm  
JOURNAL t-1 inhibitors  
Patent: WO 0215977-A 4 28-FEB-2002;  
FEATURES Amgen Inc. (US)  
source 1..819  
Location/Qualifiers  
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sig\_peptide 95..175  
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BASE COUNT 156 a 288 c 218 g 157 t  
ORIGIN

Query Match 84.0%; Score 669.4; DB 6; Length 819;  
Best Local Similarity 92.0%; Pred. No. 1.8e-126;  
Matches 717; Conservative 0; Mismatches 61; Indels 1; Gaps 1;

QY 1 ATTTAAAGCTTGGCCGGAGCGCGGCTCGCCCTCCCACTCCGCGAGAGAGAG 60  
DB 5 ATTTAAAGCTTGGCCGGAGCGCGGCTCGCCCTCCCACTCCGCGAGAGAGAG 64  
QY 61 CCGCAACCGCGCGCGCGCGAG-CCCGAGCCCGCATGAGACCTCCGAGAGAGAGAG 119  
DB 65 CCGCGCCG 124  
QY 120 ATGTTAGCGTGGCTGTGCAAGGCTGTGCGACCTCCGCGAGTGCAGCTCTCAATCGC 179  
DB 125 ATGTTAGCTTGGCTGTGCAAGGCTGTGCGACCTCCGCGAGTGCAGCTCTCAATCGC 184  
QY 180 ACAGGAGACCGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 239  
DB 185 ACAGGAGATCCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 244  
QY 240 GAGCAACCACTCGGAGCTTGGAGCTTATGAACTACTGGGCGCGCGCGCGCGCG 299  
DB 245 GAGCAATCACTCGGAGCTTGGAGCTTACTGAACTACTGGGCGCGCGCGCGCGCG 304  
QY 300 GAGCGAGATTTCAACCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 359  
DB 305 GAGCGTGAATTTCAATCTCTCTGCACTGGGGGCGAGAACTCTGCCAGGCGCGCG 364  
QY 360 TTGGAAGTGTGGCGAAGCTCTCAATGACAACTGGCGCTGAGCCGAGAACTAGAGCGCTAC 419  
DB 365 TTGGAAGTGTGGCGAAGCTCTCAATGACAACTGGCGCTGAGCCGAGAACTAGAGCGCTAC 424  
QY 420 AGCCACTTCTGTGTTACTTGTGGTGGCTCAACCGTCAAGGCTGCGCACTGAGCTGGCG 479  
DB 425 AGTCACTCTGTGTGTTACTTGTGGTGGCTCAACCGTCAAGGCTGCGCACTGAGCTGGCG 484  
QY 480 CGCAGCTGGCG 539

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Db      61 GGGGAACTCTGGGGGATGTTAGCGTCTGTGTGACAGGAGCTGTGAGCACTCCCTGAGTGTG 120
QY      165 CCAGCTCTCAATGCAACAGAGGAGCCAGAGGCTGTGCTCCATCCAGAAAACCTATGAC 224
Db      121 CCAAGCTCTCAATGCAACAGAGGAGCCAGAGGCTGTGCTCCATCCAGAAAACCTATGAC 180
QY      225 CTCACCCGCTACCTGTGAGAGCAACCAACTCCGAGCTGTGCTGAGGAGCTATCTGAACCTAC 284
Db      181 CTCACCCGCTACCTGTGAGAGCAACCAACTCCGAGCTGTGCTGAGGAGCTATCTGAACCTAC 240
QY      285 GGGGCCCCCTTTCAAGAGGAGCACTTCAACCTCCGCTGTGAGGAGGAGAGAGCTGTGAGG 344
Db      241 GGGGCCCCCTTTCAAGAGGAGCACTTCAACCTCCGCTGTGAGGAGGAGAGAGCTGTGAGG 300
QY      345 AGGGGCACTGTGACTTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 404
Db      301 AGGGGCACTGTGACTTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
QY      405 AACTAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 464
Db      361 AACTAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
QY      465 AACTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 524
Db      421 AACTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
QY      525 AGCATTTGCGGGGAGTCAATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 584
Db      481 AGCATTTGCGGGGAGTCAATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540
QY      585 GAACCCACTTGTGACTCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 644
Db      541 GAACCCACTTGTGACTCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 600
QY      645 TGGCTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 704
Db      601 TGGCTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
QY      705 AAGAAGAGATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 764
Db      661 AAGAAGAGATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
QY      765 TGAATTTCTGACCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 795
Db      721 TGAATTTCTGACCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 751

RESULT 9
AY049779      680 bp      mRNA      linear      PRI 23-OCT-2001
LOCUS      Homo sapiens cardiotrophin-like cytokine (CLC) mRNA, complete cds.
DEFINITION      AY049779
ACCESSION      AY049779.1 GI:16356642
VERSION      AY049779.1
KEYWORDS      Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 680)
AUTHORS      Hu,X., Xu,Y., Zhang,B., Peng,X., Yuan,J. and Qiang,B.
TITLE      Direct Submission
JOURNAL      Submitted (30-JUL-2001) Department of Biochemistry, Institute of
Basic Medical Science, Chinese Academy of Medical Sciences, 5 Dong
Dan San Tiao, Beijing 100005, P.R. China
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BASE COUNT      125 a      239 c      191 g      125 t
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61 GGCACCTCCGAGCAAGGAGGAGCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120
208 TCCAGAAAACCTATGAGCTCAACCCGCTACCTGAGAGCAACCACTCCGAGCTTGAGCTGAGGA 267
121 TCCAGAAAACCTATGAGCTCAACCCGCTACCTGAGAGCAACCACTCCGAGCTTGAGCTGAGGA 180
268 CCTATCTGAACTACTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 327
181 CCTATCTGAACTACTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240
328 GGGGAGAGACTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 387
241 GGGGAGAGACTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
388 AACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 447
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LOCUS      Sequence 4 from patent US 5741772.
DEFINITION      AR002597
ACCESSION      AR002597
VERSION      AR002597.1 GI:3964151
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RESULT 6
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LOCUS Homo sapiens, Similar to cardiotrophin-like cytokine;
DEFINITION neurotrophin-1/B-cell stimulating factor-3, clone MGC:21195
IMAGE:4453813, mRNA, complete cds.
ACCESSION BC012939
VERSION BC012939.1 GI:15277894
KEYWORDS MGC
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 1736)
Strausberg, R.
Direct Submission
Submitted (20-AUG-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgabbs@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: villalobos@bcm.tmc.edu.
Villalobos, D.K., Luna, R.A., Hale, S.M., Huliyil, S., Lu, X., Garcia,
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Query Match 99.5%; Score 793.4; DB 6; Length 881;  
Best Local Similarity 99.9%; Pred. No. 9.2e-152;  
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VERSION AX205042.1 GI:15394277  
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ORGANISM Homo sapiens  
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REFERENCE  
1 Elson, G. and Gauchat, J.F.  
Scentifer/nnt-1 fusion protein  
Patent: WO 0155219-A 1 02-AUG-2001;  
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Query Match 99.5%; Score 793.4; DB 6; Length 881;  
Best Local Similarity 99.9%; Pred. No. 9.2e-152;  
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DEFINITION complete cds.  
ACCESSION AF176911  
VERSION AF176911.1 GI:6007640  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 797)  
AUTHORS Senaldi, G., Varnum, B. C., Sarmiento, U., Lile, J., Starnes, C.,  
Scully, S., Guo, J., Elliott, G., McNinch, J., Freeman, D.,  
Freeman, D., Manu, F., Simonet, W. S., Boone, T. and Chang, M. S.  
TITLE Novel neurotrophin-1/B-cell stimulating factor-3: a cytokine of the  
Trk family  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (20), 11458-11463 (1999)  
MEDLINE 99432254  
PUBMED 10500198  
REFERENCE 2 (bases 1 to 797)  
AUTHORS Senaldi, G., Varnum, B., Sarmiento, U., Lile, J., Starnes, C.,  
Scully, S., Guo, J., Elliott, G., McNinch, J., Freeman, D.,  
Manu, F., Simonet, W. S., Boone, T. and Chang, M. S.  
TITLE Direct Submission  
JOURNAL Submitted (11-AUG-1999) Amgen, Inc., One Amgen Center Drive,  
Thousand Oaks, CA 91320 USA  
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DEFINITION AX205024  
ACCESSION AX205024  
VERSION AX205024.1 GI:15394259  
KEYWORDS  
SOURCE Homo sapiens  
ORGANISM Homo sapiens (human)  
REFERENCE 1  
AUTHORS Elson, G., Gauthier, J. F., Plun-Pavreau, H., Chevalier, S. and Gascan, H.  
TITLE Isolated complex comprising a ntc-1 protein and in addition at  
least a c1f-1 protein and/or a scntf\_g1(a) protein  
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ACCESSION AX392086  
VERSION AX392086.1 GI:19700574  
KEYWORDS

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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REFERENCE 1  
AUTHORS Senaldi, G.  
TITLE Method and compositions for treating age-related disease using m  
t-1 inhibitors  
JOURNAL Patent: WO 0215977-A 1 28-FEB-2002;  
Amgen Inc. (US)  
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BASE COUNT 139 a 297 c 218 g 143 t  
ORIGIN

Query Match 100.0%; Score 797; DB 6; Length 797;  
Best Local Similarity 100.0%; Pred. No. 1.7e-152;  
Matches 797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATTTAAAGCTTCCCGGAGCGCGCTGCGCTTCCCACTCCGCGAGCTTCGGGAGAGAG 60  
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QY 61 CCGGACCCGGGCGGCG 120  
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: February 9, 2004, 06:10:21 ; Search time 3198.36 Seconds

(without alignments)  
10194.288 Million cell updates/sec

Title: US-09-931-704-1

Perfect score: 797  
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Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenBank  
1: gb\_ba:\*  
2: gb\_hcg:\*  
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40: em\_hcg\_mus:\*  
41: em\_hcg\_other:\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	797	100.0	797	6	AR002595
2	797	100.0	797	6	AX392086
3	797	100.0	797	6	AF176911
4	793.4	99.5	881	6	AX205024
5	793.4	99.5	881	6	AX205042
6	776.4	97.4	1736	9	BC012939
7	749.4	94.0	1589	9	AF172854
8	749.4	94.0	1710	6	BD132824
9	680	85.3	680	9	AY049779
10	669.4	84.0	819	6	AR002597
11	669.4	84.0	819	6	AX392089
12	669.4	84.0	819	10	AF176913
13	594.4	74.6	1692	6	AX205060
14	523.4	65.7	5087	6	AR002586
15	523.4	65.7	5087	6	AX392088
16	523.4	65.7	5087	6	AF176912
17	523.4	65.7	135116	2	AP002437
18	523.4	65.7	168567	9	AP003419
19	521.4	65.5	169144	2	AC005849
20	429.6	53.9	269155	10	AC109138
21	429.6	53.9	302961	2	AC140073
22	415.2	52.1	258710	2	AC135823
23	269.4	33.8	283	6	AX202145
24	86.4	10.8	63347	2	AC110526
25	80.2	10.1	396	6	BD132825
26	68.6	8.6	230732	2	BX510356
27	65	8.2	169873	2	BX324116
28	59.4	7.5	125020	9	AF429315
29	57.8	7.3	125020	9	AF429315
30	47.6	6.0	648	5	AF181480
31	47.6	6.0	648	5	AF181481
32	46.4	5.8	149120	2	AP005536
33	46.4	5.8	167672	2	AC132806
34	46.4	5.8	177719	9	AC135048
35	46.4	5.8	187727	2	AC021142
36	46.4	5.8	202414	2	AC135051
37	46.2	5.8	97826	9	AL591647
38	46.2	5.8	173609	9	AL451077
39	45.8	5.7	1901	5	AF181482
40	45.6	5.7	1107	6	BD180326
41	44.8	5.6	2265	9	BC009360
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## ALIGNMENTS

RESULT 1  
LOCUS AR002595  
DEFINITION Sequence 1 from patent US 5741772.  
ACCESSION AR002595  
VERSION AR002595.1 GI:3964149  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 797)  
AUTHORS Chang, M.-S.  
TITLE Neurotrophic factor NNT-1  
JOURNAL Patent US 5741772-A 1 21-APR-1998;  
FEATURES location/contigs